

SEQUENCE LISTING



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TECH CENTER 1600/2800

09/603,124

<110> Pompejus, Markus
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<120> CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
INVOLVED IN HOMEOSTASIS AND ADAPTATION

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Val Thr Thr Pro His
1 5
ttg gat tct gca caa gat att gat ctg tcc cgc gtc cac ctc atc ggt 163
Leu Asp Ser Ala Gln Asp Ile Asp Leu Ser Arg Val His Leu Ile Gly
10 15 20
att ggc gga gcc gga atg tct ggc gtt gcc cga atc ctg ctt gcc cgc 211
Ile Gly Gly Ala Gly Met Ser Gly Val Ala Arg Ile Leu Leu Ala Arg
25 30 35
ggt aag aca gtc act ggt tcc gat gcc aaa gat tcc cgc acc ttg ctt 259
Gly Lys Thr Val Thr Gly Ser Asp Ala Lys Asp Ser Arg Thr Leu Leu
40 45 50
cca ctc cgc gcc gtg gga gcc acc atc gca gtg gga cac gct gcg gaa 307
Pro Leu Arg Ala Val Gly Ala Thr Ile Ala Val Gly His Ala Ala Glu
55 60 65
aac ctt gag ctt tcc ggc gaa ctt ccc acc gtc gtg gtg acc tct ttt 355
Asn Leu Glu Leu Ser Gly Glu Leu Pro Thr Val Val Val Thr Ser Phe
70 75 80 85
gcc gcc att ccg caa gac aac ccg gaa ctt gtt cgt gca cgt gaa gaa 403

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Gly	Ser	Thr	Gln	Val	Leu	Ile	Ala	Gly	Thr	His	Gly	Lys	Thr	Ser	Thr		
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acc	tct	atg	tct	gtg	gta	gct	atg	cag	gca	gcg	ggc	atg	gat	cca	agc	547	
Thr	Ser	Met	Ser	Val	Val	Ala	Met	Gln	Ala	Ala	Gly	Met	Asp	Pro	Ser		
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Phe	Ala	Ile	Gly	Gly	Gln	Leu	Asn	Lys	Ala	Gly	Thr	Asn	Ala	His	His		
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Leu	Leu	Arg	Tyr	Lys	Phe	Asn	Val	Ala	Val	Val	Thr	Asn	Val	Glu	Pro		
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gac	cac	ctg	gac	ttc	ttt	aaa	acc	cct	gaa	gcc	tac	ttc	caa	gtg	ttc	739	
Asp	His	Leu	Asp	Phe	Phe	Lys	Thr	Pro	Glu	Ala	Tyr	Phe	Gln	Val	Phe		
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Asp	Asp	Phe	Ala	Gly	Arg	Ile	Thr	Pro	Asn	Gly	Lys	Leu	Val	Val	Cys		
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Leu	Asn	Asp	Pro	His	Ala	Ala	Glu	Leu	Gly	Glu	Arg	Ser	Val	Arg	Lys		
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Gly	Ile	Lys	Thr	Val	Gly	Tyr	Gly	Thr	Ala	Asp	Ala	Val	Gln	Ala	His		
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cct	gag	gtt	cca	gcg	atg	gct	acc	atc	gtg	gat	tcc	caa	gtt	gtc	gca	931	
Pro	Glu	Val	Pro	Ala	Met	Ala	Thr	Ile	Val	Asp	Ser	Gln	Val	Val	Ala		
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Glu	Gly	Thr	Arg	Ala	Thr	Ile	Asn	Ile	Asp	Gly	Gln	Glu	Val	Ser	Val		
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att	ctt	caa	atc	cct	ggg	gat	cac	atg	gta	ctc	aac	ggg	gca	gcc	gcc	1027	
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ctg	ctg	gcc	gga	tac	ctg	gtg	ggg	ggg	gac	gtc	gac	aag	ctt	gtt	gaa	1075	
Leu	Leu	Ala	Gly	Tyr	Leu	Val	Gly	Gly	Asp	Val	Asp	Lys	Leu	Val	Glu		
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Gly	Leu	Ser	Asp	Phe	Ser	Gly	Val	Arg	Arg	Arg	Phe	Glu	Phe	His	Gly		

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	Ala Ile Glu Gly Gly Lys Phe Asn Gly Ala Ala Ile Tyr Asp Asp Tyr		Ala Ala Ile Tyr Asp Asp Tyr			
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	gca cac cac cca acg gaa gta act gca gtg ctc agc gct gcg cgc acc		gca gtg ctc agc gct gcg cgc acc			1219
	Ala His His Pro Thr Glu Val Thr Ala Val Leu Ser Ala Ala Arg Thr		Ala Val Leu Ser Ala Ala Arg Thr			
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	Arg Val Lys Ala Ala Gly Lys Gly Arg Val Ile Val Ala Phe Gln Pro		Arg Val Ile Val Ala Phe Gln Pro			
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	cat tta tac tca cgc acc ata gaa ttc caa aag gag ttc gcg ggg gca		caa aag gag ttc gcg ggg gca			1315
	His Leu Tyr Ser Arg Thr Ile Glu Phe Gln Lys Glu Phe Ala Gly Ala		Gln Lys Glu Phe Ala Gly Ala			
		390	395		400	405
	ctg tca ctg gca gac gct gcc gtg gtg ctt gag att tac gga gcg cgc		gtg gtg ctt gag att tac gga gcg cgc			1363
	Leu Ser Leu Ala Asp Ala Ala Val Val Leu Glu Ile Tyr Gly Ala Arg		Val Val Leu Glu Ile Tyr Gly Ala Arg			
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	Glu Gln Pro Val Asp Gly Val Ser Ser Glu Ile Ile Thr Asp Ala Met		Glu Ile Ile Thr Asp Ala Met			
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	Thr Ile Pro Val Val Tyr Glu Pro Asn Phe Ser Ala Val Pro Glu Arg		Pro Asn Phe Ser Ala Val Pro Glu Arg			
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	Ile Ala Glu Ile Ala Gly Pro Asn Asp Ile Val Leu Thr Met Gly Ala		Asp Ile Val Leu Thr Met Gly Ala			
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	Gly Ser Val Thr Met Leu Ala Pro Glu Ile Leu Asp Gln Leu Gln Asn		Pro Glu Ile Leu Asp Gln Leu Gln Asn			
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<212> PRT

<213> Corynebacterium glutamicum

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 Val Val Thr Ser Phe Ala Ala Ile Pro Gln Asp Asn Pro Glu Leu Val
 85 90 95
 Arg Ala Arg Glu Glu Gly Ile Pro Val Ile Arg Arg Ser Asp Leu Leu
 100 105 110
 Gly Glu Leu Leu Glu Gly Ser Thr Gln Val Leu Ile Ala Gly Thr His
 115 120 125
 Gly Lys Thr Ser Thr Thr Ser Met Ser Val Val Ala Met Gln Ala Ala
 130 135 140
 Gly Met Asp Pro Ser Phe Ala Ile Gly Gly Gln Leu Asn Lys Ala Gly
 145 150 155 160
 Thr Asn Ala His His Gly Thr Gly Glu Val Phe Ile Ala Glu Ala Asp
 165 170 175
 Glu Ser Asp Ala Ser Leu Leu Arg Tyr Lys Pro Asn Val Ala Val Val
 180 185 190
 Thr Asn Val Glu Pro Asp His Leu Asp Phe Phe Lys Thr Pro Glu Ala
 195 200 205
 Tyr Phe Gln Val Phe Asp Asp Phe Ala Gly Arg Ile Thr Pro Asn Gly
 210 215 220
 Lys Leu Val Val Cys Leu Asn Asp Pro His Ala Ala Glu Leu Gly Glu
 225 230 235 240
 Arg Ser Val Arg Lys Gly Ile Lys Thr Val Gly Tyr Gly Thr Ala Asp
 245 250 255
 Ala Val Gln Ala His Pro Glu Val Pro Ala Met Ala Thr Ile Val Asp
 260 265 270
 Ser Gln Val Val Ala Glu Gly Thr Arg Ala Thr Ile Asn Ile Asp Gly
 275 280 285
 Gln Glu Val Ser Val Ile Leu Gln Ile Pro Gly Asp His Met Val Leu
 290 295 300
 Asn Gly Ala Ala Ala Leu Leu Ala Gly Tyr Leu Val Gly Gly Asp Val
 305 310 315 320
 Asp Lys Leu Val Glu Gly Leu Ser Asp Phe Ser Gly Val Arg Arg Arg
 325 330 335
 Phe Glu Phe His Gly Ala Ile Glu Gly Gly Lys Phe Asn Gly Ala Ala
 340 345 350
 Ile Tyr Asp Asp Tyr Ala His His Pro Thr Glu Val Thr Ala Val Leu
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 Ser Ala Ala Arg Thr Arg Val Lys Ala Ala Gly Lys Gly Arg Val Ile
 370 375 380
 Val Ala Phe Gln Pro His Leu Tyr Ser Arg Thr Ile Glu Phe Gln Lys

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385          390          395          400
Glu Phe Ala Gly Ala Leu Ser Leu Ala Asp Ala Ala Val Val Leu Glu
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Ile Tyr Gly Ala Arg Glu Gln Pro Val Asp Gly Val Ser Ser Glu Ile
          420          425          430
Ile Thr Asp Ala Met Thr Ile Pro Val Val Tyr Glu Pro Asn Phe Ser
          435          440          445
Ala Val Pro Glu Arg Ile Ala Glu Ile Ala Gly Pro Asn Asp Ile Val
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Leu Thr Met Gly Ala Gly Ser Val Thr Met Leu Ala Pro Glu Ile Leu
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Asp Gln Leu Gln Asn Asn
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cat tta cct cag gcg ctg cag ggc cgt att ctt gtg gcc ggc gct ggt 163
His Leu Pro Gln Ala Leu Gln Gly Arg Ile Leu Val Ala Gly Ala Gly
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gtt tcc ggc ctg tcc att gca aag atg ctc agt gag ttg cat tgc gat 211
Val Ser Gly Leu Ser Ile Ala Lys Met Leu Ser Glu Leu His Cys Asp
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gtt gtg gtc gcc gac gat aac gaa act gca cgt cac atg ctc att gaa 259
Val Val Val Ala Asp Asp Asn Glu Thr Ala Arg His Met Leu Ile Glu
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Val Val Asp Val Ala Asp Ile Ser Thr Ala Gln Ala Gln Glu Gln Leu
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cat acg tgg ctc gca gtc acc ggc acc aac ggt aaa acc acc acc aca	499
His Thr Trp Leu Ala Val Thr Gly Thr Asn Gly Lys Thr Thr Thr Thr	
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tca atg ctc gcc gcg atg atg aat gag ggc ggt ttt act gcc aag gca	547
Ser Met Leu Ala Ala Met Met Asn Glu Gly Gly Phe Thr Ala Lys Ala	
135 140 145	
gtg ggc aat atc ggc atc ccg gtg tct gag gct ttg gta gcg aaa aac	595
Val Gly Asn Ile Gly Ile Pro Val Ser Glu Ala Leu Val Ala Lys Asn	
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Arg Ile Asp Val Leu Val Ala Glu Leu Ser Ser Phe Gln Leu His Trp	
170 175 180	
tct cca acc ttc acc cct gat gct ggc gtg gtg ctc aac ttg gct gag	691
Ser Pro Thr Phe Thr Pro Asp Ala Gly Val Val Leu Asn Leu Ala Glu	
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Asp His Ile Asp Trp His Gly Ser Met Arg Asp Tyr Ala Leu Ala Lys	
200 205 210	
atg gaa gtg ctc aag ggc aag gtc gcc atc att ggg gca gac gat cct	787
Met Glu Val Leu Lys Gly Lys Val Ala Ile Ile Gly Ala Asp Asp Pro	
215 220 225	
tat ttg gtg cag ctg act tct gaa gca gac ttg agt ggt ctc att gga	835
Tyr Leu Val Gln Leu Thr Ser Glu Ala Asp Leu Ser Gly Leu Ile Gly	
230 235 240 245	
ttt acc gtc aat gag cct gca acc ggc cag ttg ggt gtg aaa gcg ggg	883
Phe Thr Val Asn Glu Pro Ala Thr Gly Gln Leu Gly Val Lys Ala Gly	
250 255 260	
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Glu Leu Val Asp Asn Ala Tyr Gly Asn Asn Val Val Leu Ala Ser Ala	
265 270 275	
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Asp Gly Ile Asn Pro Ala Gly Pro Ala Gly Val Leu Asp Ala Leu Ala	
280 285 290	
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Ala Ala Ala Val Ala Arg Ser Gln Gly Val Ala Pro Glu Ala Ile Ala	
295 300 305	
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Arg Ala Leu Asp Ser Phe Glu Val Ala Gly His Arg Gly Gln Val Val	
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gcc gag cat gac ggt gtt cat ttc att gac aac tcc aag gcg acc aac	1123
Ala Glu His Asp Gly Val His Phe Ile Asp Asn Ser Lys Ala Thr Asn	
330 335 340	

ccc cac gct gct gat tct gcg cta gct ggg cat gat tca gtc att tgg 1171
 Pro His Ala Ala Asp Ser Ala Leu Ala Gly His Asp Ser Val Ile Trp
 345 350 355

 gtt gtc ggc gga cag ctc aaa ggc gcg gac att gcg cca ctg gtg aaa 1219
 Val Val Gly Gly Gln Leu Lys Gly Ala Asp Ile Ala Pro Leu Val Lys
 360 365 370

 aag cac gaa cag cgc atc aag gca gca ttg gtg ttg ggc gca gat cgt 1267
 Lys His Glu Gln Arg Ile Lys Ala Ala Leu Val Leu Gly Ala Asp Arg
 375 380 385

 gct gaa atc gtg gca gcg ttg aag gaa cac gcg tcg cag gcc tct gta 1315
 Ala Glu Ile Val Ala Ala Leu Lys Glu His Ala Ser Gln Ala Ser Val
 390 395 400 405

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 Phe Val Thr Asp Lys Thr Glu Pro Phe Glu Ala Met Glu Glu Ile Val
 410 415 420

 act gag gca ttt agc atc agc gaa ccc ggc gat acc gtg ttg ctt gcc 1411
 Thr Glu Ala Phe Ser Ile Ser Glu Pro Gly Asp Thr Val Leu Leu Ala
 425 430 435

 cct gcc gct gcg tct ttg gac atg ttc aaa ggc atg ggc cag cgt ggc 1459
 Pro Ala Ala Ala Ser Leu Asp Met Phe Lys Gly Met Gly Gln Arg Gly
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 Glu Lys Gly
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<210> 4

<211> 472

<212> PRT

<213> Corynebacterium glutamicum

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 35 40 45

 His Met Leu Ile Glu Val Val Asp Val Ala Asp Ile Ser Thr Ala Gln
 50 55 60

 Ala Gln Glu Gln Leu Asp Ser Phe Ser Ile Val Val Thr Ser Pro Gly
 65 70 75 80

 Trp Arg Pro Thr Ser Thr Leu Leu Val Asp Ala His Arg Gln Gly Leu
 85 90 95

Glu Val Ile Gly Asp Val Glu Leu Ala Trp Arg Leu Asp Gln Ala Gly
 100 105 110
 Val Phe Gly Glu Pro His Thr Trp Leu Ala Val Thr Gly Thr Asn Gly
 115 120 125
 Lys Thr Thr Thr Thr Ser Met Leu Ala Ala Met Met Asn Glu Gly Gly
 130 135 140
 Phe Thr Ala Lys Ala Val Gly Asn Ile Gly Ile Pro Val Ser Glu Ala
 145 150 155 160
 Leu Val Ala Lys Asn Arg Ile Asp Val Leu Val Ala Glu Leu Ser Ser
 165 170 175
 Phe Gln Leu His Trp Ser Pro Thr Phe Thr Pro Asp Ala Gly Val Val
 180 185 190
 Leu Asn Leu Ala Glu Asp His Ile Asp Trp His Gly Ser Met Arg Asp
 195 200 205
 Tyr Ala Leu Ala Lys Met Glu Val Leu Lys Gly Lys Val Ala Ile Ile
 210 215 220
 Gly Ala Asp Asp Pro Tyr Leu Val Gln Leu Thr Ser Glu Ala Asp Leu
 225 230 235 240
 Ser Gly Leu Ile Gly Phe Thr Val Asn Glu Pro Ala Thr Gly Gln Leu
 245 250 255
 Gly Val Lys Ala Gly Glu Leu Val Asp Asn Ala Tyr Gly Asn Asn Val
 260 265 270
 Val Leu Ala Ser Ala Asp Gly Ile Asn Pro Ala Gly Pro Ala Gly Val
 275 280 285
 Leu Asp Ala Leu Ala Ala Ala Val Ala Arg Ser Gln Gly Val Ala
 290 295 300
 Pro Glu Ala Ile Ala Arg Ala Leu Asp Ser Phe Glu Val Ala Gly His
 305 310 315 320
 Arg Gly Gln Val Val Ala Glu His Asp Gly Val His Phe Ile Asp Asn
 325 330 335
 Ser Lys Ala Thr Asn Pro His Ala Ala Asp Ser Ala Leu Ala Gly His
 340 345 350
 Asp Ser Val Ile Trp Val Val Gly Gly Gln Leu Lys Gly Ala Asp Ile
 355 360 365
 Ala Pro Leu Val Lys Lys His Glu Gln Arg Ile Lys Ala Ala Leu Val
 370 375 380
 Leu Gly Ala Asp Arg Ala Glu Ile Val Ala Ala Leu Lys Glu His Ala
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 Ser Gln Ala Ser Val Phe Val Thr Asp Lys Thr Glu Pro Phe Glu Ala
 405 410 415
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Pro	Ala	Pro	Leu	Arg	Arg	Leu	Arg	Ser	Ala	Ala	Ala	Ile	Ile	Ser	Ala	
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aaa	gtt	gcg	aca	tcc	gcg	tcc	aaa	gcc	aca	ggc	cgc	gga	tcc	ggt	ggc	211
Lys	Val	Ala	Thr	Ser	Ala	Ser	Lys	Ala	Thr	Gly	Arg	Gly	Ser	Gly	Gly	
			25					30					35			
atg	atc	ggc	gga	ctg	gtg	gcc	agc	aag	gta	gac	ccg	gac	atc	atg	tcc	259
Met	Ile	Gly	Gly	Leu	Val	Ala	Ser	Lys	Val	Asp	Pro	Asp	Ile	Met	Ser	
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aac	ctc	atc	aac	aac	cgc	cca	aca	gtg	ctg	gtc	acg	ggc	aca	aat	ggc	307
Asn	Leu	Ile	Asn	Asn	Arg	Pro	Thr	Val	Leu	Val	Thr	Gly	Thr	Asn	Gly	
	55					60					65					
aag	tcc	acc	acc	acc	cgc	atg	ctg	gcc	gcc	gcg	atg	cgc	agc	act	tac	355
Lys	Ser	Thr	Thr	Thr	Arg	Met	Leu	Ala	Ala	Ala	Met	Arg	Ser	Thr	Tyr	
	70				75					80					85	
acc	gtc	gcc	acc	aat	gaa	ggc	ggc	gac	aac	atg	gac	gcc	ggc	atc	att	403
Thr	Val	Ala	Thr	Asn	Glu	Gly	Gly	Asp	Asn	Met	Asp	Ala	Gly	Ile	Ile	
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Leu	Val	Leu	Leu	Asn	Leu	Ser	Arg	Asp	Gln	Leu	Asp	Arg	Val	Gly	Glu	
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Ile	Asn	Lys	Ile	Glu	Arg	Val	Leu	Arg	Asp	Ala	Val	Arg	Ser	Arg	Pro	
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caa	ggt	gaa	tcc	gcc	acc	tgc	cca	cgc	acc	gaa	tcc	cgc	atc	ctc	cac	739
Gln	Gly	Glu	Ser	Ala	Thr	Cys	Pro	Arg	Thr	Glu	Ser	Arg	Ile	Leu	His	
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Ser	Pro	Ser	Gly	Asp	Leu	Thr	Leu	Asp	Leu	Asn	Leu	Pro	Gly	Gln	Ala	
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gaa	aac	ctc	tcc	gtc	aaa	gcc	tcc	ggc	gag	cgc	ggc	acc	gac	ctg	gca	1219
Glu	Asn	Leu	Ser	Val	Lys	Ala	Ser	Gly	Glu	Arg	Gly	Thr	Asp	Leu	Ala	
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Val Arg Leu Thr Tyr Ala Glu Ile Asp His Glu Leu Ile Ser Asn Pro
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gtc gac gcc atc gca gcc tgc cct cct ggc cgc atc gaa gtc ctc gcc 1315
 Val Asp Ala Ile Ala Ala Cys Pro Pro Gly Arg Ile Glu Val Leu Ala
 390 395 400 405

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Pro Asp Ile Met Ser Asn Leu Ile Asn Asn Arg Pro Thr Val Leu Val
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Thr Gly Thr Asn Gly Lys Ser Thr Thr Thr Arg Met Leu Ala Ala Ala
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Asp Ala Gly Ile Ile Ser Ala Leu Leu Ala Gly Arg Asn Ala Ser His
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Val Val Leu Glu Val Asp Glu Leu His Val Pro Ala Ala Ile Glu Arg
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Leu Lys Pro Asp Ala Leu Val Leu Leu Asn Leu Ser Arg Asp Gln Leu
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Asp Arg Val Gly Glu Ile Asn Lys Ile Glu Arg Val Leu Arg Asp Ala
 145 150 155 160

Val Arg Ser Arg Pro Glu Met Thr Val Ile Ala Asn Cys Asp Asp Val
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Leu Val Thr Ser Val Ala Phe Asp Ala Glu Asn Val Ile Trp Val Gly
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Ser Arg Ile Leu His Asp Gly Arg His Trp Ser Ala Glu Lys Thr Leu
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 225 230 235 240
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 245 250 255
 Leu Pro Gly Gln Ala Asn Arg Gly Asn Ala Ala Gln Ala Ile Ala Ala
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 Ser Thr Val Phe Asn Val Pro Val Ser Ser Ala Leu Pro Ala Val Asn
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 Ser Val Asn Asn Val Ala Gly Arg Tyr Ser Thr Ile Thr Val Gly Glu
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 His Lys Val His Leu Leu Leu Ala Lys Asn Pro Ala Gly Trp Gln Glu
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 Ala Leu Ser Met Val Asp Arg Thr Ala Asp Gly Leu Val Ile Val Val
 325 330 335
 Asn Gly Gln Val Ala Asp Gly Glu Asp Leu Ser Trp Leu Trp Asp Val
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 Arg Phe Glu Asp Phe Glu Asn Leu Ser Val Lys Ala Ser Gly Glu Arg
 355 360 365
 Gly Thr Asp Leu Ala Val Arg Leu Thr Tyr Ala Glu Ile Asp His Glu
 370 375 380
 Leu Ile Ser Asn Pro Val Asp Ala Ile Ala Ala Cys Pro Pro Gly Arg
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Thr	Leu	Val	Ser	Ser	Ser	Val	Glu	Phe	Asp	Ser	Arg	Ser	Leu	Thr	Pro	
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Val Asp Gly His Asp Phe Ala Ala Thr Ala Ile Glu Lys Gly Ala Val
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Ala Val Leu Ala Ala Arg Glu Val Asp Val Pro Ala Ile Val Val Pro
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Pro Val Lys Ile Gln Glu Ser Asn Ala Asp Ile Tyr Ala His Asp Pro
 85 90 95

Asp Gly His Gly Ala Ala Val Val Glu Ala Leu Ser Arg Leu Ala Arg
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His Val Val Asp Ile Cys Val Ala Gly His Gln Leu Asn Val Val Ala
 115 120 125

Ile Thr Gly Ser Ala Gly Lys Thr Ser Thr Lys Asp Phe Ile Ala Thr
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Val Leu Asp Gln Asp Gly Pro Thr Val Ala Pro Pro Gly Ser Phe Asn
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Asn Glu Leu Gly Leu Pro His Thr Ala Leu Arg Cys Thr Thr Asp Thr
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Lys Tyr Leu Val Ala Glu Met Ser Ala Arg Gly Ile Gly His Ile Lys
 180 185 190

His Leu Thr Glu Ile Ala Pro Pro Arg Ile Ala Ala Val Leu Asn Val
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Gly His Ala His Leu Gly Glu Phe Gly Ser Arg Glu Asn Ile Ala Gln
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Ala Lys Gly Glu Ile Ile Glu Ala Leu Pro Ser Lys Lys Thr Ser Ser
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Val Pro Val Leu Asn Thr Asp Pro Phe Val Ala Arg Met Ala Pro Arg
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Lys Ala Arg Val Val Trp Phe Thr Thr Asp Ala Gly Gln Ala Lys Lys																20
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Ser Asp Tyr Trp Ala Thr Ser Ile Ser Leu Asp Ala Val Ala Arg Ala																35
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Ser Phe Thr Leu Asn Thr Lys Asp Gly Ser Trp Pro Val Thr Leu Gln																50
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Val Phe Gly Glu His Gln Val Ala Asn Ala Leu Ala Ala Ala Ile																65
55 60																
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Ala Met Glu Ala Gly Val Ala Pro Glu Leu Val Val Ala Gly Leu Glu																85
70 75 80																
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Ala His Ser Ala Ala Ser Ala His Arg Met Asp Val Lys Thr Arg Ala																100
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105 110																
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120 125																
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 Met Thr Leu Gly Glu
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 Ile Ala Asp Ile Val Gly Gly Arg Leu Thr Gly Gly Ala Gln Glu Asp
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 Thr Leu Val Ser Ser Val Glu Phe Asp Ser Arg Ser Leu Thr Pro
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Glu Ser Asn Ala Asp Ile Tyr Ala His Asp Pro Asp Gly His Gly Ala
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Ala Val Val Glu Ala Leu Ser Arg Leu Ala Arg His Val Val Asp Ile
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Cys Val Ala Gly His Gln Leu Asn Val Val Ala Ile Thr Gly Ser Ala
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Gly Lys Thr Ser Thr Lys Asp Phe Ile Ala Thr Val Leu Asp Gln Asp
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Gly Pro Thr Val Ala Pro Pro Gly Ser Phe Asn Asn Glu Leu Gly Leu
      150                      155                      160                      165

cca cac acc gcg ctc cgc tgc aca acc gat act aag tat ttg gtg gct 643
Pro His Thr Ala Leu Arg Cys Thr Thr Asp Thr Lys Tyr Leu Val Ala
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gag atg tcc gcg cgt ggc att gga cat att aag cac ctg aca gag att 691
Glu Met Ser Ala Arg Gly Ile Gly His Ile Lys His Leu Thr Glu Ile
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gct ccg cca cgg att gca gct gtg ctc aac gtc ggc cat gcg cac ctg 739
Ala Pro Pro Arg Ile Ala Ala Val Leu Asn Val Gly His Ala His Leu
      200                      205                      210

ggt gaa ttt gga tcc cgc gag aat atc gcg cag gca aaa ggc gag atc 787
Gly Glu Phe Gly Ser Arg Glu Asn Ile Ala Gln Ala Lys Gly Glu Ile
      215                      220                      225

att gaa gcg ctg ccc tcg aag aaa acg gct cgg tac cag tcc 829
Ile Glu Ala Leu Pro Ser Lys Lys Thr Ala Arg Tyr Gln Ser
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<211> 243

<212> PRT

<213> Corynebacterium glutamicum

<400> 14

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 Val Asp Gly His Asp Phe Ala Ala Thr Ala Ile Glu Lys Gly Ala Val
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 Ala Val Leu Ala Ala Arg Glu Val Asp Val Pro Ala Ile Val Val Pro
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 Pro Val Lys Ile Gln Glu Ser Asn Ala Asp Ile Tyr Ala His Asp Pro
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 Asp Gly His Gly Ala Ala Val Val Glu Ala Leu Ser Arg Leu Ala Arg
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 His Val Val Asp Ile Cys Val Ala Gly His Gln Leu Asn Val Val Ala
 115 120 125
 Ile Thr Gly Ser Ala Gly Lys Thr Ser Thr Lys Asp Phe Ile Ala Thr
 130 135 140
 Val Leu Asp Gln Asp Gly Pro Thr Val Ala Pro Pro Gly Ser Phe Asn
 145 150 155 160
 Asn Glu Leu Gly Leu Pro His Thr Ala Leu Arg Cys Thr Thr Asp Thr
 165 170 175
 Lys Tyr Leu Val Ala Glu Met Ser Ala Arg Gly Ile Gly His Ile Lys
 180 185 190
 His Leu Thr Glu Ile Ala Pro Pro Arg Ile Ala Ala Val Leu Asn Val
 195 200 205
 Gly His Ala His Leu Gly Glu Phe Gly Ser Arg Glu Asn Ile Ala Gln
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 Ala Lys Gly Glu Ile Ile Glu Ala Leu Pro Ser Lys Lys Thr Ala Arg
 225 230 235 240
 Tyr Gln Ser

<210> 15

<211> 1686

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1663)

<223> RXA02710

<400> 15

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Met Ala Thr Thr Leu
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ctg gac ctc acc aaa ctt atc gat ggc atc ctc aag ggc tct gcc cag 163
Leu Asp Leu Thr Lys Leu Ile Asp Gly Ile Leu Lys Gly Ser Ala Gln
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ggc gtt ccc gct cac gca gta ggg gaa caa gca atc gcg gct att ggt 211
Gly Val Pro Ala His Ala Val Gly Glu Gln Ala Ile Ala Ala Ile Gly
25 30 35
ctt gac tcc tcc agc tta cct acc tcg gac gct att ttt gct gca gtt 259
Leu Asp Ser Ser Ser Leu Pro Thr Ser Asp Ala Ile Phe Ala Ala Val
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cca gga acc cgc act cac ggc gca cag ttt gca ggt acg gat aac gct 307
Pro Gly Thr Arg Thr His Gly Ala Gln Phe Ala Gly Thr Asp Asn Ala
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Ala Lys Ala Val Ala Ile Leu Thr Asp Ala Ala Gly Leu Glu Val Leu
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aac gaa gca gga gag acc cgc cca gtc atc gtt gtt gat gat gtc cgc 403
Asn Glu Ala Gly Glu Thr Arg Pro Val Ile Val Val Asp Asp Val Arg
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gca gta ctt ggc gca gca tca tca agc att tat ggc gat cct tca aaa 451
Ala Val Leu Gly Ala Ala Ser Ser Ser Ile Tyr Gly Asp Pro Ser Lys
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gat ttc acg ctc att gga gtc act gga acc tca ggt aaa acc acc acc 499
Asp Phe Thr Leu Ile Gly Val Thr Gly Thr Ser Gly Lys Thr Thr Thr
120 125 130
agc tac ctc ttg gaa aaa gga ctc atg gag gca ggc cac aaa gtt ggt 547
Ser Tyr Leu Leu Glu Lys Gly Leu Met Glu Ala Gly His Lys Val Gly
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Leu Ile Gly Thr Thr Gly Thr Arg Ile Asp Gly Glu Glu Val Pro Thr
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aag ctc acc act cca gaa gcg ccg act ctg cag gca ttg ttt gct cga 643
Lys Leu Thr Thr Pro Glu Ala Pro Thr Leu Gln Ala Leu Phe Ala Arg
170 175 180
atg cgc gat cac ggt gtc acc cac gtg gtg atg gaa gta tcc agc cat 691
Met Arg Asp His Gly Val Thr His Val Val Met Glu Val Ser Ser His
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gca ttg tca ttg ggc aga gtt gcg ggt tcc cac ttt gat gta gct gcg 739
Ala Leu Ser Leu Gly Arg Val Ala Gly Ser His Phe Asp Val Ala Ala
200 205 210
ttt acc aac ctg tcg cag gat cac ctt gat ttc cac ccc acc atg gat 787
Phe Thr Asn Leu Ser Gln Asp His Leu Asp Phe His Pro Thr Met Asp
215 220 225

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Asp Tyr Phe Asp Ala Lys Ala Leu Phe Phe Arg Ala Asp Ser Pro Leu	
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Val Ala Asp Lys Gln Val Val Cys Val Asp Ser Trp Gly Gln Arg	
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atg gcc agc gtg gca gcg gat gtg caa aca gta tcc acc ctt ggg caa	931
Met Ala Ser Val Ala Ala Asp Val Gln Thr Val Ser Thr Leu Gly Gln	
265 270 275	
gaa gca gac ttc agc gct aca gac atc aat gtc agc gac tct ggc gcc	979
Glu Ala Asp Phe Ser Ala Thr Asp Ile Asn Val Ser Asp Ser Gly Ala	
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cag agt ttt aag atc aac gcc ccc tca aac cag tcc tac cag gtc gag	1027
Gln Ser Phe Lys Ile Asn Ala Pro Ser Asn Gln Ser Tyr Gln Val Glu	
295 300 305	
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Ala Ala Ala Ala Arg Val Gly Val Asp Gly Glu Ala Phe Ala Arg Gly	
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Met Ser Lys Val Ala Val Pro Gly Arg Met Glu Arg Ile Asp Glu Gly	
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Gln Asp Phe Leu Ala Val Val Asp Tyr Ala His Lys Pro Ala Ala Val	
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gct gct gtg ttg gat acg ttg agg acc cag att gac ggg cgc ctc gga	1267
Ala Ala Val Leu Asp Thr Leu Arg Thr Gln Ile Asp Gly Arg Leu Gly	
375 380 385	
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Val Val Ile Gly Ala Gly Asp Arg Asp Ser Thr Lys Arg Gly Pro	
390 395 400 405	
atg ggg cag ttg tcc gca cag cgt gct gat cta gtt att gtc act gat	1363
Met Gly Gln Leu Ser Ala Gln Arg Ala Asp Leu Val Ile Val Thr Asp	
410 415 420	
gac aac cct cgt tca gag gtg cct gcc acg att cgc gca gca gtc act	1411
Asp Asn Pro Arg Ser Glu Val Pro Ala Thr Ile Arg Ala Ala Val Thr	
425 430 435	
gca gga gca cag cag ggt gct tca gag tcc gaa cga ccg gtg gaa gtc	1459
Ala Gly Ala Gln Gln Gly Ala Ser Glu Ser Glu Arg Pro Val Glu Val	
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cta gaa att ggt gac cgt gca gaa gca att cgc gtt ttg gtc gag tgg	1507
Leu Glu Ile Gly Asp Arg Ala Glu Ala Ile Arg Val Leu Val Glu Trp	
455 460 465	

gca cag cct gga gat ggc att gta gta gct gga aaa ggc cat gaa gtt 1555
 Ala Gln Pro Gly Asp Gly Ile Val Val Ala Gly Lys Gly His Glu Val
 470 475 480 485
 gga caa cta gtt gct ggt gtc acc cac cat ttt gat gac cgc gaa gaa 1603
 Gly Gln Leu Val Ala Gly Val Thr His His Phe Asp Asp Arg Glu Glu
 490 495 500
 gtt cgc gct gct ttg aca gaa aag ctc aac aat aaa ctt ccc ctt act 1651
 Val Arg Ala Ala Leu Thr Glu Lys Leu Asn Asn Lys Leu Pro Leu Thr
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 acg gaa gaa gga taggccacag tcatgatcac aat 1686
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<210> 16

<211> 521

<212> PRT

<213> *Corynebacterium glutamicum*

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 Ile Ala Ala Ile Gly Leu Asp Ser Ser Ser Leu Pro Thr Ser Asp Ala
 35 40 45
 Ile Phe Ala Ala Val Pro Gly Thr Arg Thr His Gly Ala Gln Phe Ala
 50 55 60
 Gly Thr Asp Asn Ala Ala Lys Ala Val Ala Ile Leu Thr Asp Ala Ala
 65 70 75 80
 Gly Leu Glu Val Leu Asn Glu Ala Gly Glu Thr Arg Pro Val Ile Val
 85 90 95
 Val Asp Asp Val Arg Ala Val Leu Gly Ala Ala Ser Ser Ser Ile Tyr
 100 105 110
 Gly Asp Pro Ser Lys Asp Phe Thr Leu Ile Gly Val Thr Gly Thr Ser
 115 120 125
 Gly Lys Thr Thr Thr Ser Tyr Leu Leu Glu Lys Gly Leu Met Glu Ala
 130 135 140
 Gly His Lys Val Gly Leu Ile Gly Thr Thr Gly Thr Arg Ile Asp Gly
 145 150 155 160
 Glu Glu Val Pro Thr Lys Leu Thr Thr Pro Glu Ala Pro Thr Leu Gln
 165 170 175
 Ala Leu Phe Ala Arg Met Arg Asp His Gly Val Thr His Val Val Met
 180 185 190
 Glu Val Ser Ser His Ala Leu Ser Leu Gly Arg Val Ala Gly Ser His
 195 200 205

Phe Asp Val Ala Ala Phe Thr Asn Leu Ser Gln Asp His Leu Asp Phe
 210 215 220
 His Pro Thr Met Asp Asp Tyr Phe Asp Ala Lys Ala Leu Phe Phe Arg
 225 230 235 240
 Ala Asp Ser Pro Leu Val Ala Asp Lys Gln Val Val Cys Val Asp Asp
 245 250 255
 Ser Trp Gly Gln Arg Met Ala Ser Val Ala Ala Asp Val Gln Thr Val
 260 265 270
 Ser Thr Leu Gly Gln Glu Ala Asp Phe Ser Ala Thr Asp Ile Asn Val
 275 280 285
 Ser Asp Ser Gly Ala Gln Ser Phe Lys Ile Asn Ala Pro Ser Asn Gln
 290 295 300
 Ser Tyr Gln Val Glu Leu Ala Leu Pro Gly Ala Phe Asn Val Ala Asn
 305 310 315 320
 Ala Thr Leu Ala Phe Ala Ala Ala Ala Arg Val Gly Val Asp Gly Glu
 325 330 335
 Ala Phe Ala Arg Gly Met Ser Lys Val Ala Val Pro Gly Arg Met Glu
 340 345 350
 Arg Ile Asp Glu Gly Gln Asp Phe Leu Ala Val Val Asp Tyr Ala His
 355 360 365
 Lys Pro Ala Ala Val Ala Ala Val Leu Asp Thr Leu Arg Thr Gln Ile
 370 375 380
 Asp Gly Arg Leu Gly Val Val Ile Gly Ala Gly Gly Asp Arg Asp Ser
 385 390 395 400
 Thr Lys Arg Gly Pro Met Gly Gln Leu Ser Ala Gln Arg Ala Asp Leu
 405 410 415
 Val Ile Val Thr Asp Asp Asn Pro Arg Ser Glu Val Pro Ala Thr Ile
 420 425 430
 Arg Ala Ala Val Thr Ala Gly Ala Gln Gln Gly Ala Ser Glu Ser Glu
 435 440 445
 Arg Pro Val Glu Val Leu Glu Ile Gly Asp Arg Ala Glu Ala Ile Arg
 450 455 460
 Val Leu Val Glu Trp Ala Gln Pro Gly Asp Gly Ile Val Val Ala Gly
 465 470 475 480
 Lys Gly His Glu Val Gly Gln Leu Val Ala Gly Val Thr His His Phe
 485 490 495

 Asp Asp Arg Glu Glu Val Arg Ala Ala Leu Thr Glu Lys Leu Asn Asn
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 Lys Leu Pro Leu Thr Thr Glu Glu Gly
 515 520

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				Met	Ala	Asn	Tyr	Thr								
				1				5								
gtc	cct	gga	atc	aac	gag	aat	gac	gca	aag	cag	ctt	att	gat	gga	ctg	163
Val	Pro	Gly	Ile	Asn	Glu	Asn	Asp	Ala	Lys	Gln	Leu	Ile	Asp	Gly	Leu	
			10						15					20		
cag	gag	cgt	ctc	acc	gac	tac	aac	gat	ctt	cac	ctc	atc	ttg	aag	cac	211
Gln	Glu	Arg	Leu	Thr	Asp	Tyr	Asn	Asp	Leu	His	Leu	Ile	Leu	Lys	His	
			25					30					35			
gtg	cac	tgg	aac	gtc	act	ggc	ccc	aac	ttc	att	gct	gtt	cac	gaa	atg	259
Val	His	Trp	Asn	Val	Thr	Gly	Pro	Asn	Phe	Ile	Ala	Val	His	Glu	Met	
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ctc	gac	cca	cag	gtt	gac	ctt	gtt	cgt	ggc	tat	gct	gac	gaa	gtt	gca	307
Leu	Asp	Pro	Gln	Val	Asp	Leu	Val	Arg	Gly	Tyr	Ala	Asp	Glu	Val	Ala	
	55					60					65					
gag	cgc	att	ttc	acc	ctc	gga	ggc	gca	cca	gtt	gga	acc	cca	gaa	ggc	355
Glu	Arg	Ile	Phe	Thr	Leu	Gly	Gly	Ala	Pro	Val	Gly	Thr	Pro	Glu	Gly	
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cac	gtt	gct	gac	cgc	acc	cca	ctg	caa	tat	gag	cgc	aat	gcc	gga	aat	403
His	Val	Ala	Asp	Arg	Thr	Pro	Leu	Gln	Tyr	Glu	Arg	Asn	Ala	Gly	Asn	
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gtc	caa	gca	cac	ctc	act	gac	ctc	aat	cgc	gtg	tac	acc	caa	gtg	ctg	451
Val	Gln	Ala	His	Leu	Thr	Asp	Leu	Asn	Arg	Val	Tyr	Thr	Gln	Val	Leu	
			105					110					115			
acc	gga	gtt	cgc	gag	tcc	atg	gca	tca	gcc	ggc	cca	gtg	gat	cca	gta	499
Thr	Gly	Val	Arg	Glu	Ser	Met	Ala	Ser	Ala	Gly	Pro	Val	Asp	Pro	Val	
		120					125					130				
act	gaa	gac	atc	tac	atc	agc	cag	gcc	gcg	gag	ctg	gag	aaa	ttc	cag	547
Thr	Glu	Asp	Ile	Tyr	Ile	Ser	Gln	Ala	Ala	Glu	Leu	Glu	Lys	Phe	Gln	
	135					140					145					
tggttc	atc	cgc	gca	cac	att	gtt	gat	gta	gac	gga	aac	atc	caa	gag	595	
Trp	Phe	Ile	Arg	Ala	His	Ile	Val	Asp	Val	Asp	Gly	Asn	Ile	Gln	Glu	
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Leu Ile Leu Lys His Val His Trp Asn Val Thr Gly Pro Asn Phe Ile
          35          40          45
Ala Val His Glu Met Leu Asp Pro Gln Val Asp Leu Val Arg Gly Tyr
          50          55          60
Ala Asp Glu Val Ala Glu Arg Ile Phe Thr Leu Gly Gly Ala Pro Val
  65          70          75          80
Gly Thr Pro Glu Gly His Val Ala Asp Arg Thr Pro Leu Gln Tyr Glu
          85          90          95
Arg Asn Ala Gly Asn Val Gln Ala His Leu Thr Asp Leu Asn Arg Val
          100          105          110
Tyr Thr Gln Val Leu Thr Gly Val Arg Glu Ser Met Ala Ser Ala Gly
          115          120          125
Pro Val Asp Pro Val Thr Glu Asp Ile Tyr Ile Ser Gln Ala Ala Glu
          130          135          140
Leu Glu Lys Phe Gln Trp Phe Ile Arg Ala His Ile Val Asp Val Asp
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Gly Asn Ile Gln Glu
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                                         Val Asp Phe Trp Thr
                                         1             5
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att ctc gac acc atg act tcc ctc ctt act ccc att gca atc cgt gga 163
Ile Leu Asp Thr Met Thr Ser Leu Leu Thr Pro Ile Ala Ile Arg Gly
          10             15             20

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tta gaa att ccc aat agg atg tgg ctc gcg ccc atg tgc cag tac caa	211
Leu Glu Ile Pro Asn Arg Met Trp Leu Ala Pro Met Cys Gln Tyr Gln	
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gcc aat aac ctc gat ggg gtt cca ctt gat tgg cac ctc gtg cat tac	259
Ala Asn Asn Leu Asp Gly Val Pro Leu Asp Trp His Leu Val His Tyr	
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gga gcc cga gct gtt ggc ggc ttc gga ctc ctc atc gcg gaa tcc acc	307
Gly Ala Arg Ala Val Gly Gly Phe Gly Leu Leu Ile Ala Glu Ser Thr	
55 60 65	
ggc att agt cca gag gga aga atc tca tcg cgt tgc act ggc cta tgg	355
Gly Ile Ser Pro Glu Gly Arg Ile Ser Ser Arg Cys Thr Gly Leu Trp	
70 75 80 85	
aat gag gcc caa gtt gag gca tgg gag aga att aca aat ttt gtc cac	403
Asn Glu Ala Gln Val Glu Ala Trp Glu Arg Ile Thr Asn Phe Val His	
90 95 100	
gct caa ggt gga ctg atc ggt gtg caa ctt aac cat gca ggc cgc aaa	451
Ala Gln Gly Gly Leu Ile Gly Val Gln Leu Asn His Ala Gly Arg Lys	
105 110 115	
gcg agc aca tat ccg gcc ctt cct aac ttc cct act ggt act caa tca	499
Ala Ser Thr Tyr Pro Ala Leu Pro Asn Phe Pro Thr Gly Thr Gln Ser	
120 125 130	
gtt gac gag ggt gga tgg gaa acc ttt ggg cct agt gct gtc gct cag	547
Val Asp Glu Gly Gly Trp Glu Thr Phe Gly Pro Ser Ala Val Ala Gln	
135 140 145	
ccg ggg ctt gca gat ccg acc gaa ttg acc cgc gaa ggt att gaa aag	595
Pro Gly Leu Ala Asp Pro Thr Glu Leu Thr Arg Glu Gly Ile Glu Lys	
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gtt att cag gat ttc gct gct gct gca gag cgc gcg gtg cgt gca ggg	643
Val Ile Gln Asp Phe Ala Ala Ala Ala Glu Arg Ala Val Arg Ala Gly	
170 175 180	
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Phe Asp Ala Val Glu Val His Gly Ala His Gly Tyr Leu Leu His Gln	
185 190 195	
ttc ctc act ccc ctc gca aat aaa cgt act gat att tat gga ggt tcg	739
Phe Leu Thr Pro Leu Ala Asn Lys Arg Thr Asp Ile Tyr Gly Gly Ser	
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Phe Glu Asn Arg Thr Arg Leu Phe Arg Glu Val Ala Gln Ala Ile Arg	
215 220 225	
gca gtg att ccg ggc tcg atg cca ctg att gcc cgg atc tct gcc acg	835
Ala Val Ile Pro Gly Ser Met Pro Leu Ile Ala Arg Ile Ser Ala Thr	
230 235 240 245	
gac tgg att gat gat gaa cct tcg tgg gat gac gat caa acc gtc tcg	883
Asp Trp Ile Asp Asp Glu Pro Ser Trp Asp Asp Asp Gln Thr Val Ser	
250 255 260	
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Leu Val Ser Gly Ser Glu Lys Ala Gly Cys Gly Cys Ser Arg Tyr Phe
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 cac cgg agg tgc agt acc cgc gac aat ccc tgt gga gcc gag cta tca 979
 His Arg Arg Cys Ser Thr Arg Asp Asn Pro Cys Gly Ala Glu Leu Ser
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 agt gaa att tgc tcg tcg tgt gaa gca aga ggt ggg tat ccc tac ctc 1027
 Ser Glu Ile Cys Ser Ser Cys Glu Ala Arg Gly Gly Tyr Pro Tyr Leu
 295 300 305
 cgc ggt tgg att aat tac tca tgt ggg tca ggc gca ggg gca tct 1072
 Arg Gly Trp Ile Asn Tyr Ser Cys Gly Ser Gly Ala Gly Ala Ser
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 <212> PRT
 <213> Corynebacterium glutamicum

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 Met Cys Gln Tyr Gln Ala Asn Asn Leu Asp Gly Val Pro Leu Asp Trp
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 His Leu Val His Tyr Gly Ala Arg Ala Val Gly Gly Phe Gly Leu Leu
 50 55 60
 Ile Ala Glu Ser Thr Gly Ile Ser Pro Glu Gly Arg Ile Ser Ser Arg
 65 70 75 80
 Cys Thr Gly Leu Trp Asn Glu Ala Gln Val Glu Ala Trp Glu Arg Ile
 85 90 95
 Thr Asn Phe Val His Ala Gln Gly Gly Leu Ile Gly Val Gln Leu Asn
 100 105 110
 His Ala Gly Arg Lys Ala Ser Thr Tyr Pro Ala Leu Pro Asn Phe Pro
 115 120 125
 Thr Gly Thr Gln Ser Val Asp Glu Gly Gly Trp Glu Thr Phe Gly Pro
 130 135 140
 Ser Ala Val Ala Gln Pro Gly Leu Ala Asp Pro Thr Glu Leu Thr Arg
 145 150 155 160
 Glu Gly Ile Glu Lys Val Ile Gln Asp Phe Ala Ala Ala Ala Glu Arg
 165 170 175
 Ala Val Arg Ala Gly Phe Asp Ala Val Glu Val His Gly Ala His Gly
 180 185 190
 Tyr Leu Leu His Gln Phe Leu Thr Pro Leu Ala Asn Lys Arg Thr Asp

195	200	205
Ile Tyr Gly Gly Ser Phe Glu Asn Arg Thr Arg Leu Phe Arg Glu Val		
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Ala Gln Ala Ile Arg Ala Val Ile Pro Gly Ser Met Pro Leu Ile Ala		
225	230	235
Arg Ile Ser Ala Thr Asp Trp Ile Asp Asp Glu Pro Ser Trp Asp Asp		
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Asp Gln Thr Val Ser Leu Val Ser Gly Ser Glu Lys Ala Gly Cys Gly		
	260	265
Cys Ser Arg Tyr Phe His Arg Arg Cys Ser Thr Arg Asp Asn Pro Cys		
	275	280
Gly Ala Glu Leu Ser Ser Glu Ile Cys Ser Ser Cys Glu Ala Arg Gly		
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Gly Tyr Pro Tyr Leu Arg Gly Trp Ile Asn Tyr Ser Cys Gly Ser Gly		
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Ala Gly Ala Ser		

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(967)
 <223> RXS02560

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 Met Gln Gly Asn Ser
 1 5
 ctt aat ctg gca gac aac agc gag aga aag aag ccc atg ccg tca cca 163
 Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys Pro Met Pro Ser Pro
 10 15 20
 gga gaa ctt tta gcc gcc cgc tac gga caa cct gca acc tgg acg cca 211
 Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro Ala Thr Trp Thr Pro
 25 30 35
 ccg cag tgg aat gag acg ctt gat gtc att cac cag cat cga tca gtt 259
 Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His Gln His Arg Ser Val
 40 45 50

cgc agg tgg ttg gat aaa ccg gtt gat gat gac acc atc cgc acc att 307
 Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp Thr Ile Arg Thr Ile
 55 60 65
 att tcc gcc gca caa tcg gct gga acc tct tcc aat aag cag gtc att 355

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tct	gtc	atc	gtg	gtt	aaa	gat	cct	gag	ctg	agg	aaa	ggc	ctc	gcg	ggg	403
Ser	Val	Ile	Val	Val	Lys	Asp	Pro	Glu	Leu	Arg	Lys	Gly	Leu	Ala	Gly	
				90					95					100		
atc	act	cgc	cag	atg	ttt	ccg	cac	ctt	gag	cag	gtt	ccc	gcg	gtg	ctg	451
Ile	Thr	Arg	Gln	Met	Phe	Pro	His	Leu	Glu	Gln	Val	Pro	Ala	Val	Leu	
			105					110					115			
att	tgg	ttg	att	gat	tat	tcc	cga	atc	agt	gcg	gtg	gca	gcc	aga	gaa	499
Ile	Trp	Leu	Ile	Asp	Tyr	Ser	Arg	Ile	Ser	Ala	Val	Ala	Ala	Arg	Glu	
		120					125					130				
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ttc	ctc	gac	gcc	gga	atc	gca	gct	caa	aac	gct	gca	att	gct	gcg	gag	595
Phe	Leu	Asp	Ala	Gly	Ile	Ala	Ala	Gln	Asn	Ala	Ala	Ile	Ala	Ala	Glu	
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Ser	Leu	Gly	Leu	Gly	Thr	Leu	Tyr	Leu	Gly	Ser	Val	Arg	Asn	Asp	Ala	
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gaa	gcc	gtg	cac	aaa	ttg	ctt	ggc	ctt	cca	cct	gag	atc	gtg	cct	gtc	691
Glu	Ala	Val	His	Lys	Leu	Leu	Gly	Leu	Pro	Pro	Glu	Ile	Val	Pro	Val	
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Val	Gly	Leu	Glu	Met	Gly	His	Ala	Asp	Pro	Pro	Glu	Pro	Ala	Gly	Ile	
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aaa	cct	ccc	ctg	cca	caa	gaa	gcc	att	gtt	cac	tgg	gat	acc	tac	acc	787
Lys	Pro	Pro	Leu	Pro	Gln	Glu	Ala	Ile	Val	His	Trp	Asp	Thr	Tyr	Thr	
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gag	aaa	aac	ctc	gaa	ctt	atc	gat	tcc	tac	gac	cgc	gcc	ctc	gac	act	835
Glu	Lys	Asn	Leu	Glu	Leu	Ile	Asp	Ser	Tyr	Asp	Arg	Ala	Leu	Asp	Thr	
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tac	tat	tct	cgc	tac	ggc	cag	cac	cag	ctc	tgg	tcg	aag	cag	acg	gcg	883
Tyr	Tyr	Ser	Arg	Tyr	Gly	Gln	His	Gln	Leu	Trp	Ser	Lys	Gln	Thr	Ala	
				250					255					260		
cat	agg	gcg	gcg	tcg	aaa	agc	ttt	tca	aaa	acc	aac	agg	cag	ttc	ctt	931
His	Arg	Ala	Ala	Ser	Lys	Ser	Phe	Ser	Lys	Thr	Asn	Arg	Gln	Phe	Leu	
			265					270					275			
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Gln His Arg Ser Val Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp
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Asn Lys Gln Val Ile Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg
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Lys Gly Leu Ala Gly Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln
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Val Pro Ala Val Leu Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala
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Val Ala Ala Arg Glu Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp
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Glu Ala Ala Trp Gly Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala
145           150           155           160

Ala Ile Ala Ala Glu Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser
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Val Arg Asn Asp Ala Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro
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Glu Ile Val Pro Val Val Gly Leu Glu Met Gly His Ala Asp Pro Pro
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Glu Pro Ala Gly Ile Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His
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Trp Asp Thr Tyr Thr Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp
225           230           235           240

Arg Ala Leu Asp Thr Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp
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Ser Lys Gln Thr Ala His Arg Ala Ala Ser Lys Ser Phe Ser Lys Thr
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 Met Ala Val Tyr Glu
 1 5
 ctc cca gaa ctc gac tac gca tac gac gct ctc gag cca cac atc gtc 163
 Leu Pro Glu Leu Asp Tyr Ala Tyr Asp Ala Leu Glu Pro His Ile Val
 10 15 20
 gct gaa atc atg gag ctt gac cag tcc aag gac cac gca acc tac gtt 211
 Ala Glu Ile Met Glu Leu Asp Gln Ser Lys Asp His Ala Thr Tyr Val
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 Met Leu Asp Met Trp

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gag cac gct ttc tac ctg cag tac atg aac gtt aag gca gat tac gtc 163
 Glu His Ala Phe Tyr Leu Gln Tyr Met Asn Val Lys Ala Asp Tyr Val
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aag gct gtt tgg aac gtc ttc aac tgg gac gac gca aga gca cgc ttc 211
 Lys Ala Val Trp Asn Val Phe Asn Trp Asp Asp Ala Arg Ala Arg Phe
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 Val Ser Lys Val Leu
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aga gtt ggc gat cgc agc ccg cgc gtg gca gaa gtg cgc act acg ctc 163
 Arg Val Gly Asp Arg Ser Pro Arg Val Ala Glu Val Arg Thr Thr Leu
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gct cgc ctc ggt gtg att gaa ggc tat tcc agg gag atg tct gca aag 211
 Ala Arg Leu Gly Val Ile Glu Gly Tyr Ser Arg Glu Met Ser Ala Lys
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 Thr Glu Ser Gln Lys Phe His Glu Glu Glu Thr Leu Phe Asp Glu Glu
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Asp	Leu	Met	Leu	Ser	Leu	His	Cys	Asp	Ser	Tyr	Pro	Asn	Glu	Lys	Ala	
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Leu Arg Leu Thr Arg Met Pro Met Val Glu Val Val Thr Gly Tyr Leu			
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Thr Asn Pro Asp Asp Leu Ala Val Leu Thr Asp Pro Gln Met Arg Asp			
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His Ile Ala Glu Ala Ile Val Val Ala Val Lys Arg Leu Tyr Leu Leu			
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Leu Phe Asp Glu Glu Leu Ser Leu Ser Ile Lys Ser Phe Gln Gln Ala
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Arg Gly Val Val Pro Ser Gly Leu Ile Asp Asp Pro Thr Leu Arg Ala
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Ile Arg Glu Ala Ser Tyr Thr Leu Gly Thr Arg Val Leu Ala Tyr Gln
85 90 95

Pro Gly Asn Gln Leu Val Gly Asp Asp Val Val Glu Ile Gln Ser His
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Leu Gln Glu Leu Gly Phe Tyr Ala Asp Arg Val Asp Gly His Phe Gly
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Glu Leu Thr His Lys Ala Val Met Asn Tyr Gln Leu Asn Tyr Gly Met
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Gln Val Asp Gly Ile Cys Gly Pro Asp Thr Ile Arg Ala Leu Ser Arg

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Glu Arg Met Arg Asn Ala Gly Pro Arg Leu Ala Gly Lys Arg Val Val						
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Ile Asp Pro Ala Leu Gly Gly Ser Asn Lys Gly Gln Ile Val Lys Gly						
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Pro Tyr Gly Glu Ile Ser Glu Glu Glu Ile Leu Trp Asp Leu Ala Thr						
		210		215		220
Arg Leu Glu Gly Arg Met Ile Ala Thr Gly Met Glu Thr Ile Leu Ser						
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Arg Pro His Met Asp Asp Pro Ser Ser Arg Asp Arg Ala Ser Ile Ala						
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Asn Ala Phe Gly Ala Asp Leu Met Leu Ser Leu His Cys Asp Ser Tyr						
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Pro Asn Glu Lys Ala Asn Gly Val Ala Ser Phe Tyr Phe Gly Ser Glu						
		275		280		285
Asn Gly Thr Asn Ser Leu Thr Gly Glu Thr Leu Ser Ala Tyr Ile Gln						
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Lys Glu Ile Val Ala Arg Thr Pro Leu Asn Asn Cys Gly Ser His Ala						
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Arg Thr Trp Asp Leu Leu Arg Leu Thr Arg Met Pro Met Val Glu Val						
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Val Thr Gly Tyr Leu Thr Asn Pro Asp Asp Leu Ala Val Leu Thr Asp						
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Pro Gln Met Arg Asp His Ile Ala Glu Ala Ile Val Val Ala Val Lys						
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Arg Leu Tyr Leu Leu Asp Glu Glu Ala Gln Pro Lys Thr Gly Thr Phe						
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<223> RXA02641

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Thr Gly Gly Ser Ser Gly Gly Thr Asp Leu Leu Asn Gly Ala Asn Ser	505	510	515	
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Glu Gln Leu Leu Thr Gly Leu Gly Ser Ile Ala Ala Val Leu Ile Ala	520	525	530	
gcg tct ttg gct gat ggt ggc ctg aat ggt ctg atc agc aat gtt ggt				1747
Ala Ser Leu Ala Asp Gly Gly Leu Asn Gly Leu Ile Ser Asn Val Gly	535	540	545	
agc aac aac ggc gtc cca gtg ctt ggc gat atc aag atc act gac gtc				1795
Ser Asn Asn Gly Val Pro Val Leu Gly Asp Ile Lys Ile Thr Asp Val	550	555	560	565
atc cca atc gtt gat acc gcg atc aac cta acc gga gac aat aag tac				1843
Ile Pro Ile Val Asp Thr Ala Ile Asn Leu Thr Gly Asp Asn Lys Tyr	570	575	580	
tct cgc ggt tgg aac gac ctg aac aac acg ctt gga cca gtg ctt ggc				1891
Ser Arg Gly Trp Asn Asp Leu Asn Asn Thr Leu Gly Pro Val Leu Gly	585	590	595	
gct gcc act ggt ggc gaa acc acc gtg aag tac acc agc gac cag aac				1939
Ala Ala Thr Gly Gly Glu Thr Thr Val Lys Tyr Thr Ser Asp Gln Asn	600	605	610	
tct gag gtt act ttc gtg ccg ttt gaa aat ggc atc atg gtg tct tcc				1987
Ser Glu Val Thr Phe Val Pro Phe Glu Asn Gly Ile Met Val Ser Ser	615	620	625	
cct gag gct gga act cac ggc ctg tgg ggc gca atc ggt gac gcg tgg				2035
Pro Glu Ala Gly Thr His Gly Leu Trp Gly Ala Ile Gly Asp Ala Trp	630	635	640	645
gct cag cag ggc gct gac ctt ggc cct ctg gga ctt cca acc agt aat				2083
Ala Gln Gln Gly Ala Asp Leu Gly Pro Leu Gly Leu Pro Thr Ser Asn	650	655	660	
gaa tac acc gtt ggc gaa cag ctt cgt gtt gat ttc cag aat ggt tac				2131
Glu Tyr Thr Val Gly Glu Gln Leu Arg Val Asp Phe Gln Asn Gly Tyr	665	670	675	
atc act tac gat tct gcg act ggc cag gca agc att cag ctg aac				2176
Ile Thr Tyr Asp Ser Ala Thr Gly Gln Ala Ser Ile Gln Leu Asn	680	685	690	
tagtctcaat tagagccgaa aac				2199

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<211> 692

<212> PRT

<213> Corynebacterium glutamicum

<400> 30

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Ala Ala Gly Thr Gln Tyr Leu Asn Thr Gln Gly Glu Gly Ile Gly Pro
 20 25 30

Val Ala Val Gln Asn Asp Ser Glu Ser Phe Asn Ser Gly Thr Asn Val
 35 40 45

Val Val Glu Asp Ala Ala Val Thr Ala Gln Gly Glu Gly Gly Gly Ala
 50 55 60

Arg Thr Val Lys Glu Phe Gln Arg Asp Gln Gln Phe Ser Ser Phe Ala
 65 70 75 80

Leu Thr Trp Thr Gly Lys Lys Asp Ile Thr Ala Phe Val Arg Ala Glu
 85 90 95

Gln Glu Asp Gly Thr Trp Ser Gln Trp Tyr Asp Leu Glu Pro Met Val
 100 105 110

Asn Glu Asp Gln Gly Thr Asn Gly Thr Glu Leu Ile Trp His Gly Pro
 115 120 125

Thr Asn Lys Ile Gln Val Ser Thr Leu Asn Val Asp Leu Phe Gly Ala
 130 135 140

Asp Ala Ala Ala Ala Asp Glu Asn Gly Gln Asp Ile Pro Ala Val Asp
 145 150 155 160

Ala Ala Glu Ala Ala Pro Ala Ala Glu Pro Ala Pro Ala Glu Ala Pro
 165 170 175

Val Glu Glu Ala Pro Ala Pro Val Ala Glu Pro Ala Pro Ala Ala Glu
 180 185 190

Pro Ile Ala Glu Pro Val Ala Asp Tyr Ser Ala Asn Asp Gly Leu Ala
 195 200 205

Pro Leu Pro Ser Asn Tyr Gly Asp Ile Gln Pro Val Ala Asp Val Asp
 210 215 220

Asp Gly Leu Asn Ala Val Phe Ile Asp Gly Asn Ala Asp Ala Gly Val
 225 230 235 240

Gly Ile Ala Asn Val Ala Asp Thr Asp Gly Met Pro Lys Val Ile Ser
 245 250 255

Arg Ala Gly Trp Gly Ala Asp Glu Ser Leu Arg Cys Ser Asn Pro Thr
 260 265 270

Ile Asp Asp Gly Val Ser Ala Ile Thr Ile His His Thr Ala Gly Ser
 275 280 285

Asn Asn Tyr Thr Glu Ala Gln Ala Ala Ala Gln Val Arg Ser Ala Tyr
 290 295 300

Ser Tyr His Ala Lys Asn Leu Gly Trp Cys Asp Ile Gly Tyr Gln Ser
 305 310 315 320

Leu Val Asp Lys Tyr Gly Asn Ile Tyr Glu Gly Arg Ala Gly Gly Met
 325 330 335
 Thr Asn Ala Val Gln Gly Ala His Ala Gly Gly Phe Asn Gln Asn Thr
 340 345 350
 Trp Ala Ile Ser Met Ile Gly Asp Tyr Ser Tyr Asn Ala Pro Pro Gln
 355 360 365
 Glu Thr Ile Asn Ala Val Gly Glu Leu Ala Gly Trp Arg Ala Lys Val
 370 375 380
 Ala Gly Phe Asp Pro Thr Gly Thr Asp Thr His Tyr Ser Glu Gly Thr
 385 390 395 400
 Ser Tyr Ala Lys Tyr Ser Tyr Gly Thr Arg Val Ser Leu Pro Asn Ile
 405 410 415
 Leu Ala His Arg Asn Val Gly Leu Thr Ala Cys Pro Gly Asp Ala Gly
 420 425 430
 Tyr Ala Gln Met Glu Asn Ile Arg Gln Ile Val Lys Ala Lys Tyr Thr
 435 440 445
 Ser Leu Gln Asn Gly Asn Thr Gly Gly Thr Thr Thr Thr Pro Ala Thr
 450 455 460
 Thr Pro Lys Glu Thr Ser Thr Ser Asn Ala Pro Ser Thr Thr Thr Ala
 465 470 475 480
 Gln Leu Val Thr Pro Ala Glu Pro Gln Gln Tyr Ser Glu Ser Asp Ala
 485 490 495
 Leu Ala Ala Leu Leu Thr Gly Gly Ser Ser Gly Gly Thr Asp Leu Leu
 500 505 510
 Asn Gly Ala Asn Ser Glu Gln Leu Leu Thr Gly Leu Gly Ser Ile Ala
 515 520 525
 Ala Val Leu Ile Ala Ala Ser Leu Ala Asp Gly Gly Leu Asn Gly Leu
 530 535 540
 Ile Ser Asn Val Gly Ser Asn Asn Gly Val Pro Val Leu Gly Asp Ile
 545 550 555 560
 Lys Ile Thr Asp Val Ile Pro Ile Val Asp Thr Ala Ile Asn Leu Thr
 565 570 575
 Gly Asp Asn Lys Tyr Ser Arg Gly Trp Asn Asp Leu Asn Asn Thr Leu
 580 585 590
 Gly Pro Val Leu Gly Ala Ala Thr Gly Gly Glu Thr Thr Val Lys Tyr
 595 600 605

 Thr Ser Asp Gln Asn Ser Glu Val Thr Phe Val Pro Phe Glu Asn Gly
 610 615 620
 Ile Met Val Ser Ser Pro Glu Ala Gly Thr His Gly Leu Trp Gly Ala
 625 630 635 640

Ile Gly Asp Ala Trp Ala Gln Gln Gly Ala Asp Leu Gly Pro Leu Gly
645 650 655

Leu Pro Thr Ser Asn Glu Tyr Thr Val Gly Glu Gln Leu Arg Val Asp
660 665 670

Phe Gln Asn Gly Tyr Ile Thr Tyr Asp Ser Ala Thr Gly Gln Ala Ser
675 680 685

Ile Gln Leu Asn
690

<210> 31
<211> 1377
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1354)
<223> RXA00135

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Val Lys Asp Lys Phe
1 5

tta gtc act ggt gga gca cag ctg cag ggc gct gta aaa gtt tac ggc 163
Leu Val Thr Gly Gly Ala Gln Leu Gln Gly Ala Val Lys Val Tyr Gly
10 15 20

gca aaa aac agc gtt ttg aag ctc atg gca gca gca ctt ctc gct gaa 211
Ala Lys Asn Ser Val Leu Lys Leu Met Ala Ala Ala Leu Leu Ala Glu
25 30 35

ggc aca aca act cta acc aat tgc ccc gaa atc ctc gac gtc ccc ctg 259
Gly Thr Thr Thr Leu Thr Asn Cys Pro Glu Ile Leu Asp Val Pro Leu
40 45 50

atg cgc gac gtc ctc gtt ggt ctt ggc tgc gat gtc acc atc gac ggc 307
Met Arg Asp Val Leu Val Gly Leu Gly Cys Asp Val Thr Ile Asp Gly
55 60 65

tca acc gta acc att act acc cct gca gaa ctc agc tcc aat gct gac 355
Ser Thr Val Thr Ile Thr Thr Pro Ala Glu Leu Ser Ser Asn Ala Asp
70 75 80 85

ttc cca gca gtc acc caa ttc cgt gca tcc gta tgt gtg ctt ggt cca 403
Phe Pro Ala Val Thr Gln Phe Arg Ala Ser Val Cys Val Leu Gly Pro
90 95 100

ttg aca gca cgt tgt ggt cgc gca gtt gta tcc ctt ccc ggc ggt gac 451
Leu Thr Ala Arg Cys Gly Arg Ala Val Val Ser Leu Pro Gly Gly Asp
105 110 115

gcc att gga tcc cgt cca ctc gac atg cat caa agc ggc ctg gaa aag 499
Ala Ile Gly Ser Arg Pro Leu Asp Met His Gln Ser Gly Leu Glu Lys
120 125 130

ctt ggt gcc acc acc cgc att tcc cac ggt gca gta gtt gca gaa gct	547
Leu Gly Ala Thr Thr Arg Ile Ser His Gly Ala Val Val Ala Glu Ala	
135 140 145	
gaa aag ctc gtc ggt gcc aac atc acc ctg gat ttc ccg tcc gtc ggc	595
Glu Lys Leu Val Gly Ala Asn Ile Thr Leu Asp Phe Pro Ser Val Gly	
150 155 160 165	
gcc acc gaa aac atc ctc act gca tcc gtc atg gca gaa gga cgc aca	643
Ala Thr Glu Asn Ile Leu Thr Ala Ser Val Met Ala Glu Gly Arg Thr	
170 175 180	
gta tta gat aac gca gcg cgc gaa cca gaa att gtt gat ctc tgc cgt	691
Val Leu Asp Asn Ala Ala Arg Glu Pro Glu Ile Val Asp Leu Cys Arg	
185 190 195	
atg ctt cga tcc atg ggc gcc aac att gaa ggt gaa gga agc cca ccc	739
Met Leu Arg Ser Met Gly Ala Asn Ile Glu Gly Glu Gly Ser Pro Pro	
200 205 210	
atc acc atc gaa ggc gta gag aaa ctc acc cca act cag cac gaa gta	787
Ile Thr Ile Glu Gly Val Glu Lys Leu Thr Pro Thr Gln His Glu Val	
215 220 225	
atc ggc gac cgc atc gtt gcc gga acg tgg gca tac gcc gct gcg atg	835
Ile Gly Asp Arg Ile Val Ala Gly Thr Trp Ala Tyr Ala Ala Ala Met	
230 235 240 245	
act cgt ggc gat att aca gtt ggc gga atc gca cca agg tat ctg cac	883
Thr Arg Gly Asp Ile Thr Val Gly Gly Ile Ala Pro Arg Tyr Leu His	
250 255 260	
ctt cca ttg gaa aag ctc aag atc gcc ggc gcc aag gtg gaa acc tac	931
Leu Pro Leu Glu Lys Leu Lys Ile Ala Gly Ala Lys Val Glu Thr Tyr	
265 270 275	
gaa aac ggc ttc cgc gtc caa atg gat aag cag cct gag gca acc gac	979
Glu Asn Gly Phe Arg Val Gln Met Asp Lys Gln Pro Glu Ala Thr Asp	
280 285 290	
tac caa acc ctc ccg ttc cca ggg ttc cct aca gat ctg caa ccc atg	1027
Tyr Gln Thr Leu Pro Phe Pro Gly Phe Pro Thr Asp Leu Gln Pro Met	
295 300 305	
gca att gga atc aac gca gta tct aat gga act tca gta att aca gag	1075
Ala Ile Gly Ile Asn Ala Val Ser Asn Gly Thr Ser Val Ile Thr Glu	
310 315 320 325	
aat gtc ttt gaa tca cga ttc cgc ttc gtc gat gaa atg ctt cgc ctg	1123
Asn Val Phe Glu Ser Arg Phe Arg Phe Val Asp Glu Met Leu Arg Leu	
330 335 340	
ggc gct gac gcg aat gtc gat ggg cac cac gta gta atc cga gga att	1171
Gly Ala Asp Ala Asn Val Asp Gly His His Val Val Ile Arg Gly Ile	
345 350 355	
gaa cag ctt tcc tct act tcc gtg tgg tct tca gat atc cgt gca gga	1219
Glu Gln Leu Ser Ser Thr Ser Val Trp Ser Ser Asp Ile Arg Ala Gly	
360 365 370	

gca gga ctg gtt ctt gcc gcc ctt tgc gca gac gga gtg acc gaa gtt 1267
 Ala Gly Leu Val Leu Ala Ala Leu Cys Ala Asp Gly Val Thr Glu Val
 375 380 385

cac gat gtt ttc cac atc gac cgc gga tac ccc aac ttc gtg gaa aat 1315
 His Asp Val Phe His Ile Asp Arg Gly Tyr Pro Asn Phe Val Glu Asn
 390 395 400 405

ctg cag aaa ctc gga gcg acc atc gaa agg gtt tct tcc taacgaagcc 1364
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ttcccatcaa gca 1377

<210> 32

<211> 418

<212> PRT

<213> Corynebacterium glutamicum

<400> 32

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 35 40 45

Leu Asp Val Pro Leu Met Arg Asp Val Leu Val Gly Leu Gly Cys Asp
 50 55 60

Val Thr Ile Asp Gly Ser Thr Val Thr Ile Thr Thr Pro Ala Glu Leu
 65 70 75 80

Ser Ser Asn Ala Asp Phe Pro Ala Val Thr Gln Phe Arg Ala Ser Val
 85 90 95

Cys Val Leu Gly Pro Leu Thr Ala Arg Cys Gly Arg Ala Val Val Ser
 100 105 110

Leu Pro Gly Gly Asp Ala Ile Gly Ser Arg Pro Leu Asp Met His Gln
 115 120 125

Ser Gly Leu Glu Lys Leu Gly Ala Thr Thr Arg Ile Ser His Gly Ala
 130 135 140

Val Val Ala Glu Ala Glu Lys Leu Val Gly Ala Asn Ile Thr Leu Asp
 145 150 155 160

Phe Pro Ser Val Gly Ala Thr Glu Asn Ile Leu Thr Ala Ser Val Met
 165 170 175

Ala Glu Gly Arg Thr Val Leu Asp Asn Ala Ala Arg Glu Pro Glu Ile
 180 185 190

Val Asp Leu Cys Arg Met Leu Arg Ser Met Gly Ala Asn Ile Glu Gly
 195 200 205

Glu Gly Ser Pro Pro Ile Thr Ile Glu Gly Val Glu Lys Leu Thr Pro

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      210              215              220
Thr  Gln  His  Glu  Val  Ile  Gly  Asp  Arg  Ile  Val  Ala  Gly  Thr  Trp  Ala
225              230              235              240
Tyr  Ala  Ala  Ala  Met  Thr  Arg  Gly  Asp  Ile  Thr  Val  Gly  Gly  Ile  Ala
      245              250              255
Pro  Arg  Tyr  Leu  His  Leu  Pro  Leu  Glu  Lys  Leu  Lys  Ile  Ala  Gly  Ala
      260              265              270
Lys  Val  Glu  Thr  Tyr  Glu  Asn  Gly  Phe  Arg  Val  Gln  Met  Asp  Lys  Gln
      275              280              285
Pro  Glu  Ala  Thr  Asp  Tyr  Gln  Thr  Leu  Pro  Phe  Pro  Gly  Phe  Pro  Thr
      290              295              300
Asp  Leu  Gln  Pro  Met  Ala  Ile  Gly  Ile  Asn  Ala  Val  Ser  Asn  Gly  Thr
305              310              315              320
Ser  Val  Ile  Thr  Glu  Asn  Val  Phe  Glu  Ser  Arg  Phe  Arg  Phe  Val  Asp
      325              330              335
Glu  Met  Leu  Arg  Leu  Gly  Ala  Asp  Ala  Asn  Val  Asp  Gly  His  His  Val
      340              345              350
Val  Ile  Arg  Gly  Ile  Glu  Gln  Leu  Ser  Ser  Thr  Ser  Val  Trp  Ser  Ser
      355              360              365
Asp  Ile  Arg  Ala  Gly  Ala  Gly  Leu  Val  Leu  Ala  Ala  Leu  Cys  Ala  Asp
370              375              380
Gly  Val  Thr  Glu  Val  His  Asp  Val  Phe  His  Ile  Asp  Arg  Gly  Tyr  Pro
385              390              395              400
Asn  Phe  Val  Glu  Asn  Leu  Gln  Lys  Leu  Gly  Ala  Thr  Ile  Glu  Arg  Val
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Ser  Ser

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<210> 33
<211> 1221
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(1198)
<223> RXA02706

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<400> 33
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cgacgattct cgtcggaacg tggaaggaca gtagaaaaca atg caa cag att atg 115
              Met Gln Gln Ile Met
              1              5

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gtc agt gga acg gtt gcg ttc ctc gtc tca atc ttt ctc acc ccg gtg 163
Val Ser Gly Thr Val Ala Phe Leu Val Ser Ile Phe Leu Thr Pro Val

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ttg	atc	cgt	tat	ttc	act	aac	cgc	cag	ttg	ggc	cag	gaa	atc	cgt	gaa	211
Leu	Ile	Arg	Tyr	Phe	Thr	Asn	Arg	Gln	Leu	Gly	Gln	Glu	Ile	Arg	Glu	
25				30				35								
gaa	ggc	ctg	cag	tct	cac	ttg	cgt	aag	cgt	ggc	act	cca	acc	atg	ggt	259
Glu	Gly	Leu	Gln	Ser	His	Leu	Arg	Lys	Arg	Gly	Thr	Pro	Thr	Met	Gly	
40				45				50								
ggc	att	gcg	att	atc	gcg	ggc	att	gtt	gtg	gcc	tat	gtg	ttt	acc	aat	307
Gly	Ile	Ala	Ile	Ile	Ala	Gly	Ile	Val	Val	Ala	Tyr	Val	Phe	Thr	Asn	
55				60				65								
atc	ttg	gcc	atg	atc	caa	ggc	gtt	ggt	gga	ttc	aca	gtc	tcc	ggc	ttg	355
Ile	Leu	Ala	Met	Ile	Gln	Gly	Val	Gly	Gly	Phe	Thr	Val	Ser	Gly	Leu	
70				75				80				85				
ctc	gtg	ttg	ggt	ctg	acc	ttg	ggc	ctt	ggt	gcc	act	ggt	ttc	gcc	gat	403
Leu	Val	Leu	Gly	Leu	Thr	Leu	Gly	Leu	Gly	Ala	Thr	Gly	Phe	Ala	Asp	
90				95				100								
gac	ttc	atc	aag	ctg	tac	atg	aac	cga	aac	ctt	ggt	ttg	aac	aag	acc	451
Asp	Phe	Ile	Lys	Leu	Tyr	Met	Asn	Arg	Asn	Leu	Gly	Leu	Asn	Lys	Thr	
105				110				115								
gct	aag	ctg	gtg	tct	cag	ctg	gcc	att	gcg	ttg	atc	ttt	ggt	ttt	ttg	499
Ala	Lys	Leu	Val	Ser	Gln	Leu	Ala	Ile	Ala	Leu	Ile	Phe	Gly	Phe	Leu	
120				125				130								
gta	ctg	cag	ttt	ccc	gat	gaa	aac	ggt	ctg	acc	cca	gca	tca	acc	cac	547
Val	Leu	Gln	Phe	Pro	Asp	Glu	Asn	Gly	Leu	Thr	Pro	Ala	Ser	Thr	His	
135				140				145								
ctg	tca	ttc	att	cgc	gat	atc	gac	acc	att	gac	ctt	ggc	ttc	ggg	ggc	595
Leu	Ser	Phe	Ile	Arg	Asp	Ile	Asp	Thr	Ile	Asp	Leu	Gly	Phe	Gly	Gly	
150				155				160				165				
agc	gtt	ttt	ggc	atc	atc	gtg	ttc	ctc	atc	ttt	atc	tac	gtt	gtg	gtc	643
Ser	Val	Phe	Gly	Ile	Ile	Val	Phe	Leu	Ile	Phe	Ile	Tyr	Val	Val	Val	
170				175				180								
agc	gcg	tgg	tcg	aat	gcc	gtg	aac	atc	act	gac	ggt	ttg	gat	ggt	ttg	691
Ser	Ala	Trp	Ser	Asn	Ala	Val	Asn	Ile	Thr	Asp	Gly	Leu	Asp	Gly	Leu	
185				190				195								
gcc	gca	ggt	acc	aca	gca	ttt	gtc	atg	ggt	gct	tac	acc	ttg	atc	acg	739
Ala	Ala	Gly	Thr	Thr	Ala	Phe	Val	Met	Gly	Ala	Tyr	Thr	Leu	Ile	Thr	
200				205				210								
ttc	tgg	cag	ttc	cga	aac	tcc	tgc	gat	act	gca	gtg	gaa	gcg	ggt	tgc	787
Phe	Trp	Gln	Phe	Arg	Asn	Ser	Cys	Asp	Thr	Ala	Val	Glu	Ala	Gly	Cys	
215				220				225								
tat	acg	gtg	cgt	gat	cca	ctg	gat	ttg	tcc	gtg	ttg	tgt	gct	gct	ggt	835
Tyr	Thr	Val	Arg	Asp	Pro	Leu	Asp	Leu	Ser	Val	Leu	Cys	Ala	Ala	Gly	
230				235				240				245				

atc ttc atg ggc gat act ggt tct ttg gca ctg ggc ggt ttg gtt gca 931
 Ile Phe Met Gly Asp Thr Gly Ser Leu Ala Leu Gly Gly Leu Val Ala
 265 270 275
 ggt att tct gtg gtt agt cgc acc gag ctg ctc atg gtt atc atc ggc 979
 Gly Ile Ser Val Val Ser Arg Thr Glu Leu Leu Met Val Ile Ile Gly
 280 285 290
 gcg ctg ttt gtc att gag atc gct tct gtt gcg atc cag atc ggc gtg 1027
 Ala Leu Phe Val Ile Glu Ile Ala Ser Val Ala Ile Gln Ile Gly Val
 295 300 305
 ttt aag acc cgc ggt aag cgt gtg ttc aaa atg gct ccg atc cac cac 1075
 Phe Lys Thr Arg Gly Lys Arg Val Phe Lys Met Ala Pro Ile His His
 310 315 320 325
 cac ttc gag gcc ctt ggg tgg gct gaa act acc gtg acc atc cgt ttc 1123
 His Phe Glu Ala Leu Gly Trp Ala Glu Thr Thr Val Thr Ile Arg Phe
 330 335 340
 tgg ctg atc gcg atc atg gct gtg ttg gcg ggt gtc ggt gtg ttt tac 1171
 Trp Leu Ile Ala Ile Met Ala Val Leu Ala Gly Val Gly Val Phe Tyr
 345 350 355
 agc gac tgg ctc cac tta gcg gag gta taaataatta tgggttctct gtc 1221
 Ser Asp Trp Leu His Leu Ala Glu Val
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<210> 34

<211> 366

<212> PRT

<213> Corynebacterium glutamicum

<400> 34

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 Gln Glu Ile Arg Glu Glu Gly Leu Gln Ser His Leu Arg Lys Arg Gly
 35 40 45
 Thr Pro Thr Met Gly Gly Ile Ala Ile Ile Ala Gly Ile Val Val Ala
 50 55 60
 Tyr Val Phe Thr Asn Ile Leu Ala Met Ile Gln Gly Val Gly Gly Phe
 65 70 75 80
 Thr Val Ser Gly Leu Leu Val Leu Gly Leu Thr Leu Gly Leu Gly Ala
 85 90 95
 Thr Gly Phe Ala Asp Asp Phe Ile Lys Leu Tyr Met Asn Arg Asn Leu
 100 105 110
 Gly Leu Asn Lys Thr Ala Lys Leu Val Ser Gln Leu Ala Ile Ala Leu
 115 120 125
 Ile Phe Gly Phe Leu Val Leu Gln Phe Pro Asp Glu Asn Gly Leu Thr

130	135	140
Pro Ala Ser Thr His Leu Ser Phe Ile Arg Asp Ile Asp Thr Ile Asp 145	150	155
Leu Gly Phe Gly Gly Ser Val Phe Gly Ile Ile Val Phe Leu Ile Phe 165	170	175
Ile Tyr Val Val Val Ser Ala Trp Ser Asn Ala Val Asn Ile Thr Asp 180	185	190
Gly Leu Asp Gly Leu Ala Ala Gly Thr Thr Ala Phe Val Met Gly Ala 195	200	205
Tyr Thr Leu Ile Thr Phe Trp Gln Phe Arg Asn Ser Cys Asp Thr Ala 210	215	220
Val Glu Ala Gly Cys Tyr Thr Val Arg Asp Pro Leu Asp Leu Ser Val 225	230	235
Leu Cys Ala Ala Gly Leu Gly Ala Thr Leu Gly Phe Leu Trp Trp Asn 245	250	255
Ala Ala Pro Ala Lys Ile Phe Met Gly Asp Thr Gly Ser Leu Ala Leu 260	265	270
Gly Gly Leu Val Ala Gly Ile Ser Val Val Ser Arg Thr Glu Leu Leu 275	280	285
Met Val Ile Ile Gly Ala Leu Phe Val Ile Glu Ile Ala Ser Val Ala 290	295	300
Ile Gln Ile Gly Val Phe Lys Thr Arg Gly Lys Arg Val Phe Lys Met 305	310	315
Ala Pro Ile His His His Phe Glu Ala Leu Gly Trp Ala Glu Thr Thr 325	330	335
Val Thr Ile Arg Phe Trp Leu Ile Ala Ile Met Ala Val Leu Ala Gly 340	345	350
Val Gly Val Phe Tyr Ser Asp Trp Leu His Leu Ala Glu Val 355	360	365

<210> 35

<211> 972

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

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<223> RXA02411

<400> 35

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ttggacggat aaaaagggaa gcaacgcgag gtggcttatg atg gca acc gtg act 115

Met Ala Thr Val Thr
1 5

gat ttc agt gga tct atg att gaa cgc ccc gtg cca ggt gct gat gcg	163
Asp Phe Ser Gly Ser Met Ile Glu Arg Pro Val Pro Gly Ala Asp Ala	
10 15 20	
ccg att gga att ttt gat tct gga gtt ggc gga tta acc gta gct cgc	211
Pro Ile Gly Ile Phe Asp Ser Gly Val Gly Gly Leu Thr Val Ala Arg	
25 30 35	
aca atc atc gat caa ttg cca cat gaa tca gtt att tat atc ggt gat	259
Thr Ile Ile Asp Gln Leu Pro His Glu Ser Val Ile Tyr Ile Gly Asp	
40 45 50	
act gcc aat ggc cct tat ggt ccg ttg cct atc gct aag gtc cgt gag	307
Thr Ala Asn Gly Pro Tyr Gly Pro Leu Pro Ile Ala Lys Val Arg Glu	
55 60 65	
cac gcc atc cgc att gcc gat gag ttg gtg gaa cgc gga tgc aag atg	355
His Ala Ile Arg Ile Ala Asp Glu Leu Val Glu Arg Gly Cys Lys Met	
70 75 80 85	
att gtc att gcc tgc aac act gcg tcc gct gcg ttt ctc cga gat gcc	403
Ile Val Ile Ala Cys Asn Thr Ala Ser Ala Ala Phe Leu Arg Asp Ala	
90 95 100	
cgt gaa cga tac agt gtg cca gtc gtg gaa gtt att ctt ccc gca gta	451
Arg Glu Arg Tyr Ser Val Pro Val Val Glu Val Ile Leu Pro Ala Val	
105 110 115	
agg cgt gcg gtg gca tcc acc cgc aat ggc aaa gtg ggc gtg atc ggc	499
Arg Arg Ala Val Ala Ser Thr Arg Asn Gly Lys Val Gly Val Ile Gly	
120 125 130	
aca gtg gga acc att aac tcc ggt gcg tac cag gat ctt ttc tct gca	547
Thr Val Gly Thr Ile Asn Ser Gly Ala Tyr Gln Asp Leu Phe Ser Ala	
135 140 145	
agc ccc tcc att gtg gtc aac gca gtg gca tgc cca cgg ttt gtg gat	595
Ser Pro Ser Ile Val Val Asn Ala Val Ala Cys Pro Arg Phe Val Asp	
150 155 160 165	
ttc gtg gaa cgc gga att acc agc ggc agg cag atc ctc aac att gcg	643
Phe Val Glu Arg Gly Ile Thr Ser Gly Arg Gln Ile Leu Asn Ile Ala	
170 175 180	
cag gat tat tta gag cct ttg caa gca gaa ggg gtg gac acc ctc gtg	691
Gln Asp Tyr Leu Glu Pro Leu Gln Ala Glu Gly Val Asp Thr Leu Val	
185 190 195	
ctt gga tgc acc cac tat cca ctg ctt tcc ggt gtc att cag ttg gca	739
Leu Gly Cys Thr His Tyr Pro Leu Leu Ser Gly Val Ile Gln Leu Ala	
200 205 210	
atg ggg gac cac gta agt ttg gtc tct agc gcg gaa gaa act gcg aaa	787
Met Gly Asp His Val Ser Leu Val Ser Ser Ala Glu Glu Thr Ala Lys	
215 220 225	
gac gtg ctg aga att ttg agc cag caa gat ctt tta gcc gat ccg gac	835
Asp Val Leu Arg Ile Leu Ser Gln Gln Asp Leu Leu Ala Asp Pro Asp	
230 235 240 245	

atg cat cct gag cca agt tat agc ttt gaa tca aca ggc gat ccg gaa 883
 Met His Pro Glu Pro Ser Tyr Ser Phe Glu Ser Thr Gly Asp Pro Glu
 250 255 260

atc ttt gcg caa tta agc cgc cga ttc ctt gga cca att gtt tcc caa 931
 Ile Phe Ala Gln Leu Ser Arg Arg Phe Leu Gly Pro Ile Val Ser Gln
 265 270 275

gtg aga caa aac gag gga taacccccagg tgtgtgttct acc 972
 Val Arg Gln Asn Glu Gly
 280

<210> 36

<211> 283

<212> PRT

<213> Corynebacterium glutamicum

<400> 36

Met Ala Thr Val Thr Asp Phe Ser Gly Ser Met Ile Glu Arg Pro Val
 1 5 10 15

Pro Gly Ala Asp Ala Pro Ile Gly Ile Phe Asp Ser Gly Val Gly Gly
 20 25 30

Leu Thr Val Ala Arg Thr Ile Ile Asp Gln Leu Pro His Glu Ser Val
 35 40 45

Ile Tyr Ile Gly Asp Thr Ala Asn Gly Pro Tyr Gly Pro Leu Pro Ile
 50 55 60

Ala Lys Val Arg Glu His Ala Ile Arg Ile Ala Asp Glu Leu Val Glu
 65 70 75 80

Arg Gly Cys Lys Met Ile Val Ile Ala Cys Asn Thr Ala Ser Ala Ala
 85 90 95

Phe Leu Arg Asp Ala Arg Glu Arg Tyr Ser Val Pro Val Val Glu Val
 100 105 110

Ile Leu Pro Ala Val Arg Arg Ala Val Ala Ser Thr Arg Asn Gly Lys
 115 120 125

Val Gly Val Ile Gly Thr Val Gly Thr Ile Asn Ser Gly Ala Tyr Gln
 130 135 140

Asp Leu Phe Ser Ala Ser Pro Ser Ile Val Val Asn Ala Val Ala Cys
 145 150 155 160

Pro Arg Phe Val Asp Phe Val Glu Arg Gly Ile Thr Ser Gly Arg Gln
 165 170 175

Ile Leu Asn Ile Ala Gln Asp Tyr Leu Glu Pro Leu Gln Ala Glu Gly
 180 185 190

Val Asp Thr Leu Val Leu Gly Cys Thr His Tyr Pro Leu Leu Ser Gly
 195 200 205

Val Ile Gln Leu Ala Met Gly Asp His Val Ser Leu Val Ser Ser Ala
 210 215 220

Glu Glu Thr Ala Lys Asp Val Leu Arg Ile Leu Ser Gln Gln Asp Leu
 225 230 235 240

Leu Ala Asp Pro Asp Met His Pro Glu Pro Ser Tyr Ser Phe Glu Ser
 245 250 255

Thr Gly Asp Pro Glu Ile Phe Ala Gln Leu Ser Arg Arg Phe Leu Gly
 260 265 270

Pro Ile Val Ser Gln Val Arg Gln Asn Glu Gly
 275 280

<210> 37
 <211> 1203
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1180)
 <223> RXN01022

<400> 37
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 taagaaggct gagtagtctt aggttgtaag cttcaatgct gtg agc aac tct aat 115
 Val Ser Asn Ser Asn
 1 5

tct gga aaa gtc cgc gtc gca gtc gtt tat ggt ggt cgc agt tct gag 163
 Ser Gly Lys Val Arg Val Ala Val Val Tyr Gly Gly Arg Ser Ser Glu
 10 15 20

cac tcc gtc tcc tgc gtc tcc gct ggt gct atc atg gcc cat ctc gat 211
 His Ser Val Ser Cys Val Ser Ala Gly Ala Ile Met Ala His Leu Asp
 25 30 35

cct gag aag tac gat gtg att ccc gtc ggc att act gtc gac ggc gcg 259
 Pro Glu Lys Tyr Asp Val Ile Pro Val Gly Ile Thr Val Asp Gly Ala
 40 45 50

tgg gtt gtt ggt gaa acc gat cca cag aag cta act ctc atc gat cgc 307
 Trp Val Val Gly Glu Thr Asp Pro Gln Lys Leu Thr Leu Ile Asp Arg
 55 60 65

acc atg cct gag gtg gag cat cat gaa gag gtt cgc cca agc ctg gat 355
 Thr Met Pro Glu Val Glu His His Glu Glu Val Arg Pro Ser Leu Asp
 70 75 80 85

ccc gca cac cgt gga gag ttc cac ttt tcc gat ggc agc ttg tat gcc 403
 Pro Ala His Arg Gly Glu Phe His Phe Ser Asp Gly Ser Leu Tyr Ala
 90 95 100

acc gct gat gtg att ttc cct gtg ctg cat ggt cgt ttt ggt gaa gac 451
 Thr Ala Asp Val Ile Phe Pro Val Leu His Gly Arg Phe Gly Glu Asp
 105 110 115

ggc act gtg cag ggt ctg ttt gca ctg tct gat att ccg gtc gtt ggc 499
 Gly Thr Val Gln Gly Leu Phe Ala Leu Ser Asp Ile Pro Val Val Gly
 120 125 130

cca ggt gtg ctg gcc tct gct gcg gga atg gac aag gaa tac act aag	547
Pro Gly Val Leu Ala Ser Ala Ala Gly Met Asp Lys Glu Tyr Thr Lys	
135 140 145	
aag ctc atg gca gcg gaa ggg ctg ccc gtt ggc cgt gag gtg att cta	595
Lys Leu Met Ala Ala Glu Gly Leu Pro Val Gly Arg Glu Val Ile Leu	
150 155 160 165	
cgt gat cgt acc gag ctg acc gag gca gaa aag aac ctg ctg ggc ctg	643
Arg Asp Arg Thr Glu Leu Thr Glu Ala Glu Lys Asn Leu Leu Gly Leu	
170 175 180	
cct gta ttt gtg aag cct gcg cgt ggt ggc tca tcg att ggt atc tct	691
Pro Val Phe Val Lys Pro Ala Arg Gly Gly Ser Ser Ile Gly Ile Ser	
185 190 195	
cgt gtt act gcg tgg gag gat ttt aat aag gct gtg ggg ctt gct cgt	739
Arg Val Thr Ala Trp Glu Asp Phe Asn Lys Ala Val Gly Leu Ala Arg	
200 205 210	
gcc cat gat gag aag gtc att gtg gaa tca gag atc gtt ggc tct gag	787
Ala His Asp Glu Lys Val Ile Val Glu Ser Glu Ile Val Gly Ser Glu	
215 220 225	
gtg gag tgt ggc gtg ctg cag tat cca gac ggt cgt atc gtg gcg tct	835
Val Glu Cys Gly Val Leu Gln Tyr Pro Asp Gly Arg Ile Val Ala Ser	
230 235 240 245	
gtt cct gcg ttg ctg tct ggc acc gaa tca ggc gct ggt gga ttc tat	883
Val Pro Ala Leu Leu Ser Gly Thr Glu Ser Gly Ala Gly Gly Phe Tyr	
250 255 260	
gac ttt gat acc aag tac ttg gac aac gtt gtt act gca gag atc cca	931
Asp Phe Asp Thr Lys Tyr Leu Asp Asn Val Val Thr Ala Glu Ile Pro	
265 270 275	
gca ccg ctt gat gag aag acc acg gaa ctg atc cag tct ttg gct gtg	979
Ala Pro Leu Asp Glu Lys Thr Thr Glu Leu Ile Gln Ser Leu Ala Val	
280 285 290	
gaa tct ttc cag gct ctt gcg tgt gaa ggc ctt gct cgc gtg gac ttc	1027
Glu Ser Phe Gln Ala Leu Ala Cys Glu Gly Leu Ala Arg Val Asp Phe	
295 300 305	
ttt gtt acc gcc aat ggt cct gtg ctc aat gag atc aac acc atg cca	1075
Phe Val Thr Ala Asn Gly Pro Val Leu Asn Glu Ile Asn Thr Met Pro	
310 315 320 325	
gga ttt acc ccc att tcc atg tac cca cag atg ttc act gca tca ggc	1123
Gly Phe Thr Pro Ile Ser Met Tyr Pro Gln Met Phe Thr Ala Ser Gly	
330 335 340	
gtg gct tat gag gaa ttg ttg gat gtg ttg gtg cag cag gca ttg cac	1171
Val Ala Tyr Glu Glu Leu Leu Asp Val Leu Val Gln Gln Ala Leu His	
345 350 355	
cgc gac aac tagcatcaaa taaaaacagc ccc	1203
Arg Asp Asn	
360	

<210> 38
 <211> 360
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 38

Val Ser Asn Ser Asn Ser Gly Lys Val Arg Val Ala Val Val Tyr Gly
 1 5 10 15

Gly Arg Ser Ser Glu His Ser Val Ser Cys Val Ser Ala Gly Ala Ile
 20 25 30

Met Ala His Leu Asp Pro Glu Lys Tyr Asp Val Ile Pro Val Gly Ile
 35 40 45

Thr Val Asp Gly Ala Trp Val Val Gly Glu Thr Asp Pro Gln Lys Leu
 50 55 60

Thr Leu Ile Asp Arg Thr Met Pro Glu Val Glu His His Glu Glu Val
 65 70 75 80

Arg Pro Ser Leu Asp Pro Ala His Arg Gly Glu Phe His Phe Ser Asp
 85 90 95

Gly Ser Leu Tyr Ala Thr Ala Asp Val Ile Phe Pro Val Leu His Gly
 100 105 110

Arg Phe Gly Glu Asp Gly Thr Val Gln Gly Leu Phe Ala Leu Ser Asp
 115 120 125

Ile Pro Val Val Gly Pro Gly Val Leu Ala Ser Ala Ala Gly Met Asp
 130 135 140

Lys Glu Tyr Thr Lys Lys Leu Met Ala Ala Glu Gly Leu Pro Val Gly
 145 150 155 160

Arg Glu Val Ile Leu Arg Asp Arg Thr Glu Leu Thr Glu Ala Glu Lys
 165 170 175

Asn Leu Leu Gly Leu Pro Val Phe Val Lys Pro Ala Arg Gly Gly Ser
 180 185 190

Ser Ile Gly Ile Ser Arg Val Thr Ala Trp Glu Asp Phe Asn Lys Ala
 195 200 205

Val Gly Leu Ala Arg Ala His Asp Glu Lys Val Ile Val Glu Ser Glu
 210 215 220

Ile Val Gly Ser Glu Val Glu Cys Gly Val Leu Gln Tyr Pro Asp Gly
 225 230 235 240

Arg Ile Val Ala Ser Val Pro Ala Leu Leu Ser Gly Thr Glu Ser Gly
 245 250 255

Ala Gly Gly Phe Tyr Asp Phe Asp Thr Lys Tyr Leu Asp Asn Val Val
 260 265 270

Thr Ala Glu Ile Pro Ala Pro Leu Asp Glu Lys Thr Thr Glu Leu Ile
 275 280 285

Gln Ser Leu Ala Val Glu Ser Phe Gln Ala Leu Ala Cys Glu Gly Leu
 290 295 300

Ala Arg Val Asp Phe Phe Val Thr Ala Asn Gly Pro Val Leu Asn Glu
 305 310 315 320

Ile Asn Thr Met Pro Gly Phe Thr Pro Ile Ser Met Tyr Pro Gln Met
 325 330 335

Phe Thr Ala Ser Gly Val Ala Tyr Glu Glu Leu Leu Asp Val Leu Val
 340 345 350

Gln Gln Ala Leu His Arg Asp Asn
 355 360

<210> 39
 <211> 827
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(804)
 <223> FRXA01022

<400> 39
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 His Phe Ser Asp Gly Ser Leu Tyr Ala Thr Ala Asp Val Ile Phe Pro
 1 5 10 15

gtg ctg cat ggt cgt ttt ggt gaa gac ggc act gtg cag ggt ctg ttt 96
 Val Leu His Gly Arg Phe Gly Glu Asp Gly Thr Val Gln Gly Leu Phe
 20 25 30

gca ctg tct gat att ccg gtc gtt ggc cca ggt gtg ctg gcc tct gct 144
 Ala Leu Ser Asp Ile Pro Val Val Gly Pro Gly Val Leu Ala Ser Ala
 35 40 45

gcg gga atg gac aag gaa tac act aag aag ctc atg gca gcg gaa ggg 192
 Ala Gly Met Asp Lys Glu Tyr Thr Lys Lys Leu Met Ala Ala Glu Gly
 50 55 60

ctg ccc gtt ggc cgt gag gtg att cta cgt gat cgt acc gag ctg acc 240
 Leu Pro Val Gly Arg Glu Val Ile Leu Arg Asp Arg Thr Glu Leu Thr
 65 70 75 80

gag gca gaa aag aac ctg ctg ggc ctg cct gta ttt gtg aag cct gcg 288
 Glu Ala Glu Lys Asn Leu Leu Gly Leu Pro Val Phe Val Lys Pro Ala
 85 90 95

cgt ggt ggc tca tcg att ggt atc tct cgt gtt act gcg tgg gag gat 336
 Arg Gly Gly Ser Ser Ile Gly Ile Ser Arg Val Thr Ala Trp Glu Asp
 100 105 110

ttt aat aag gct gtg ggg ctt gct cgt gcc cat gat gag aag gtc att 384
 Phe Asn Lys Ala Val Gly Leu Ala Arg Ala His Asp Glu Lys Val Ile
 115 120 125

gtg gaa tca gag atc gtt ggc tct gag gtg gag tgt ggc gtg ctg cag 432
 Val Glu Ser Glu Ile Val Gly Ser Glu Val Glu Cys Gly Val Leu Gln

130	135	140	
tat cca gac ggt cgt atc gtg gcg tct gtt cct gcg ttg ctg tct ggc			480
Tyr Pro Asp Gly Arg Ile Val Ala Ser Val Pro Ala Leu Leu Ser Gly			
145	150	155	160
acc gaa tca ggc gct ggt gga ttc tat gac ttt gat acc aag tac ttg			528
Thr Glu Ser Gly Ala Gly Gly Phe Tyr Asp Phe Asp Thr Lys Tyr Leu			
	165	170	175
gac aac gtt gtt act gca gag atc cca gca ccg ctt gat gag aag acc			576
Asp Asn Val Val Thr Ala Glu Ile Pro Ala Pro Leu Asp Glu Lys Thr			
	180	185	190
acg gaa ctg atc cag tct ttg gct gtg gaa tct ttc cag gct ctt gcg			624
Thr Glu Leu Ile Gln Ser Leu Ala Val Glu Ser Phe Gln Ala Leu Ala			
	195	200	205
tgt gaa ggc ctt gct cgc gtg gac ttc ttt gtt acc gcc aat ggt cct			672
Cys Glu Gly Leu Ala Arg Val Asp Phe Phe Val Thr Ala Asn Gly Pro			
	210	215	220
gtg ctc aat gag atc aac acc atg cca gga ttt acc ccc att tcc atg			720
Val Leu Asn Glu Ile Asn Thr Met Pro Gly Phe Thr Pro Ile Ser Met			
	225	230	235
tac cca cag atg ttc act gca tca ggc gtg gct tat gag gaa ttg ttg			768
Tyr Pro Gln Met Phe Thr Ala Ser Gly Val Ala Tyr Glu Glu Leu Leu			
	245	250	255
gat gtg ttg gtg cag cag gca ttg cac cgc gac aac tagcatcaaa			814
Asp Val Leu Val Gln Gln Ala Leu His Arg Asp Asn			
	260	265	
taaaaacagc ccc			827

<210> 40
 <211> 268
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 40
 His Phe Ser Asp Gly Ser Leu Tyr Ala Thr Ala Asp Val Ile Phe Pro
 1 5 10 15
 Val Leu His Gly Arg Phe Gly Glu Asp Gly Thr Val Gln Gly Leu Phe
 20 25 30
 Ala Leu Ser Asp Ile Pro Val Val Gly Pro Gly Val Leu Ala Ser Ala
 35 40 45
 Ala Gly Met Asp Lys Glu Tyr Thr Lys Lys Leu Met Ala Ala Glu Gly
 50 55 60
 Leu Pro Val Gly Arg Glu Val Ile Leu Arg Asp Arg Thr Glu Leu Thr
 65 70 75 80
 Glu Ala Glu Lys Asn Leu Leu Gly Leu Pro Val Phe Val Lys Pro Ala
 85 90 95

Arg Gly Gly Ser Ser Ile Gly Ile Ser Arg Val Thr Ala Trp Glu Asp
 100 105 110

Phe Asn Lys Ala Val Gly Leu Ala Arg Ala His Asp Glu Lys Val Ile
 115 120 125

Val Glu Ser Glu Ile Val Gly Ser Glu Val Glu Cys Gly Val Leu Gln
 130 135 140

Tyr Pro Asp Gly Arg Ile Val Ala Ser Val Pro Ala Leu Leu Ser Gly
 145 150 155 160

Thr Glu Ser Gly Ala Gly Gly Phe Tyr Asp Phe Asp Thr Lys Tyr Leu
 165 170 175

Asp Asn Val Val Thr Ala Glu Ile Pro Ala Pro Leu Asp Glu Lys Thr
 180 185 190

Thr Glu Leu Ile Gln Ser Leu Ala Val Glu Ser Phe Gln Ala Leu Ala
 195 200 205

Cys Glu Gly Leu Ala Arg Val Asp Phe Phe Val Thr Ala Asn Gly Pro
 210 215 220

Val Leu Asn Glu Ile Asn Thr Met Pro Gly Phe Thr Pro Ile Ser Met
 225 230 235 240

Tyr Pro Gln Met Phe Thr Ala Ser Gly Val Ala Tyr Glu Glu Leu Leu
 245 250 255

Asp Val Leu Val Gln Gln Ala Leu His Arg Asp Asn
 260 265

<210> 41
 <211> 1212
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1189)
 <223> RXA02703

<400> 41
 caaagcaggc ctaccgagcg ccgttccgag agtcgcgcga tgattggcgt gacaaccgca 60

accgcagata aatgtgaaat caggagaact acgaataaag atg gct aac tcc cca 115
 Met Ala Asn Ser Pro
 1 5

aaa ccc atg cgg gtt gtc gtt gct ggt ggc ggt acc gca gga cat att 163
 Lys Pro Met Arg Val Val Val Ala Gly Gly Gly Thr Ala Gly His Ile
 10 15 20

gag cct gcg ttg gca gtg gct gaa gcg ctg cgc gat aag cac ggt gca 211
 Glu Pro Ala Leu Ala Val Ala Glu Ala Leu Arg Asp Lys His Gly Ala
 25 30 35

aca gtt tcg gct tta ggt act gct cgt ggt ttg gaa aca acc ctg gtg 259
 Thr Val Ser Ala Leu Gly Thr Ala Arg Gly Leu Glu Thr Thr Leu Val

40	45	50	
cct gat cgt ggg ttt gag ctt cat ctc atc gag ccg gtt cca gtc cca Pro Asp Arg Gly Phe Glu Leu His Leu Ile Glu Pro Val Pro Val Pro 55 60 65			307
cgc aag ccc aat atg gat ttg ttg aag ctc cca ttc cgg gta gct aag Arg Lys Pro Asn Met Asp Leu Leu Lys Leu Pro Phe Arg Val Ala Lys 70 75 80 85			355
gca tta ggc caa gca cgc aag gca ctg aag gac aca gac gct caa gcg Ala Leu Gly Gln Ala Arg Lys Ala Leu Lys Asp Thr Asp Ala Gln Ala 90 95 100			403
gtc atc ggc ttt ggc ggt tat gta tct gct ccg gct tat atg gcg gcg Val Ile Gly Phe Gly Gly Tyr Val Ser Ala Pro Ala Tyr Met Ala Ala 105 110 115			451
aag tct ttg ggc ttg cca ttt ttt gtc cac gaa gcc aac gcc cgt gca Lys Ser Leu Gly Leu Pro Phe Phe Val His Glu Ala Asn Ala Arg Ala 120 125 130			499
ggc atg gcc aac aaa ttg ggc gtc aag ctc ggt ggc gtt ggc ctt aat Gly Met Ala Asn Lys Leu Gly Val Lys Leu Gly Gly Val Gly Leu Asn 135 140 145			547
gct gtt gct ggt tcc ggc atg gac ggc gac gtg gtg ggc att ccg att Ala Val Ala Gly Ser Gly Met Asp Gly Asp Val Val Gly Ile Pro Ile 150 155 160 165			595
cgt gct gtt tta agt ggc gcg cgg gat gag tcc gca gct gac cga gcc Arg Ala Val Leu Ser Gly Ala Arg Asp Glu Ser Ala Ala Asp Arg Ala 170 175 180			643
agg gac act tgg ggt ttg gac aag gac cgc caa acc att ttt gtc acc Arg Asp Thr Trp Gly Leu Asp Lys Asp Arg Gln Thr Ile Phe Val Thr 185 190 195			691
ggt ggt tcg cag ggc tct gtg agt atc aac aag gcc gtc gag caa gct Gly Gly Ser Gln Gly Ser Val Ser Ile Asn Lys Ala Val Glu Gln Ala 200 205 210			739
gta gat cag ctg gtg gag gca ggt ttc cag gtg ctc cac gcc gtg ggt Val Asp Gln Leu Val Glu Ala Gly Phe Gln Val Leu His Ala Val Gly 215 220 225			787
aag aaa aac gag ttg cct gca gcg aaa ccc ggc tac cat ccc gtt ccg Lys Lys Asn Glu Leu Pro Ala Ala Lys Pro Gly Tyr His Pro Val Pro 230 235 240 245			835
ttt atc gac gat atg cag gct gcc tac acc gtt gct gat ctt atc gtg Phe Ile Asp Asp Met Gln Ala Ala Tyr Thr Val Ala Asp Leu Ile Val 250 255 260			883
tgc cgc tcc ggc gcg atg acg gtt gca gag gtc acc gcc gcc gcc gtc Cys Arg Ser Gly Ala Met Thr Val Ala Glu Val Thr Ala Ala Gly Val 265 270 275			931
ccc gcg att tat gtc ccg ctg cct cac ggc aac ggt gag cag gct ctc Pro Ala Ile Tyr Val Pro Leu Pro His Gly Asn Gly Glu Gln Ala Leu 280 285 290			979

aac gcc cag gct gtc att aaa gct ggt gcc gca cgc cag atc gac gac 1027
 Asn Ala Gln Ala Val Ile Lys Ala Gly Ala Ala Arg Gln Ile Asp Asp
 295 300 305

 gcg gac ttc acc gcc cag acg ctt atc gac gcc acc ctt gac att ctc 1075
 Ala Asp Phe Thr Ala Gln Thr Leu Ile Asp Ala Thr Leu Asp Ile Leu
 310 315 320 325

 ctt cat ccc tcc aca cac caa tcg atg tcg gac gca gct aaa acc tcc 1123
 Leu His Pro Ser Thr His Gln Ser Met Ser Asp Ala Ala Lys Thr Ser
 330 335 340

 acc gca ggt aac gcc tcc acg gtg att gca gac atg att gct gca act 1171
 Thr Ala Gly Asn Ala Ser Thr Val Ile Ala Asp Met Ile Ala Ala Thr
 345 350 355

 atc aat agc caa cac aac taaaacgacc agctcaacgc aaa 1212
 Ile Asn Ser Gln His Asn
 360

<210> 42
 <211> 363
 <212> PRT
 <213> Corynebacterium glutamicum.

<400> 42
 Met Ala Asn Ser Pro Lys Pro Met Arg Val Val Val Ala Gly Gly Gly
 1 5 10 15

 Thr Ala Gly His Ile Glu Pro Ala Leu Ala Val Ala Glu Ala Leu Arg
 20 25 30

 Asp Lys His Gly Ala Thr Val Ser Ala Leu Gly Thr Ala Arg Gly Leu
 35 40 45

 Glu Thr Thr Leu Val Pro Asp Arg Gly Phe Glu Leu His Leu Ile Glu
 50 55 60

 Pro Val Pro Val Pro Arg Lys Pro Asn Met Asp Leu Leu Lys Leu Pro
 65 70 75 80

 Phe Arg Val Ala Lys Ala Leu Gly Gln Ala Arg Lys Ala Leu Lys Asp
 85 90 95

 Thr Asp Ala Gln Ala Val Ile Gly Phe Gly Gly Tyr Val Ser Ala Pro
 100 105 110

 Ala Tyr Met Ala Ala Lys Ser Leu Gly Leu Pro Phe Phe Val His Glu
 115 120 125

 Ala Asn Ala Arg Ala Gly Met Ala Asn Lys Leu Gly Val Lys Leu Gly
 130 135 140

~~Gly Val Gly Leu Asn Ala Val Ala Gly Ser Gly Met Asp Gly Asp Val~~
~~145 150 155 160~~

 Val Gly Ile Pro Ile Arg Ala Val Leu Ser Gly Ala Arg Asp Glu Ser
 165 170 175

Ala Ala Asp Arg Ala Arg Asp Thr Trp Gly Leu Asp Lys Asp Arg Gln
 180 185 190

Thr Ile Phe Val Thr Gly Gly Ser Gln Gly Ser Val Ser Ile Asn Lys
 195 200 205

Ala Val Glu Gln Ala Val Asp Gln Leu Val Glu Ala Gly Phe Gln Val
 210 215 220

Leu His Ala Val Gly Lys Lys Asn Glu Leu Pro Ala Ala Lys Pro Gly
 225 230 235 240

Tyr His Pro Val Pro Phe Ile Asp Asp Met Gln Ala Ala Tyr Thr Val
 245 250 255

Ala Asp Leu Ile Val Cys Arg Ser Gly Ala Met Thr Val Ala Glu Val
 260 265 270

Thr Ala Ala Gly Val Pro Ala Ile Tyr Val Pro Leu Pro His Gly Asn
 275 280 285

Gly Glu Gln Ala Leu Asn Ala Gln Ala Val Ile Lys Ala Gly Ala Ala
 290 295 300

Arg Gln Ile Asp Asp Ala Asp Phe Thr Ala Gln Thr Leu Ile Asp Ala
 305 310 315 320

Thr Leu Asp Ile Leu Leu His Pro Ser Thr His Gln Ser Met Ser Asp
 325 330 335

Ala Ala Lys Thr Ser Thr Ala Gly Asn Ala Ser Thr Val Ile Ala Asp
 340 345 350

Met Ile Ala Ala Thr Ile Asn Ser Gln His Asn
 355 360

<210> 43
 <211> 2235
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(2212)
 <223> RXA02711

<400> 43
 aaaacctcca ggcgattcca caagaagcag cagctccgcc gtatcagacc aacctgttc 60

cttatgctgc aaccaccgga caagcaggtg gcgcagggca gtg act ttc ccc agc 115
 Val Thr Phe Pro Ser
 1 5

aat ggc aga agt cgg ggc gag cgt gcg gga cgt gaa gat acg tcc cgc 163
 Asn Gly Arg Ser Arg Gly Glu Arg Ala Gly Arg Glu Asp Thr Ser Arg
 10 15 20

cgt tcg gcg tat cag gac gaa agc aga aga gcc gct aga gag cgc gaa 211
 Arg Ser Ala Tyr Gln Asp Glu Ser Arg Arg Ala Ala Arg Glu Arg Glu
 25 30 35

ctt	acg	cga	cgc	agc	ggg	aaa	gct	aaa	ggc	gta	aac	caa	gaa	gaa	gga	259
Leu	Thr	Arg	Arg	Ser	Gly	Lys	Ala	Lys	Gly	Val	Asn	Gln	Glu	Glu	Gly	
		40					45					50				
gtg	acc	tac	cgg	cct	aaa	tct	tca	acc	cag	ggc	ggc	gca	cgc	aag	cga	307
Val	Thr	Tyr	Arg	Pro	Lys	Ser	Ser	Thr	Gln	Gly	Gly	Ala	Arg	Lys	Arg	
	55					60					65					
cgt	gtg	aac	atg	gtt	acc	gct	atc	gca	ttg	gtc	atc	gct	ggc	gta	ctg	355
Arg	Val	Asn	Met	Val	Thr	Ala	Ile	Ala	Leu	Val	Ile	Ala	Gly	Val	Leu	
	70					75				80					85	
atc	att	cgc	ctc	ggc	tgg	gtc	caa	gtt	gtc	tgg	gga	cca	gaa	ctg	tcc	403
Ile	Ile	Arg	Leu	Gly	Trp	Val	Gln	Val	Val	Trp	Gly	Pro	Glu	Leu	Ser	
				90					95					100		
ctc	aat	gct	tgc	gaa	cag	cgc	acc	cgc	gtg	tac	gta	gat	cct	gca	cgt	451
Leu	Asn	Ala	Ser	Glu	Gln	Arg	Thr	Arg	Val	Tyr	Val	Asp	Pro	Ala	Arg	
			105					110					115			
cgt	gga	agc	atc	gtg	gac	cgc	gaa	gga	aac	cag	atg	gcg	tac	acg	atg	499
Arg	Gly	Ser	Ile	Val	Asp	Arg	Glu	Gly	Asn	Gln	Met	Ala	Tyr	Thr	Met	
		120					125					130				
cag	gca	cgt	tgc	ctg	acg	gtt	tct	ccg	aac	atc	atg	cgt	gag	gaa	tta	547
Gln	Ala	Arg	Ser	Leu	Thr	Val	Ser	Pro	Asn	Ile	Met	Arg	Glu	Glu	Leu	
	135					140					145					
aag	acc	gga	act	gat	ttg	gcc	ttg	cgt	ttg	gcg	gct	gaa	gaa	acc	gat	595
Lys	Thr	Gly	Thr	Asp	Leu	Ala	Leu	Arg	Leu	Ala	Ala	Glu	Glu	Thr	Asp	
	150				155					160					165	
ccg	gaa	aac	gtg	gcc	agc	tat	gtg	acc	atc	gaa	gaa	ggc	aac	gcg	tat	643
Pro	Glu	Asn	Val	Ala	Ser	Tyr	Val	Thr	Ile	Glu	Glu	Gly	Asn	Ala	Tyr	
				170					175					180		
gtt	ttt	gcg	tct	gaa	gaa	cag	cgc	gaa	acc	att	ctg	tcc	gac	aag	gta	691
Val	Phe	Ala	Ser	Glu	Glu	Gln	Arg	Glu	Thr	Ile	Leu	Ser	Asp	Lys	Val	
			185					190					195			
gaa	gag	cgc	att	caa	agc	att	gcg	gat	cgg	atc	cct	gag	atc	atc	aaa	739
Glu	Glu	Arg	Ile	Gln	Ser	Ile	Ala	Asp	Arg	Ile	Pro	Glu	Ile	Ile	Lys	
		200					205					210				
tcc	cat	gac	caa	gat	gtc	act	gga	att	tcc	tct	gag	gag	atc	ctg	gac	787
Ser	His	Asp	Gln	Asp	Val	Thr	Gly	Ile	Ser	Ser	Glu	Glu	Ile	Leu	Asp	
	215					220					225					
aag	ctc	aat	gct	gat	agc	cag	tat	gag	gtg	ctc	gtc	cgc	aat	gtt	gat	835
Lys	Leu	Asn	Ala	Asp	Ser	Gln	Tyr	Glu	Val	Leu	Val	Arg	Asn	Val	Asp	
	230				235					240					245	
ccc	gat	gta	gcg	tca	gaa	atc	acc	gat	gag	atg	ccc	agc	gtc	gca	gct	883
Pro	Asp	Val	Ala	Ser	Glu	Ile	Thr	Asp	Glu	Met	Pro	Ser	Val	Ala	Ala	
				250					255				260			
gat	cat	caa	gac	atc	cgc	caa	tac	cca	aac	ggc	gcg	att	ggg	gaa	aac	931
Asp	His	Gln	Asp	Ile	Arg	Gln	Tyr	Pro	Asn	Gly	Ala	Ile	Gly	Glu	Asn	
			265				270						275			

atc atc ggt cga atc agc atg gac ggc gaa ggc cag ttc ggc ttt gag	979
Ile Ile Gly Arg Ile Ser Met Asp Gly Glu Gly Gln Phe Gly Phe Glu	
280 285 290	
gct tcc aac gat tcc ctg ttg gca gga aac aac ggt cgc tca acc cag	1027
Ala Ser Asn Asp Ser Leu Leu Ala Gly Asn Asn Gly Arg Ser Thr Gln	
295 300 305	
gac atg tcc att ttg gga caa gca ata ccg ggc acg ttg agg gat caa	1075
Asp Met Ser Ile Leu Gly Gln Ala Ile Pro Gly Thr Leu Arg Asp Gln	
310 315 320 325	
att cca gcc att gat ggt gcc agc gtt gaa ctc acc gtt gat ctg gat	1123
Ile Pro Ala Ile Asp Gly Ala Ser Val Glu Leu Thr Val Asp Leu Asp	
330 335 340	
ctg caa acc tat gtg cag cag gca ttg gag cag gcg aaa gct aac tcc	1171
Leu Gln Thr Tyr Val Gln Gln Ala Leu Glu Gln Ala Lys Ala Asn Ser	
345 350 355	
ggg gca gaa aac gcc tcc gct gtg gtt ctt gat gcc aag acc gct gag	1219
Gly Ala Glu Asn Ala Ser Ala Val Val Leu Asp Ala Lys Thr Ala Glu	
360 365 370	
gtt ttg gcg atg gca aac acc gat acc atc aac ccc aac gaa gac acg	1267
Val Leu Ala Met Ala Asn Thr Asp Thr Ile Asn Pro Asn Glu Asp Thr	
375 380 385	
gga aag cag att gag cag ggc aag agc ttt gac aat cct tct gtc acc	1315
Gly Lys Gln Ile Glu Gln Gly Lys Ser Phe Asp Asn Pro Ser Val Thr	
390 395 400 405	
cac ccc ttc gag cct ggt tct gta gcc aag gtg att act gca gca ggc	1363
His Pro Phe Glu Pro Gly Ser Val Ala Lys Val Ile Thr Ala Ala Gly	
410 415 420	
gta att caa gag ggc ttg act act cca gat gaa gtg ttg cag gta ccg	1411
Val Ile Gln Glu Gly Leu Thr Thr Pro Asp Glu Val Leu Gln Val Pro	
425 430 435	
ggc agt att gaa atg gcc ggt gtt tct gtc ggt gat gcg tgg gac cac	1459
Gly Ser Ile Glu Met Ala Gly Val Ser Val Gly Asp Ala Trp Asp His	
440 445 450	
ggg gtc gtt ccc tac acc act gca gga att ttt ggt aag tcc tcg aat	1507
Gly Val Val Pro Tyr Thr Thr Ala Gly Ile Phe Gly Lys Ser Ser Asn	
455 460 465	
gta ggc act ctg atg ctt gcg cag cgt ctt ggt gaa gat aaa ttt gct	1555
Val Gly Thr Leu Met Leu Ala Gln Arg Leu Gly Glu Asp Lys Phe Ala	
470 475 480 485	
gat tac ctg gaa cga ttc ggt gtg gga cag cca acg ggt att gag ctt	1603
Asp Tyr Leu Glu Arg Phe Gly Val Gly Gln Pro Thr Gly Ile Glu Leu	
490 495 500	
ccg agc gaa tcc caa ggc ctg ctg ccc gca cgt gag cag tgg tct ggc	1651
Pro Ser Glu Ser Gln Gly Leu Leu Pro Ala Arg Glu Gln Trp Ser Gly	
505 510 515	
ggg act ttt gct aac ctg ccc atc ggt cag ggt atg tcg atc acc acg	1699

Gly Thr Phe Ala Asn Leu Pro Ile Gly Gln Gly Met Ser Ile Thr Thr
 520 525 530
 ttg caa atg gct gga atc tac caa gcc ttg gcc aac gat ggt gaa cgc 1747
 Leu Gln Met Ala Gly Ile Tyr Gln Ala Leu Ala Asn Asp Gly Glu Arg
 535 540 545
 att caa ccg cgg atc atc aag agc gtg act gat tct gac gga aca gtc 1795
 Ile Gln Pro Arg Ile Ile Lys Ser Val Thr Asp Ser Asp Gly Thr Val
 550 555 560 565
 cta gag cag cca gaa ccc gat aaa atc cag gtt gtc agc gct gaa gct 1843
 Leu Glu Gln Pro Glu Pro Asp Lys Ile Gln Val Val Ser Ala Glu Ala
 570 575 580
 gcc cgc acc acg gtg gat atg ttt agg tct gtc acc cag gtt gat cca 1891
 Ala Arg Thr Thr Val Asp Met Phe Arg Ser Val Thr Gln Val Asp Pro
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 act gga gtg caa caa ggt acc gct cca gac gcc tcc att gag ggt tat 1939
 Thr Gly Val Gln Gln Gly Thr Ala Pro Asp Ala Ser Ile Glu Gly Tyr
 600 605 610
 caa atc tca ggt aag aca ggt acg gcg cag aaa gtt gac ccc aac acg 1987
 Gln Ile Ser Gly Lys Thr Gly Thr Ala Gln Lys Val Asp Pro Asn Thr
 615 620 625
 ggc gcg tac tct aac tcg caa tac tgg att acc ttc gcg ggt att gca 2035
 Gly Ala Tyr Ser Asn Ser Gln Tyr Trp Ile Thr Phe Ala Gly Ile Ala
 630 635 640 645
 ccc gct gat gat cct cga ttt gtt gta gcc atc atg ctt gat gag cca 2083
 Pro Ala Asp Asp Pro Arg Phe Val Val Ala Ile Met Leu Asp Glu Pro
 650 655 660
 gaa cgc gga gtc cac ggt ggt ggc ggc caa acc gca gca cct ttg ttc 2131
 Glu Arg Gly Val His Gly Gly Gly Gln Thr Ala Ala Pro Leu Phe
 665 670 675
 aaa gac atc gcc acc tgg ttg ctc aac cgc gac aac atc cca ctg tct 2179
 Lys Asp Ile Ala Thr Trp Leu Leu Asn Arg Asp Asn Ile Pro Leu Ser
 680 685 690
 gca gcc acc gaa ccg atc atc ctt caa gct caa taactcaaac agaagtgtct 2232
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 ttt 2235

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<211> 704

<212> PRT

<213> Corynebacterium glutamicum

<400> 44

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Ala Arg Glu Arg Glu Leu Thr Arg Arg Ser Gly Lys Ala Lys Gly Val
35 40 45

Asn Gln Glu Glu Gly Val Thr Tyr Arg Pro Lys Ser Ser Thr Gln Gly
50 55 60

Gly Ala Arg Lys Arg Arg Val Asn Met Val Thr Ala Ile Ala Leu Val
65 70 75 80

Ile Ala Gly Val Leu Ile Ile Arg Leu Gly Trp Val Gln Val Val Trp
85 90 95

Gly Pro Glu Leu Ser Leu Asn Ala Ser Glu Gln Arg Thr Arg Val Tyr
100 105 110

Val Asp Pro Ala Arg Arg Gly Ser Ile Val Asp Arg Glu Gly Asn Gln
115 120 125

Met Ala Tyr Thr Met Gln Ala Arg Ser Leu Thr Val Ser Pro Asn Ile
130 135 140

Met Arg Glu Glu Leu Lys Thr Gly Thr Asp Leu Ala Leu Arg Leu Ala
145 150 155 160

Ala Glu Glu Thr Asp Pro Glu Asn Val Ala Ser Tyr Val Thr Ile Glu
165 170 175

Glu Gly Asn Ala Tyr Val Phe Ala Ser Glu Glu Gln Arg Glu Thr Ile
180 185 190

Leu Ser Asp Lys Val Glu Glu Arg Ile Gln Ser Ile Ala Asp Arg Ile
195 200 205

Pro Glu Ile Ile Lys Ser His Asp Gln Asp Val Thr Gly Ile Ser Ser
210 215 220

Glu Glu Ile Leu Asp Lys Leu Asn Ala Asp Ser Gln Tyr Glu Val Leu
225 230 235 240

Val Arg Asn Val Asp Pro Asp Val Ala Ser Glu Ile Thr Asp Glu Met
245 250 255

Pro Ser Val Ala Ala Asp His Gln Asp Ile Arg Gln Tyr Pro Asn Gly
260 265 270

Ala Ile Gly Glu Asn Ile Ile Gly Arg Ile Ser Met Asp Gly Glu Gly
275 280 285

Gln Phe Gly Phe Glu Ala Ser Asn Asp Ser Leu Leu Ala Gly Asn Asn
290 295 300

Gly Arg Ser Thr Gln Asp Met Ser Ile Leu Gly Gln Ala Ile Pro Gly
305 310 315 320

~~Thr Leu Arg Asp Gln Ile Pro Ala Ile Asp Gly Ala Ser Val Glu Leu~~
325 330 335

Thr Val Asp Leu Asp Leu Gln Thr Tyr Val Gln Gln Ala Leu Glu Gln
340 345 350

Ala Lys Ala Asn Ser Gly Ala Glu Asn Ala Ser Ala Val Val Leu Asp
 355 360 365
 Ala Lys Thr Ala Glu Val Leu Ala Met Ala Asn Thr Asp Thr Ile Asn
 370 375 380
 Pro Asn Glu Asp Thr Gly Lys Gln Ile Glu Gln Gly Lys Ser Phe Asp
 385 390 395 400
 Asn Pro Ser Val Thr His Pro Phe Glu Pro Gly Ser Val Ala Lys Val
 405 410 415
 Ile Thr Ala Ala Gly Val Ile Gln Glu Gly Leu Thr Thr Pro Asp Glu
 420 425 430
 Val Leu Gln Val Pro Gly Ser Ile Glu Met Ala Gly Val Ser Val Gly
 435 440 445
 Asp Ala Trp Asp His Gly Val Val Pro Tyr Thr Thr Ala Gly Ile Phe
 450 455 460
 Gly Lys Ser Ser Asn Val Gly Thr Leu Met Leu Ala Gln Arg Leu Gly
 465 470 475 480
 Glu Asp Lys Phe Ala Asp Tyr Leu Glu Arg Phe Gly Val Gly Gln Pro
 485 490 495
 Thr Gly Ile Glu Leu Pro Ser Glu Ser Gln Gly Leu Leu Pro Ala Arg
 500 505 510
 Glu Gln Trp Ser Gly Gly Thr Phe Ala Asn Leu Pro Ile Gly Gln Gly
 515 520 525
 Met Ser Ile Thr Thr Leu Gln Met Ala Gly Ile Tyr Gln Ala Leu Ala
 530 535 540
 Asn Asp Gly Glu Arg Ile Gln Pro Arg Ile Ile Lys Ser Val Thr Asp
 545 550 555 560
 Ser Asp Gly Thr Val Leu Glu Gln Pro Glu Pro Asp Lys Ile Gln Val
 565 570 575
 Val Ser Ala Glu Ala Ala Arg Thr Thr Val Asp Met Phe Arg Ser Val
 580 585 590
 Thr Gln Val Asp Pro Thr Gly Val Gln Gln Gly Thr Ala Pro Asp Ala
 595 600 605
 Ser Ile Glu Gly Tyr Gln Ile Ser Gly Lys Thr Gly Thr Ala Gln Lys
 610 615 620
 Val Asp Pro Asn Thr Gly Ala Tyr Ser Asn Ser Gln Tyr Trp Ile Thr
 625 630 635 640
 Phe Ala Gly Ile Ala Pro Ala Asp Asp Pro Arg Phe Val Val Ala Ile
 645 650 655
 Met Leu Asp Glu Pro Glu Arg Gly Val His Gly Gly Gly Gly Gln Thr
 660 665 670
 Ala Ala Pro Leu Phe Lys Asp Ile Ala Thr Trp Leu Leu Asn Arg Asp

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Asn Ile Pro Leu Ser Ala	Ala Thr Glu Pro Ile	Ile Leu Gln Ala Gln
690	695	700

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 <223> RXA02859

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Gln Tyr Thr Val Asp Gln Leu Leu His Gly Leu Leu Leu Ala Ser Gly	
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aac gat gcg gcg tat ctg ttg gct cag gaa ctt ggt ggg gat caa gca	96
Asn Asp Ala Ala Tyr Leu Leu Ala Gln Glu Leu Gly Gly Asp Gln Ala	
20 25 30	
acc ctg gag aaa gta aac gcg ctg gcc aag gag ttg ggc act caa gac	144
Thr Leu Glu Lys Val Asn Ala Leu Ala Lys Glu Leu Gly Thr Gln Asp	
35 40 45	
acc ttc gtt gcc act tat tcc ggt ttg gat gcg ccg gga atg tcg acc	192
Thr Phe Val Ala Thr Tyr Ser Gly Leu Asp Ala Pro Gly Met Ser Thr	
50 55 60	
tcc gca tac gac atg tca ttg att tat cag cat gcg tgg cag aac ccg	240
Ser Ala Tyr Asp Met Ser Leu Ile Tyr Gln His Ala Trp Gln Asn Pro	
65 70 75 80	
gtt ttc gag tcg att atc tcc acc gat cac att gat ttc cct ggt tgg	288
Val Phe Glu Ser Ile Ile Ser Thr Asp His Ile Asp Phe Pro Gly Trp	
85 90 95	
ggc gac aat gag ggt ttc caa gtc tgg aac gat aac gcc ttg ttc atg	336
Gly Asp Asn Glu Gly Phe Gln Val Trp Asn Asp Asn Ala Leu Phe Met	
100 105 110	
aac gat cct gat ggc atc ggc ggc aag acc ggc tac acc gac gac gcg	384
Asn Asp Pro Asp Gly Ile Gly Gly Lys Thr Gly Tyr Thr Asp Asp Ala	
115 120 125	
aac cac acc ttt gtc ggc ggt ctc gat cgg ggt ggt cgc cgc ctc gcc	432
Asn His Thr Phe Val Gly Gly Leu Asp Arg Gly Gly Arg Arg Leu Ala	
130 135 140	
gcc gta ctc ttg gat tcc acc gtc agc gac att cgt ccg tgg gaa caa	480
Ala Val Leu Leu Asp Ser Thr Val Ser Asp Ile Arg Pro Trp Glu Gln	
145 150 155 160	
gca cga ttg ctt atc gac gcc tcc ctc ccc atc acg ccg ggg tcc ggc	528
Ala Arg Leu Leu Ile Asp Ala Ser Leu Pro Ile Thr Pro Gly Ser Gly	
165 170 175	

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gtg ggc cag ctg ggc tcc ggc agc gcg aac gat gtg gca ccg gcg acc 576
Val Gly Gln Leu Gly Ser Gly Ser Ala Asn Asp Val Ala Pro Ala Thr
      180                      185                      190

cca gaa tta cca gaa ccc acc gac aac ctg act tca ggt gag ggt ggg 624
Pro Glu Leu Pro Glu Pro Thr Asp Asn Leu Thr Ser Gly Glu Gly Gly
      195                      200                      205

tcg cag aac acg ctg ctt aag ctc gtg gtg ccc atc gga atc atc gtg 672
Ser Gln Asn Thr Leu Leu Lys Leu Val Val Pro Ile Gly Ile Ile Val
      210                      215                      220

ctg ttg cta atc gcc gca cta gcg tgg aca ttc aga tct ccc aag aaa 720
Leu Leu Leu Ile Ala Ala Leu Ala Trp Thr Phe Arg Ser Pro Lys Lys
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aag aac taggtgttct tcttcacgac ctc 749
Lys Asn

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<210> 46
<211> 242
<212> PRT
<213> Corynebacterium glutamicum

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Asn Asp Ala Ala Tyr Leu Leu Ala Gln Glu Leu Gly Gly Asp Gln Ala
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Thr Leu Glu Lys Val Asn Ala Leu Ala Lys Glu Leu Gly Thr Gln Asp
      35          40          45

Thr Phe Val Ala Thr Tyr Ser Gly Leu Asp Ala Pro Gly Met Ser Thr
      50          55          60

Ser Ala Tyr Asp Met Ser Leu Ile Tyr Gln His Ala Trp Gln Asn Pro
      65          70          75          80

Val Phe Glu Ser Ile Ile Ser Thr Asp His Ile Asp Phe Pro Gly Trp
      85          90          95

Gly Asp Asn Glu Gly Phe Gln Val Trp Asn Asp Asn Ala Leu Phe Met
      100         105         110

Asn Asp Pro Asp Gly Ile Gly Gly Lys Thr Gly Tyr Thr Asp Asp Ala
      115         120         125

Asn His Thr Phe Val Gly Gly Leu Asp Arg Gly Gly Arg Arg Leu Ala
      130         135         140

Ala Val Leu Leu Asp Ser Thr Val Ser Asp Ile Arg Pro Trp Glu Gln
-----145-----150-----155-----160-----

Ala Arg Leu Leu Ile Asp Ala Ser Leu Pro Ile Thr Pro Gly Ser Gly
      165          170          175

Val Gly Gln Leu Gly Ser Gly Ser Ala Asn Asp Val Ala Pro Ala Thr

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180 185 190

Pro Glu Leu Pro Glu Pro Thr Asp Asn Leu Thr Ser Gly Glu Gly Gly
195 200 205

Ser Gln Asn Thr Leu Leu Lys Leu Val Val Pro Ile Gly Ile Ile Val
210 215 220

Leu Leu Leu Ile Ala Ala Leu Ala Trp Thr Phe Arg Ser Pro Lys Lys
225 230 235 240

Lys Asn

<210> 47
<211> 1149
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1126)
<223> RXA00569

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Met Arg Leu Lys Lys
1 5

cag ctt ctt ggc agc ctg tta gtt gtc atc gtg gtt ttg tcc atc gcc 163
Gln Leu Leu Gly Ser Leu Leu Val Val Ile Val Val Leu Ser Ile Ala
10 15 20

gta gca acc acc aaa caa caa aaa ggc ttc gtc aca ggt cag ccc acc 211
Val Ala Thr Thr Lys Gln Gln Lys Gly Phe Val Thr Gly Gln Pro Thr
25 30 35

ggt gcg ctt aac ctc tcc gac atc ctc gac tcc gaa gaa ctt ggc gag 259
Gly Ala Leu Asn Leu Ser Asp Ile Leu Asp Ser Glu Glu Leu Gly Glu
40 45 50

tat cac ctc atg tca gcc gcc atc atc act ggt aac act gta gat ttc 307
Tyr His Leu Met Ser Ala Ala Ile Ile Thr Gly Asn Thr Val Asp Phe
55 60 65

agc ggg ctc ggc gca ggt cca gac gac cct ttt gaa atc gca tcg att 355
Ser Gly Leu Gly Ala Gly Pro Asp Asp Pro Phe Glu Ile Ala Ser Ile
70 75 80 85

acg aag atc ttc acc ggt gag ctg ctt cga ctt cag att gag cga gga 403
Thr Lys Ile Phe Thr Gly Glu Leu Leu Arg Leu Gln Ile Glu Arg Gly
90 95 100

gag atc aca gaa tcc acg gcc gtc gga gac gtt ctt gga gaa cgt gta 451
Glu Ile Thr Glu Ser Thr Ala Val Gly Asp Val Leu Gly Glu Arg Val
105 110 115

gcc gac tcc ctc atc cgg gac ata acc gtg gaa gaa cta gcc aat cac 499

Ala	Asp	Ser	Leu	Ile	Arg	Asp	Ile	Thr	Val	Glu	Glu	Leu	Ala	Asn	His		
		120					125					130					
acc	agc	gga	cta	ccc	cgt	cta	ggc	aat	gta	gga	ctt	aga	cct	ttt	atg	547	
Thr	Ser	Gly	Leu	Pro	Arg	Leu	Gly	Asn	Val	Gly	Leu	Arg	Pro	Phe	Met		
		135				140					145						
gct	acg	ttc	ttt	gac	aag	aat	cct	tac	aaa	gac	ctc	tct	gca	gat	cga	595	
Ala	Thr	Phe	Phe	Asp	Lys	Asn	Pro	Tyr	Lys	Asp	Leu	Ser	Ala	Asp	Arg		
150				155						160					165		
gtc	atc	tct	atc	agc	aca	acg	tcc	aaa	ttg	aat	tcg	cgc	gga	gaa	ttt	643	
Val	Ile	Ser	Ile	Ser	Thr	Thr	Ser	Lys	Leu	Asn	Ser	Arg	Gly	Glu	Phe		
				170					175					180			
cac	tac	tca	aat	ctt	ggg	ttt	gct	ctg	ctt	ggc	caa	gtc	ctt	gcc	cgc	691	
His	Tyr	Ser	Asn	Leu	Gly	Phe	Ala	Leu	Leu	Gly	Gln	Val	Leu	Ala	Arg		
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Asn	Ala	Gly	Leu	Thr	Phe	Asp	Gln	Leu	Leu	Asp	Arg	Asp	Leu	Leu	Ala		
		200					205					210					
cca	ctc	aac	ctc	aat	aac	acc	aag	ctc	atg	acc	cca	gaa	tcc	ctc	gct	787	
Pro	Leu	Asn	Leu	Asn	Asn	Thr	Lys	Leu	Met	Thr	Pro	Glu	Ser	Leu	Ala		
		215				220					225						
caa	gat	gca	cct	caa	ggg	ttc	tca	aca	cct	ggc	aaa	caa	gtc	gaa	gcg	835	
Gln	Asp	Ala	Pro	Gln	Gly	Phe	Ser	Thr	Pro	Gly	Lys	Gln	Val	Glu	Ala		
230				235						240				245			
tgg	gag	atg	gat	ggc	ttt	ctc	ccc	gca	gct	ggc	ctg	cgt	tcc	acc	gcg	883	
Trp	Glu	Met	Asp	Gly	Phe	Leu	Pro	Ala	Ala	Gly	Leu	Arg	Ser	Thr	Ala		
				250					255					260			
cgc	gac	atg	gca	gtt	ttc	tgt	cag	tac	tta	ttc	aca	aaa	ggc	ccc	gcc	931	
Arg	Asp	Met	Ala	Val	Phe	Cys	Gln	Tyr	Leu	Phe	Thr	Lys	Gly	Pro	Ala		
			265					270					275				
cct	ttc	acc	tgg	caa	tcc	ctt	gaa	tcg	gcc	cct	gaa	atc	gtc	tgg	cat	979	
Pro	Phe	Thr	Trp	Gln	Ser	Leu	Glu	Ser	Ala	Pro	Glu	Ile	Val	Trp	His		
		280						285				290					
aac	gga	gag	tcc	ttt	gga	tat	agt	tcc	gta	ctc	ttc	ttt	aac	acc	gct	1027	
Asn	Gly	Glu	Ser	Phe	Gly	Tyr	Ser	Ser	Val	Leu	Phe	Phe	Asn	Thr	Ala		
		295				300					305						
aca	act	act	gcc	atc	ttc	gtt	gct	gcc	gac	gtt	gcc	aca	tct	gtc	ttc	1075	
Thr	Thr	Thr	Ala	Ile	Phe	Val	Ala	Ala	Asp	Val	Ala	Thr	Ser	Val	Phe		
310				315						320				325			
cca	att	ggt	cac	gag	ctt	tta	atg	gca	aac	tcc	act	agg	cag	gaa	tca	1123	
Pro	Ile	Gly	His	Glu	Leu	Leu	Met	Ala	Asn	Ser	Thr	Arg	Gln	Glu	Ser		
				330					335					340			

aaa-tgategattc-ccccgeetct-atc
Lys

1149

<211> 342

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 48

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Thr	Gly	Gln	Pro	Thr	Gly	Ala	Leu	Asn	Leu	Ser	Asp	Ile	Leu	Asp	Ser
		35					40					45			
Glu	Glu	Leu	Gly	Glu	Tyr	His	Leu	Met	Ser	Ala	Ala	Ile	Ile	Thr	Gly
	50					55					60				
Asn	Thr	Val	Asp	Phe	Ser	Gly	Leu	Gly	Ala	Gly	Pro	Asp	Asp	Pro	Phe
65					70					75					80
Glu	Ile	Ala	Ser	Ile	Thr	Lys	Ile	Phe	Thr	Gly	Glu	Leu	Leu	Arg	Leu
				85					90					95	
Gln	Ile	Glu	Arg	Gly	Glu	Ile	Thr	Glu	Ser	Thr	Ala	Val	Gly	Asp	Val
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Leu	Gly	Glu	Arg	Val	Ala	Asp	Ser	Leu	Ile	Arg	Asp	Ile	Thr	Val	Glu
	115						120					125			
Glu	Leu	Ala	Asn	His	Thr	Ser	Gly	Leu	Pro	Arg	Leu	Gly	Asn	Val	Gly
	130					135					140				
Leu	Arg	Pro	Phe	Met	Ala	Thr	Phe	Phe	Asp	Lys	Asn	Pro	Tyr	Lys	Asp
145					150					155					160
Leu	Ser	Ala	Asp	Arg	Val	Ile	Ser	Ile	Ser	Thr	Thr	Ser	Lys	Leu	Asn
				165					170					175	
Ser	Arg	Gly	Glu	Phe	His	Tyr	Ser	Asn	Leu	Gly	Phe	Ala	Leu	Leu	Gly
			180					185					190		
Gln	Val	Leu	Ala	Arg	Asn	Ala	Gly	Leu	Thr	Phe	Asp	Gln	Leu	Leu	Asp
		195					200					205			
Arg	Asp	Leu	Leu	Ala	Pro	Leu	Asn	Leu	Asn	Asn	Thr	Lys	Leu	Met	Thr
	210					215					220				
Pro	Glu	Ser	Leu	Ala	Gln	Asp	Ala	Pro	Gln	Gly	Phe	Ser	Thr	Pro	Gly
225					230					235					240
Lys	Gln	Val	Glu	Ala	Trp	Glu	Met	Asp	Gly	Phe	Leu	Pro	Ala	Ala	Gly
				245					250					255	
Leu	Arg	Ser	Thr	Ala	Arg	Asp	Met	Ala	Val	Phe	Cys	Gln	Tyr	Leu	Phe
			260				265						270		
Thr	Lys	Gly	Pro	Ala	Pro	Phe	Thr	Trp	Gln	Ser	Leu	Glu	Ser	Ala	Pro
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Glu	Ile	Val	Trp	His	Asn	Gly	Glu	Ser	Phe	Gly	Tyr	Ser	Ser	Val	Leu
	290					295					300				

Phe Phe Asn Thr Ala Thr Thr Thr Ala Ile Phe Val Ala Ala Asp Val
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Thr Arg Gln Glu Ser Lys
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<211> 1008

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(985)

<223> RXN03092

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Val Ser Thr Thr Asn
1 5

tct ctg aca aag ctc gtt gca tct aca gtc gcc gct ggc gtc ctt ggt 163
Ser Leu Thr Lys Leu Val Ala Ser Thr Val Ala Ala Gly Val Leu Gly
10 15 20

gcg ctc gca ctt gtg cct ttc gct agt ctt tct ggc gtt gcg gtt gcg 211
Ala Leu Ala Leu Val Pro Phe Ala Ser Leu Ser Gly Val Ala Val Ala
25 30 35

cgt acc aat gac acg atg cag acc aac ctt tca gat ctg acg gat ggt 259
Arg Thr Asn Asp Thr Met Gln Thr Asn Leu Ser Asp Leu Thr Asp Gly
40 45 50

cgc ggg ccg ggc gtc acg acg att act gat tcc act gac cag ccg att 307
Arg Gly Pro Gly Val Thr Thr Ile Thr Asp Ser Thr Asp Gln Pro Ile
55 60 65

gct tat att tat gcg cag cgg cgg ttt gag gtt ggg ggt gat cag att 355
Ala Tyr Ile Tyr Ala Gln Arg Arg Phe Glu Val Gly Gly Asp Gln Ile
70 75 80 85

tct acg tcg atg aag gat gcg atc gtt tcg att gag gat cgc agg ttc 403
Ser Thr Ser Met Lys Asp Ala Ile Val Ser Ile Glu Asp Arg Arg Phe
90 95 100

tat gag cat gat ggt gtg gat ttg cag ggc ttt ggt cgt gca atc ctg 451
Tyr Glu His Asp Gly Val Asp Leu Gln Gly Phe Gly Arg Ala Ile Leu
105 110 115

acg aac ctg gct gcg ggt ggc gtg gag cag ggt gct tcg acg att aac 499
Thr Asn Leu Ala Ala Gly Gly Val Glu Gln Gly Ala Ser Thr Ile Asn
120 125 130

cag cag tat gtg aag aac ttc ttg ctg ttg gtg gaa gct gat gat gag 547

Gln Gln Tyr Val Lys Asn Phe Leu Leu Leu Val Glu Ala Asp Asp Glu
 135 140 145
 gcg gag cag gct gct gct gtg gaa acc tcc atc cct cgt aag ctc cgt 595
 Ala Glu Gln Ala Ala Ala Val Glu Thr Ser Ile Pro Arg Lys Leu Arg
 150 155 160 165
 gag atg aag atg gcg tct gat ttg gaa aag acg ttg tcg aag gat gag 643
 Glu Met Lys Met Ala Ser Asp Leu Glu Lys Thr Leu Ser Lys Asp Glu
 170 175 180
 att ctg act cgt tat ctc aac att gtt cct ttt ggt aat ggt gct tat 691
 Ile Leu Thr Arg Tyr Leu Asn Ile Val Pro Phe Gly Asn Gly Ala Tyr
 185 190 195
 ggt gtt gag gct gcg gcg cgg acg tat ttc ggt acg tcg gct gcc gag 739
 Gly Val Glu Ala Ala Ala Arg Thr Tyr Phe Gly Thr Ser Ala Ala Glu
 200 205 210
 tta acc att cca cag tct gcg atg ctc gcg ggc att gtg cag tct tcg 787
 Leu Thr Ile Pro Gln Ser Ala Met Leu Ala Gly Ile Val Gln Ser Ser
 215 220 225
 tct tat ctc aat cca tac acc aat cac gat gct gtg ttt gag cgt cgt 835
 Ser Tyr Leu Asn Pro Tyr Thr Asn His Asp Ala Val Phe Glu Arg Arg
 230 235 240 245
 aat act gtt ttg ggc gct atg gct gat gct ggc gcg att tcc cca gac 883
 Asn Thr Val Leu Gly Ala Met Ala Asp Ala Gly Ala Ile Ser Pro Asp
 250 255 260
 gag gct tcg gct ttc cag cag gaa cct ttg ggt gtc ctg gaa acc ccg 931
 Glu Ala Ser Ala Phe Gln Gln Glu Pro Leu Gly Val Leu Glu Thr Pro
 265 270 275
 caa ggc tta tcc aat ggt tgt atc ggc gct ggc gat cgg tgg ttt ttt 979
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 ttg caa taacgctctt gcaatatctt tct 1008
 Leu Gln
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<211> 295

<212> PRT

<213> Corynebacterium glutamicum

<400> 50

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Gly Val Ala Val Ala Arg Thr Asn Asp Thr Met Gln Thr Asn Leu Ser
 35 40 45

Asp Leu Thr Asp Gly Arg Gly Pro Gly Val Thr Thr Ile Thr Asp Ser
 50 55 60

Thr Asp Gln Pro Ile Ala Tyr Ile Tyr Ala Gln Arg Arg Phe Glu Val
 65 70 75 80
 Gly Gly Asp Gln Ile Ser Thr Ser Met Lys Asp Ala Ile Val Ser Ile
 85 90 95
 Glu Asp Arg Arg Phe Tyr Glu His Asp Gly Val Asp Leu Gln Gly Phe
 100 105 110
 Gly Arg Ala Ile Leu Thr Asn Leu Ala Ala Gly Gly Val Glu Gln Gly
 115 120 125
 Ala Ser Thr Ile Asn Gln Gln Tyr Val Lys Asn Phe Leu Leu Leu Val
 130 135 140
 Glu Ala Asp Asp Glu Ala Glu Gln Ala Ala Ala Val Glu Thr Ser Ile
 145 150 155 160
 Pro Arg Lys Leu Arg Glu Met Lys Met Ala Ser Asp Leu Glu Lys Thr
 165 170 175
 Leu Ser Lys Asp Glu Ile Leu Thr Arg Tyr Leu Asn Ile Val Pro Phe
 180 185 190
 Gly Asn Gly Ala Tyr Gly Val Glu Ala Ala Ala Arg Thr Tyr Phe Gly
 195 200 205
 Thr Ser Ala Ala Glu Leu Thr Ile Pro Gln Ser Ala Met Leu Ala Gly
 210 215 220
 Ile Val Gln Ser Ser Ser Tyr Leu Asn Pro Tyr Thr Asn His Asp Ala
 225 230 235 240
 Val Phe Glu Arg Arg Asn Thr Val Leu Gly Ala Met Ala Asp Ala Gly
 245 250 255
 Ala Ile Ser Pro Asp Glu Ala Ser Ala Phe Gln Gln Glu Pro Leu Gly
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 Asp Arg Trp Phe Phe Leu Gln
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 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1033)
 <223> FRXA00594

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tct	ctg	aca	aag	ctc	gtt	gca	tct	aca	gtc	gcc	gct	ggc	gtc	ctt	ggg		163
Ser	Leu	Thr	Lys	Leu	Val	Ala	Ser	Thr	Val	Ala	Ala	Gly	Val	Leu	Gly		
				10					15					20			
gcg	ctc	gca	ctt	gtg	cct	ttc	gct	agt	ctt	tct	ggc	gtt	gcg	gtt	gcg		211
Ala	Leu	Ala	Leu	Val	Pro	Phe	Ala	Ser	Leu	Ser	Gly	Val	Ala	Val	Ala		
			25					30				35					
cgt	acc	aat	gac	acg	atg	cag	acc	aac	ctt	tca	gat	ctg	acg	gat	ggg		259
Arg	Thr	Asn	Asp	Thr	Met	Gln	Thr	Asn	Leu	Ser	Asp	Leu	Thr	Asp	Gly		
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cgc	ggg	ccg	ggc	gtc	acg	acg	att	act	gat	tcc	act	gac	cag	ccg	att		307
Arg	Gly	Pro	Gly	Val	Thr	Thr	Ile	Thr	Asp	Ser	Thr	Asp	Gln	Pro	Ile		
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gct	tat	att	tat	gcg	cag	cgg	cgg	ttt	gag	gtt	ggg	ggg	gat	cag	att		355
Ala	Tyr	Ile	Tyr	Ala	Gln	Arg	Arg	Phe	Glu	Val	Gly	Gly	Asp	Gln	Ile		
	70				75				80						85		
tct	acg	tcg	atg	aag	gat	gcg	atc	gtt	tcg	att	gag	gat	cgc	agg	ttc		403
Ser	Thr	Ser	Met	Lys	Asp	Ala	Ile	Val	Ser	Ile	Glu	Asp	Arg	Arg	Phe		
				90					95					100			
tat	gag	cat	gat	ggg	gtg	gat	ttg	cag	ggc	ttt	ggg	cgt	gca	atc	ctg		451
Tyr	Glu	His	Asp	Gly	Val	Asp	Leu	Gln	Gly	Phe	Gly	Arg	Ala	Ile	Leu		
			105					110					115				
acg	aac	ctg	gct	gcg	ggg	ggc	gtg	gag	cag	ggg	gct	tcg	acg	att	aac		499
Thr	Asn	Leu	Ala	Ala	Gly	Gly	Val	Glu	Gln	Gly	Ala	Ser	Thr	Ile	Asn		
		120					125					130					
cag	cag	tat	gtg	aag	aac	ttc	ttg	ctg	ttg	gtg	gaa	gct	gat	gat	gag		547
Gln	Gln	Tyr	Val	Lys	Asn	Phe	Leu	Leu	Leu	Val	Glu	Ala	Asp	Asp	Glu		
		135				140					145						
gcg	gag	cag	gct	gct	gct	gtg	gaa	acc	tcc	atc	cct	cgt	aag	ctc	cgt		595
Ala	Glu	Gln	Ala	Ala	Ala	Val	Glu	Thr	Ser	Ile	Pro	Arg	Lys	Leu	Arg		
	150				155					160					165		
gag	atg	aag	atg	gcg	tct	gat	ttg	gaa	aag	acg	ttg	tcg	aag	gat	gag		643
Glu	Met	Lys	Met	Ala	Ser	Asp	Leu	Glu	Lys	Thr	Leu	Ser	Lys	Asp	Glu		
				170					175					180			
att	ctg	act	cgt	tat	ctc	aac	att	gtt	cct	ttt	ggg	aat	ggg	gct	tat		691
Ile	Leu	Thr	Arg	Tyr	Leu	Asn	Ile	Val	Pro	Phe	Gly	Asn	Gly	Ala	Tyr		
			185					190					195				
ggg	gtt	gag	gct	gcg	gcg	cgg	acg	tat	ttc	ggg	acg	tcg	gct	gcc	gag		739
Gly	Val	Glu	Ala	Ala	Ala	Arg	Thr	Tyr	Phe	Gly	Thr	Ser	Ala	Ala	Glu		
		200					205					210					
tta	acc	att	cca	cag	tct	gcg	atg	ctc	gcg	ggc	att	gtg	cag	tct	tcg		787
Leu	Thr	Ile	Pro	Gln	Ser	Ala	Met	Leu	Ala	Gly	Ile	Val	Gln	Ser	Ser		
		215					220				225						
tct	tat	ctc	aat	cca	tac	acc	aat	cac	gat	gct	gtg	ttt	gag	cgt	cgt		835
Ser	Tyr	Leu	Asn	Pro	Tyr	Thr	Asn	His	Asp	Ala	Val	Phe	Glu	Arg	Arg		

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aat act gtt ttg ggc gct atg gct gat gct ggc gcg att tcc cca gac				883
Asn Thr Val Leu Gly Ala Met Ala Asp Ala Gly Ala Ile Ser Pro Asp				
	250	255	260	
gag gct tcg gct ttc cag cag gaa cct ttg ggt gtc ctg gaa acc ccg				931
Glu Ala Ser Ala Phe Gln Gln Glu Pro Leu Gly Val Leu Glu Thr Pro				
	265	270	275	
caa ggc tta tcc aat ggt tgt atc ggc gct ggc gat cgt ggt ttc ttc				979
Gln Gly Leu Ser Asn Gly Cys Ile Gly Ala Gly Asp Arg Gly Phe Phe				
	280	285	290	
tgc gat tac gct ctg caa tat ctt tct gag cag gga atc acc caa gat				1027
Cys Asp Tyr Ala Leu Gln Tyr Leu Ser Glu Gln Gly Ile Thr Gln Asp				
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atg ctg				1033
Met Leu				
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<212> PRT

<213> Corynebacterium glutamicum

<400> 52

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20 25 30

Gly Val Ala Val Ala Arg Thr Asn Asp Thr Met Gln Thr Asn Leu Ser
35 40 45

Asp Leu Thr Asp Gly Arg Gly Pro Gly Val Thr Thr Ile Thr Asp Ser
50 55 60

Thr Asp Gln Pro Ile Ala Tyr Ile Tyr Ala Gln Arg Arg Phe Glu Val
65 70 75 80

Gly Gly Asp Gln Ile Ser Thr Ser Met Lys Asp Ala Ile Val Ser Ile
85 90 95

Glu Asp Arg Arg Phe Tyr Glu His Asp Gly Val Asp Leu Gln Gly Phe
100 105 110

Gly Arg Ala Ile Leu Thr Asn Leu Ala Ala Gly Gly Val Glu Gln Gly
115 120 125

Ala Ser Thr Ile Asn Gln Gln Tyr Val Lys Asn Phe Leu Leu Leu Val
130 135 140

Glu Ala Asp Asp Glu Ala Glu Gln Ala Ala Ala Val Glu Thr Ser Ile
145 150 155 160

Pro Arg Lys Leu Arg Glu Met Lys Met Ala Ser Asp Leu Glu Lys Thr
165 170 175

Leu Ser Lys Asp Glu Ile Leu Thr Arg Tyr Leu Asn Ile Val Pro Phe
 180 185 190
 Gly Asn Gly Ala Tyr Gly Val Glu Ala Ala Ala Arg Thr Tyr Phe Gly
 195 200 205
 Thr Ser Ala Ala Glu Leu Thr Ile Pro Gln Ser Ala Met Leu Ala Gly
 210 215 220
 Ile Val Gln Ser Ser Ser Tyr Leu Asn Pro Tyr Thr Asn His Asp Ala
 225 230 235 240
 Val Phe Glu Arg Arg Asn Thr Val Leu Gly Ala Met Ala Asp Ala Gly
 245 250 255
 Ala Ile Ser Pro Asp Glu Ala Ser Ala Phe Gln Gln Glu Pro Leu Gly
 260 265 270
 Val Leu Glu Thr Pro Gln Gly Leu Ser Asn Gly Cys Ile Gly Ala Gly
 275 280 285
 Asp Arg Gly Phe Phe Cys Asp Tyr Ala Leu Gln Tyr Leu Ser Glu Gln
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 Gly Ile Thr Gln Asp Met Leu
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1522)
 <223> RXA01828

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 Val Asn Arg Ser Ile
 1 5
 cga atc aca tcc ctc ttc tct ttg ctc ctg atc ttg gtg ctc gta gca 163
 Arg Ile Thr Ser Leu Phe Ser Leu Leu Leu Ile Leu Val Leu Val Ala
 10 15 20
 aac ctc acc tgg att cag gct ttt agg gac gat gat ctt gct cag aac 211
 Asn Leu Thr Trp Ile Gln Ala Phe Arg Asp Asp Asp Leu Ala Gln Asn
 25 30 35
 cca ctg aac gca cgt ggt ttc ctg gag gcg aag tcc act ccg cgt gga 259
 Pro Leu Asn Ala Arg Gly Phe Leu Glu Ala Lys Ser Thr Pro Arg Gly
 40 45 50
 cag att tca act ggt ggc caa gta ctc gca gag tcc tcc cag gac gat 307
 Gln Ile Ser Thr Gly Gly Gln Val Leu Ala Glu Ser Ser Gln Asp Asp
 55 60 65

cag ggt ttt tac cag cgc agc tac atc acc aac ccg act gcc tac gca	355
Gln Gly Phe Tyr Gln Arg Ser Tyr Ile Thr Asn Pro Thr Ala Tyr Ala	
70 75 80 85	
ccg gtg gtt ggt tac ctc tct gat gtt tat gga gca gct ggc ctg gaa	403
Pro Val Val Gly Tyr Leu Ser Asp Val Tyr Gly Ala Ala Gly Leu Glu	
90 95 100	
ttg gga tac aac tct atc ctc aac ggc agt gac tct tcc ctg ttt acc	451
Leu Gly Tyr Asn Ser Ile Leu Asn Gly Ser Asp Ser Ser Leu Phe Thr	
105 110 115	
tcc cag tgg ctg gat gtc att tct ggc agc cct acc cat ggc gca aac	499
Ser Gln Trp Leu Asp Val Ile Ser Gly Ser Pro Thr His Gly Ala Asn	
120 125 130	
att gag ctg acc ttg gat ccc aat gcg cag caa act gct tat gaa cag	547
Ile Glu Leu Thr Leu Asp Pro Asn Ala Gln Gln Thr Ala Tyr Glu Gln	
135 140 145	
ctg agc caa agc ggc tac gag ggt gct gtg gtg gcg ctt cgc cca agc	595
Leu Ser Gln Ser Gly Tyr Glu Gly Ala Val Val Ala Leu Arg Pro Ser	
150 155 160 165	
act ggt gag gtg ctg gcc atg gcg tca tcg cca agc tat gac ccc aac	643
Thr Gly Glu Val Leu Ala Met Ala Ser Ser Pro Ser Tyr Asp Pro Asn	
170 175 180	
cag atc gtg gat cca gca acc gca gag gac gct tgg gct gag tac acc	691
Gln Ile Val Asp Pro Ala Thr Ala Glu Asp Ala Trp Ala Glu Tyr Thr	
185 190 195	
tcc act gaa ggt gca ccg ctg ctc aac cat gca acg cag gaa tca ctg	739
Ser Thr Glu Gly Ala Pro Leu Leu Asn His Ala Thr Gln Glu Ser Leu	
200 205 210	
cct cct gga tct att ttc aag atc atc act act gcg gca gct ttg gaa	787
Pro Pro Gly Ser Ile Phe Lys Ile Ile Thr Thr Ala Ala Ala Leu Glu	
215 220 225	
aac ggc tac tct gct gat tcc acc gtg act gca gag gca gca gtg acc	835
Asn Gly Tyr Ser Ala Asp Ser Thr Val Thr Ala Glu Ala Ala Val Thr	
230 235 240 245	
ctg cct ggc acc aac acc acc ttg acc aac tac ggc ggt cag aca tgt	883
Leu Pro Gly Thr Asn Thr Thr Leu Thr Asn Tyr Gly Gly Gln Thr Cys	
250 255 260	
gcg ggc ggt ggc acc act acc ctg ctc acc gct ttc cag ctc tcc tgc	931
Ala Gly Gly Gly Thr Thr Thr Leu Leu Thr Ala Phe Gln Leu Ser Cys	
265 270 275	
aat act gcg ttt gtg gag acc ggc att gat gtt ggc gcg gat gct ttg	979
Asn Thr Ala Phe Val Glu Thr Gly Ile Asp Val Gly Ala Asp Ala Leu	
280 285 290	
cgc gcg tct gcc gag gac ttc gga gtg gga caa acc tac agc ttg gga	1027
Arg Ala Ser Ala Glu Asp Phe Gly Val Gly Gln Thr Tyr Ser Leu Gly	
295 300 305	

cta gat aac gtt cct ggc ggc ttg ggt gaa atc ccc gac gat gcc gcc 1075
 Leu Asp Asn Val Pro Gly Gly Leu Gly Glu Ile Pro Asp Asp Ala Ala
 310 315 320 325

ctt gga caa tcc agc att ggc cag cgc gac gtg caa atg aac gtg ctg 1123
 Leu Gly Gln Ser Ser Ile Gly Gln Arg Asp Val Gln Met Asn Val Leu
 330 335 340

cag gcc gct gtc atg gca gga acc gta tcc aac ggt ggc gta cgc atg 1171
 Gln Ala Ala Val Met Ala Gly Thr Val Ser Asn Gly Gly Val Arg Met
 345 350 355

gaa cca tat ttg gta tcc cgc gtc acc ggt cag gac ctg agc gaa ctg 1219
 Glu Pro Tyr Leu Val Ser Arg Val Thr Gly Gln Asp Leu Ser Glu Leu
 360 365 370

agc acc cac aag ccg aaa tca gtt ggt gga gtc gag cca gaa att gca 1267
 Ser Thr His Lys Pro Lys Ser Val Gly Gly Val Glu Pro Glu Ile Ala
 375 380 385

gaa cag ttg aag act ttg atg gaa gcc tca gag cgc aat act tcg ggc 1315
 Glu Gln Leu Lys Thr Leu Met Glu Ala Ser Glu Arg Asn Thr Ser Gly
 390 395 400 405

tac acc gga att cag atc gct tcc aag act ggt acc gcg gaa cat ggt 1363
 Tyr Thr Gly Ile Gln Ile Ala Ser Lys Thr Gly Thr Ala Glu His Gly
 410 415 420

gat gaa aac aca cca cca cac acc tgg tac gtg gca ttc aac aac gac 1411
 Asp Glu Asn Thr Pro Pro His Thr Trp Tyr Val Ala Phe Asn Asn Asp
 425 430 435

att gct gtt gct gtg ttg gtg aaa gac ggc ggt gga ttt ggc acc agt 1459
 Ile Ala Val Ala Val Leu Val Lys Asp Gly Gly Gly Phe Gly Thr Ser
 440 445 450

gca act ggt ggt cag gtc gca gcc cca att ggc cga gct gtg ctt cag 1507
 Ala Thr Gly Gly Gln Val Ala Ala Pro Ile Gly Arg Ala Val Leu Gln
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gca gcc gga gga ttt taaaatatga gtcaagaaga cat 1545
 Ala Ala Gly Gly Phe
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<210> 54

<211> 474

<212> PRT

<213> Corynebacterium glutamicum

<400> 54

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Asp Leu Ala Gln Asn Pro Leu Asn Ala Arg Gly Phe Leu Glu Ala Lys
 35 40 45

Ser Thr Pro Arg Gly Gln Ile Ser Thr Gly Gly Gln Val Leu Ala Glu

50					55					60					
Ser	Ser	Gln	Asp	Asp	Gln	Gly	Phe	Tyr	Gln	Arg	Ser	Tyr	Ile	Thr	Asn
65					70					75					80
Pro	Thr	Ala	Tyr	Ala	Pro	Val	Val	Gly	Tyr	Leu	Ser	Asp	Val	Tyr	Gly
				85					90					95	
Ala	Ala	Gly	Leu	Glu	Leu	Gly	Tyr	Asn	Ser	Ile	Leu	Asn	Gly	Ser	Asp
			100					105					110		
Ser	Ser	Leu	Phe	Thr	Ser	Gln	Trp	Leu	Asp	Val	Ile	Ser	Gly	Ser	Pro
		115					120					125			
Thr	His	Gly	Ala	Asn	Ile	Glu	Leu	Thr	Leu	Asp	Pro	Asn	Ala	Gln	Gln
	130					135					140				
Thr	Ala	Tyr	Glu	Gln	Leu	Ser	Gln	Ser	Gly	Tyr	Glu	Gly	Ala	Val	Val
145					150					155					160
Ala	Leu	Arg	Pro	Ser	Thr	Gly	Glu	Val	Leu	Ala	Met	Ala	Ser	Ser	Pro
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Ser	Tyr	Asp	Pro	Asn	Gln	Ile	Val	Asp	Pro	Ala	Thr	Ala	Glu	Asp	Ala
			180					185					190		
Trp	Ala	Glu	Tyr	Thr	Ser	Thr	Glu	Gly	Ala	Pro	Leu	Leu	Asn	His	Ala
		195					200					205			
Thr	Gln	Glu	Ser	Leu	Pro	Pro	Gly	Ser	Ile	Phe	Lys	Ile	Ile	Thr	Thr
	210					215					220				
Ala	Ala	Ala	Leu	Glu	Asn	Gly	Tyr	Ser	Ala	Asp	Ser	Thr	Val	Thr	Ala
225					230					235					240
Glu	Ala	Ala	Val	Thr	Leu	Pro	Gly	Thr	Asn	Thr	Thr	Leu	Thr	Asn	Tyr
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Gly	Gly	Gln	Thr	Cys	Ala	Gly	Gly	Gly	Thr	Thr	Thr	Leu	Leu	Thr	Ala
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Phe	Gln	Leu	Ser	Cys	Asn	Thr	Ala	Phe	Val	Glu	Thr	Gly	Ile	Asp	Val
		275					280					285			
Gly	Ala	Asp	Ala	Leu	Arg	Ala	Ser	Ala	Glu	Asp	Phe	Gly	Val	Gly	Gln
	290					295					300				
Thr	Tyr	Ser	Leu	Gly	Leu	Asp	Asn	Val	Pro	Gly	Gly	Leu	Gly	Glu	Ile
305					310					315					320
Pro	Asp	Asp	Ala	Ala	Leu	Gly	Gln	Ser	Ser	Ile	Gly	Gln	Arg	Asp	Val
				325					330					335	
Gln	Met	Asn	Val	Leu	Gln	Ala	Ala	Val	Met	Ala	Gly	Thr	Val	Ser	Asn
			340					345					350		
Gly	Gly	Val	Arg	Met	Glu	Pro	Tyr	Leu	Val	Ser	Arg	Val	Thr	Gly	Gln
		355					360					365			
Asp	Leu	Ser	Glu	Leu	Ser	Thr	His	Lys	Pro	Lys	Ser	Val	Gly	Gly	Val
370						375					380				

Glu Pro Glu Ile Ala Glu Gln Leu Lys Thr Leu Met Glu Ala Ser Glu
 385 390 395 400
 Arg Asn Thr Ser Gly Tyr Thr Gly Ile Gln Ile Ala Ser Lys Thr Gly
 405 410 415
 Thr Ala Glu His Gly Asp Glu Asn Thr Pro Pro His Thr Trp Tyr Val
 420 425 430
 Ala Phe Asn Asn Asp Ile Ala Val Ala Val Leu Val Lys Asp Gly Gly
 435 440 445
 Gly Phe Gly Thr Ser Ala Thr Gly Gly Gln Val Ala Ala Pro Ile Gly
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 Arg Ala Val Leu Gln Ala Ala Gly Gly Phe
 465 470

<210> 55
 <211> 1208
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(1185)
 <223> RXA00612

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 gtt cct tct cga tat gag gtc aag ggc atg ggc tcc ggc ggt gcc gcg 96
 Val Pro Ser Arg Tyr Glu Val Lys Gly Met Gly Ser Gly Gly Ala Ala
 20 25 30
 aac tgt ccc gca aat act tac tgc gtg gaa aac gca gga tcc tac gcg 144
 Asn Cys Pro Ala Asn Thr Tyr Cys Val Glu Asn Ala Gly Ser Tyr Ala
 35 40 45
 cct cgc atg act ctg cag gac gct ctc gcg cag tcc ccc aac act gca 192
 Pro Arg Met Thr Leu Gln Asp Ala Leu Ala Gln Ser Pro Asn Thr Ala
 50 55 60
 ttc gtt gaa atg atc gag cag gtt ggc gtg gac acc gtt gtg gat ctt 240
 Phe Val Glu Met Ile Glu Gln Val Gly Val Asp Thr Val Val Asp Leu
 65 70 75 80
 tca gta aag ctg ggc ctg cga agc tac acc gat gaa ggt tcc ttc gac 288
 Ser Val Lys Leu Gly Leu Arg Ser Tyr Thr Asp Glu Gly Ser Phe Asp
 85 90 95
 ggc gaa agc tca atc gcg gac tac atg aag gac aac aac ctc ggt tct 336
 Gly Glu Ser Ser Ile Ala Asp Tyr Met Lys Asp Asn Asn Leu Gly Ser
 100 105 110
 tac act ctt gga cct acc gct gtt aac cct ctt gaa ttg tcc aat gtt 384
 Tyr Thr Leu Gly Pro Thr Ala Val Asn Pro Leu Glu Leu Ser Asn Val

115				120				125								
gct	gca	acc	att	gca	tcc	ggt	ggc	atg	tgg	tgc	gaa	ccc	aat	ccc	atc	432
Ala	Ala	Thr	Ile	Ala	Ser	Gly	Gly	Met	Trp	Cys	Glu	Pro	Asn	Pro	Ile	
	130					135					140					
gcc	agc	gtc	cat	gac	cgt	gaa	ggc	aac	gaa	gtc	tac	att	gac	cgc	cct	480
Ala	Ser	Val	His	Asp	Arg	Glu	Gly	Asn	Glu	Val	Tyr	Ile	Asp	Arg	Pro	
145					150					155					160	
gca	tgt	gag	cgc	gcc	atc	gat	gcc	gaa	acg	gct	tca	gct	ttg	gcc	gtc	528
Ala	Cys	Glu	Arg	Ala	Ile	Asp	Ala	Glu	Thr	Ala	Ser	Ala	Leu	Ala	Val	
				165					170					175		
ggc	atg	agc	aag	gat	acg	gtc	agc	gga	act	gcg	gcc	tct	gca	gcc	agc	576
Gly	Met	Ser	Lys	Asp	Thr	Val	Ser	Gly	Thr	Ala	Ala	Ser	Ala	Ala	Ser	
			180					185					190			
atg	tac	gga	tgg	tcc	ttg	cca	acc	gca	gcg	aag	acc	ggt	acc	acc	gag	624
Met	Tyr	Gly	Trp	Ser	Leu	Pro	Thr	Ala	Ala	Lys	Thr	Gly	Thr	Thr	Glu	
		195					200					205				
tcc	aac	cag	tcc	tca	gca	ttt	atg	ggc	ttc	aac	agc	aac	ttt	gcc	gca	672
Ser	Asn	Gln	Ser	Ser	Ala	Phe	Met	Gly	Phe	Asn	Ser	Asn	Phe	Ala	Ala	
	210					215					220					
gct	cca	tac	atc	tac	aat	gac	ggc	acc	tcc	acc	acc	cca	ctg	tgc	agc	720
Ala	Pro	Tyr	Ile	Tyr	Asn	Asp	Gly	Thr	Ser	Thr	Thr	Pro	Leu	Cys	Ser	
225					230					235					240	
ggc	ccc	gtc	cgc	cag	tgc	agc	agc	ggt	aac	ctc	ttc	ggc	ggt	aac	gaa	768
Gly	Pro	Val	Arg	Gln	Cys	Ser	Ser	Gly	Asn	Leu	Phe	Gly	Gly	Asn	Glu	
				245					250					255		
cca	gct	caa	aca	tgg	ttt	aac	atg	gca	agc	aac	gtc	ccc	gca	gct	tcg	816
Pro	Ala	Gln	Thr	Trp	Phe	Asn	Met	Ala	Ser	Asn	Val	Pro	Ala	Ala	Ser	
			260					265					270			
caa	gga	aca	ctg	cca	tcc	agc	agc	gat	tca	ttc	cgc	ctc	ggc	act	tcc	864
Gln	Gly	Thr	Leu	Pro	Ser	Ser	Ser	Asp	Ser	Phe	Arg	Leu	Gly	Thr	Ser	
		275					280					285				
ggc	gaa	ctc	ctc	aac	cag	gtt	gtc	ggc	caa	agc	gaa	gcc	tcc	gct	cga	912
Gly	Glu	Leu	Leu	Asn	Gln	Val	Val	Gly	Gln	Ser	Glu	Ala	Ser	Ala	Arg	
	290					295					300					
cgc	acc	ctc	gaa	gcc	aaa	ggc	tac	aag	gtc	acc	acg	cgt	tca	gtc	tcc	960
Arg	Thr	Leu	Glu	Ala	Lys	Gly	Tyr	Lys	Val	Thr	Thr	Arg	Ser	Val	Ser	
305					310					315					320	
ggc	gcc	ggc	agc	gcg	cgc	ggc	acc	gta	gtc	agc	gca	acc	cct	cag	ggt	1008
Gly	Ala	Gly	Ser	Ala	Arg	Gly	Thr	Val	Val	Ser	Ala	Thr	Pro	Gln	Gly	
				325					330					335		
gca	gtg	ctt	atc	gac	ggt	gga	acc	gtc	att	ttg	gac	atc	tcc	gac	ggc	1056
Ala	Val	Leu	Ile	Asp	Gly	Gly	Thr	Val	Ile	Leu	Asp	Ile	Ser	Asp	Gly	
			340				345					350				
aca	agc	cct	gcc	ccc	gct	gcc	acc	aac	aat	gat	gac	agc	gac	gat	gga	1104
Thr	Ser	Pro	Ala	Pro	Ala	Ala	Thr	Asn	Asn	Asp	Asp	Ser	Asp	Asp	Gly	
		355					360					365				

gac acc cct gct cca tca aca aac aac cgc gga aca acc att gaa gac 1152
 Asp Thr Pro Ala Pro Ser Thr Asn Asn Arg Gly Thr Thr Ile Glu Asp
 370 375 380

gcc atc aat gac gcc atc aac cag ttc ttc cgc tagaaatacc tagttgctca 1205
 Ala Ile Asn Asp Ala Ile Asn Gln Phe Phe Arg
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aac 1208

<210> 56

<211> 395

<212> PRT

<213> Corynebacterium glutamicum

<400> 56

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Val Pro Ser Arg Tyr Glu Val Lys Gly Met Gly Ser Gly Gly Ala Ala
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Asn Cys Pro Ala Asn Thr Tyr Cys Val Glu Asn Ala Gly Ser Tyr Ala
 35 40 45

Pro Arg Met Thr Leu Gln Asp Ala Leu Ala Gln Ser Pro Asn Thr Ala
 50 55 60

Phe Val Glu Met Ile Glu Gln Val Gly Val Asp Thr Val Val Asp Leu
 65 70 75 80

Ser Val Lys Leu Gly Leu Arg Ser Tyr Thr Asp Glu Gly Ser Phe Asp
 85 90 95

Gly Glu Ser Ser Ile Ala Asp Tyr Met Lys Asp Asn Asn Leu Gly Ser
 100 105 110

Tyr Thr Leu Gly Pro Thr Ala Val Asn Pro Leu Glu Leu Ser Asn Val
 115 120 125

Ala Ala Thr Ile Ala Ser Gly Gly Met Trp Cys Glu Pro Asn Pro Ile
 130 135 140

Ala Ser Val His Asp Arg Glu Gly Asn Glu Val Tyr Ile Asp Arg Pro
 145 150 155 160

Ala Cys Glu Arg Ala Ile Asp Ala Glu Thr Ala Ser Ala Leu Ala Val
 165 170 175

Gly Met Ser Lys Asp Thr Val Ser Gly Thr Ala Ala Ser Ala Ala Ser
 180 185 190

Met Tyr Gly Trp Ser Leu Pro Thr Ala Ala Lys Thr Gly Thr Thr Glu
 195 200 205

Ser Asn Gln Ser Ser Ala Phe Met Gly Phe Asn Ser Asn Phe Ala Ala
 210 215 220

Ala Pro Tyr Ile Tyr Asn Asp Gly Thr Ser Thr Thr Pro Leu Cys Ser

225		230		235		240
Gly Pro Val Arg	Gln Cys Ser Ser	Gly Asn Leu Phe	Gly Gly Asn Glu			
	245	250	255			
Pro Ala Gln Thr	Trp Phe Asn Met	Ala Ser Asn Val	Pro Ala Ala Ser			
	260	265	270			
Gln Gly Thr Leu	Pro Ser Ser Ser	Asp Ser Phe Arg	Leu Gly Thr Ser			
	275	280	285			
Gly Glu Leu Leu	Asn Gln Val Val	Gly Gln Ser Glu	Ala Ser Ala Arg			
	290	295	300			
Arg Thr Leu Glu	Ala Lys Gly Tyr	Lys Val Thr Thr	Arg Ser Val Ser			
	305	310	315			320
Gly Ala Gly Ser	Ala Arg Gly Thr	Val Val Ser Ala	Thr Pro Gln Gly			
	325	330	335			
Ala Val Leu Ile	Asp Gly Gly Thr	Val Ile Leu Asp	Ile Ser Asp Gly			
	340	345	350			
Thr Ser Pro Ala	Pro Ala Ala Thr	Asn Asn Asp Asp	Ser Asp Asp Gly			
	355	360	365			
Asp Thr Pro Ala	Pro Ser Thr Asn	Asn Arg Gly Thr	Thr Thr Ile Glu			
	370	375	380			
Ala Ile Asn Asp	Ala Ile Asn Gln	Phe Phe Arg				
	385	390	395			

<210> 57

<211> 1404

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1381)

<223> RXA01510

<400> 57

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	Met Lys Asn Ala Trp	
	1 5	

tgg gtt ggc tca tcg gtt ggt gta ctg att gca gtg ggg gct gtc atc	163
Trp Val Gly Ser Ser Val Gly Val Leu Ile Ala Val Gly Ala Val Ile	
	10 15 20

ggt ggt ggc gtg tgg gtg aat cat tct ggt ttt ggt ttg gat cac ccg	211
Gly Gly Gly Val Trp Val Asn His Ser Gly Phe Gly Leu Asp His Pro	
	25 30 35

gag ccc atg tcg gtg gag atg cct gag cag ctg ttt tct tct gcg att	259
Glu Pro Met Ser Val Glu Met Pro Glu Gln Leu Phe Ser Ser Ala Ile	
	40 45 50

gat ccg gat gct ttg gaa gcc cca gat ttt gcc act ttg gag aag gat	307
Asp Pro Asp Ala Leu Glu Ala Pro Asp Phe Ala Thr Leu Glu Lys Asp	
55 60 65	
ttg acc tcg cag gct gcg gat tct cgg ttg ggc act ttt gtc ggt gtt	355
Leu Thr Ser Gln Ala Ala Asp Ser Arg Leu Gly Thr Phe Val Gly Val	
70 75 80 85	
gcc agg gat gtg gaa tct ggt gag gtg gtg tgg gag cag aat cag ggg	403
Ala Arg Asp Val Glu Ser Gly Glu Val Val Trp Glu Gln Asn Gln Gly	
90 95 100	
act gcg gtg agg ccg gcg tcg gcg acg aag att ttg acg gcg gcg gtg	451
Thr Ala Val Arg Pro Ala Ser Ala Thr Lys Ile Leu Thr Ala Ala Val	
105 110 115	
gcg ttg tat gag ctt ggc cgt gag gac acc atc aca acg aag gtt gtt	499
Ala Leu Tyr Glu Leu Gly Arg Glu Asp Thr Ile Thr Thr Lys Val Val	
120 125 130	
gag ggg gag cag ccg gga acg gtg gtg att aag gcg ggt ggt gat gtc	547
Glu Gly Glu Gln Pro Gly Thr Val Val Ile Lys Ala Gly Gly Asp Val	
135 140 145	
acg ttg agt gag gag atg ctc gat gat ttg gcc acc cag ctt gag ggg	595
Thr Leu Ser Glu Glu Met Leu Asp Asp Leu Ala Thr Gln Leu Glu Gly	
150 155 160 165	
caa gat att ggc act gtg ttg atc gat acg tct att tgg cct gat gag	643
Gln Asp Ile Gly Thr Val Leu Ile Asp Thr Ser Ile Trp Pro Asp Glu	
170 175 180	
ggc ttt gct agt acg tgg gat cca gtg gat gtt gat gct ggt tat atc	691
Gly Phe Ala Ser Thr Trp Asp Pro Val Asp Val Asp Ala Gly Tyr Ile	
185 190 195	
gct gat gtg gag ccc gcg atg att gag gct gcc cgc att ggt ggg tcg	739
Ala Asp Val Glu Pro Ala Met Ile Glu Ala Ala Arg Ile Gly Gly Ser	
200 205 210	
gag ggg gat ctg ccg agg tct cat act ccg gcg tta gat gtt gcg cag	787
Glu Gly Asp Leu Pro Arg Ser His Thr Pro Ala Leu Asp Val Ala Gln	
215 220 225	
gcg ttg gcg gat cgt gtc ggc gcg gac acc gta gat gag ggc agc gct	835
Ala Leu Ala Asp Arg Val Gly Ala Asp Thr Val Asp Glu Gly Ser Ala	
230 235 240 245	
ccg gac aaa acc gtg ctg gca tcc gtg gag tct gac acg ttg gat cag	883
Pro Asp Lys Thr Val Leu Ala Ser Val Glu Ser Asp Thr Leu Asp Gln	
250 255 260	
cgt ctt gct cgg atg atg aag gat tct gac aat gtg atg gca gag ggt	931
Arg Leu Ala Arg Met Met Lys Asp Ser Asp Asn Val Met Ala Glu Gly	
265 270 275	
atc gct aag gaa gtg gcc gcg tcg aag gat ttg gct acc gat tcg gcg	979
Ile Ala Lys Glu Val Ala Ala Ser Lys Asp Leu Ala Thr Asp Ser Ala	
280 285 290	

agt acc tcg aag atg acg ttg gag att ctc aag gac aag ggc ttc gat 1027
 Ser Thr Ser Lys Met Thr Leu Glu Ile Leu Lys Asp Lys Gly Phe Asp
 295 300 305
 ttg agt ggc gtg tcc att gtg gat aat tcg ggt ttg agc ttt gac aac 1075
 Leu Ser Gly Val Ser Ile Val Asp Asn Ser Gly Leu Ser Phe Asp Asn
 310 315 320 325
 ctc att acg ccc cgc ctg ctt gat gat att ttg acc cgc gcc gcc acg 1123
 Leu Ile Thr Pro Arg Leu Leu Asp Asp Ile Leu Thr Arg Ala Ala Thr
 330 335 340
 gaa cct gag ttg agt tca cta ttg aca tcg ctg cct atc gcg cat gga 1171
 Glu Pro Glu Leu Ser Ser Leu Leu Thr Ser Leu Pro Ile Ala His Gly
 345 350 355
 acc gga acc ttg gag gat cgc tac gac gga ctc tca ggt gcg ggt tgg 1219
 Thr Gly Thr Leu Glu Asp Arg Tyr Asp Gly Leu Ser Gly Ala Gly Trp
 360 365 370
 gtg cgg gcg aaa act ggc act ctg acg gat aca tcg gca ttg gca ggg 1267
 Val Arg Ala Lys Thr Gly Thr Leu Thr Asp Thr Ser Ala Leu Ala Gly
 375 380 385
 gtg gtg acc tcg gag tcg ggg cgt gtg ttt acc ttt gct ttt gtg tct 1315
 Val Val Thr Ser Glu Ser Gly Arg Val Phe Thr Phe Ala Phe Val Ser
 390 395 400 405
 aat ggt tcc gcg att gtg ccg gcg cgt gag gct ttg gat gag atg gcg 1363
 Asn Gly Ser Ala Ile Val Pro Ala Arg Glu Ala Leu Asp Glu Met Ala
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 tcg att ctg agg gac ttt taagggtggca tccctcatcg gga 1404
 Ser Ile Leu Arg Asp Phe
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<210> 58

<211> 427

<212> PRT

<213> Corynebacterium glutamicum

<400> 58

Met Lys Asn Ala Trp Trp Val Gly Ser Ser Val Gly Val Leu Ile Ala
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 Val Gly Ala Val Ile Gly Gly Gly Val Trp Val Asn His Ser Gly Phe
 20 25 30
 Gly Leu Asp His Pro Glu Pro Met Ser Val Glu Met Pro Glu Gln Leu
 35 40 45
 Phe Ser Ser Ala Ile Asp Pro Asp Ala Leu Glu Ala Pro Asp Phe Ala
 50 55 60
 Thr Leu Glu Lys Asp Leu Thr Ser Gln Ala Ala Asp Ser Arg Leu Gly
 65 70 75 80
 Thr Phe Val Gly Val Ala Arg Asp Val Glu Ser Gly Glu Val Val Trp
 85 90 95

Glu Gln Asn Gln Gly Thr Ala Val Arg Pro Ala Ser Ala Thr Lys Ile
 100 105 110
 Leu Thr Ala Ala Val Ala Leu Tyr Glu Leu Gly Arg Glu Asp Thr Ile
 115 120 125
 Thr Thr Lys Val Val Glu Gly Glu Gln Pro Gly Thr Val Val Ile Lys
 130 135 140
 Ala Gly Gly Asp Val Thr Leu Ser Glu Glu Met Leu Asp Asp Leu Ala
 145 150 155 160
 Thr Gln Leu Glu Gly Gln Asp Ile Gly Thr Val Leu Ile Asp Thr Ser
 165 170 175
 Ile Trp Pro Asp Glu Gly Phe Ala Ser Thr Trp Asp Pro Val Asp Val
 180 185 190
 Asp Ala Gly Tyr Ile Ala Asp Val Glu Pro Ala Met Ile Glu Ala Ala
 195 200 205
 Arg Ile Gly Gly Ser Glu Gly Asp Leu Pro Arg Ser His Thr Pro Ala
 210 215 220
 Leu Asp Val Ala Gln Ala Leu Ala Asp Arg Val Gly Ala Asp Thr Val
 225 230 235 240
 Asp Glu Gly Ser Ala Pro Asp Lys Thr Val Leu Ala Ser Val Glu Ser
 245 250 255
 Asp Thr Leu Asp Gln Arg Leu Ala Arg Met Met Lys Asp Ser Asp Asn
 260 265 270
 Val Met Ala Glu Gly Ile Ala Lys Glu Val Ala Ala Ser Lys Asp Leu
 275 280 285
 Ala Thr Asp Ser Ala Ser Thr Ser Lys Met Thr Leu Glu Ile Leu Lys
 290 295 300
 Asp Lys Gly Phe Asp Leu Ser Gly Val Ser Ile Val Asp Asn Ser Gly
 305 310 315 320
 Leu Ser Phe Asp Asn Leu Ile Thr Pro Arg Leu Leu Asp Asp Ile Leu
 325 330 335
 Thr Arg Ala Ala Thr Glu Pro Glu Leu Ser Ser Leu Leu Thr Ser Leu
 340 345 350
 Pro Ile Ala His Gly Thr Gly Thr Leu Glu Asp Arg Tyr Asp Gly Leu
 355 360 365
 Ser Gly Ala Gly Trp Val Arg Ala Lys Thr Gly Thr Leu Thr Asp Thr
 370 375 380
 Ser Ala Leu Ala Gly Val Val Thr Ser Glu Ser Gly Arg Val Phe Thr
 385 390 395 400

 Phe Ala Phe Val Ser Asn Gly Ser Ala Ile Val Pro Ala Arg Glu Ala
 405 410 415
 Leu Asp Glu Met Ala Ser Ile Leu Arg Asp Phe

420

425

<210> 59
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1939)
 <223> RXN01608

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 Met Ala Leu Cys Met
 1 5

acg gtg gca ttt gct gga gga agc ctg acc gcg tgc aca cct cgt cct 163
 Thr Val Ala Phe Ala Gly Gly Ser Leu Thr Ala Cys Thr Pro Arg Pro
 10 15 20

gat acc gca gac ccc atc gca gag gaa ttc ctt caa gct tgg gca tcg 211
 Asp Thr Ala Asp Pro Ile Ala Glu Glu Phe Leu Gln Ala Trp Ala Ser
 25 30 35

caa gat ttc gac act att gcg gac atc acc gac caa gct gac ctt gcc 259
 Gln Asp Phe Asp Thr Ile Ala Asp Ile Thr Asp Gln Ala Asp Leu Ala
 40 45 50

aca gaa atg ctc agc acc agt ttc gat ggt ctg caa gca gac agc gtt 307
 Thr Glu Met Leu Ser Thr Ser Phe Asp Gly Leu Gln Ala Asp Ser Val
 55 60 65

gaa ctg act ttg gat tcc gtg gat tcc cgg gac acc atc gcc acc gcc 355
 Glu Leu Thr Leu Asp Ser Val Asp Ser Arg Asp Thr Ile Ala Thr Ala
 70 75 80 85

aat ttc tcc gtg gtg tgg aag ctt ccc cga gac aga gaa gtt tcc tac 403
 Asn Phe Ser Val Val Trp Lys Leu Pro Arg Asp Arg Glu Val Ser Tyr
 90 95 100

gac tca tcg atg acg ctg acc aag atg cgc aac gaa tgg aca gtg cgt 451
 Asp Ser Ser Met Thr Leu Thr Lys Met Arg Asn Glu Trp Thr Val Arg
 105 110 115

tgg gaa cct tcc ctc gtg cac ccc aaa ctg ggc gcc aac cag cac ctg 499
 Trp Glu Pro Ser Leu Val His Pro Lys Leu Gly Ala Asn Gln His Leu
 120 125 130

gaa ttg cgc gcc att gaa gcg cag cga gcc aac gta att tcc tcc gat 547
 Glu Leu Arg Ala Ile Glu Ala Gln Arg Ala Asn Val Ile Ser Ser Asp
 135 140 145

gga gct ccg gtt ctc gcg ccg gga agt atc tac cga gtt ttg gtt gat 595
 Gly Ala Pro Val Leu Ala Pro Gly Ser Ile Tyr Arg Val Leu Val Asp
 150 155 160 165

ccc agc gca ggg gat gcc gat gtg gtg gtc aag agg gtg gca gat tat 643

Pro	Ser	Ala	Gly	Asp	Ala	Asp	Val	Val	Val	Lys	Arg	Val	Ala	Asp	Tyr	
				170					175					180		
ttg	aat	gaa	gcc	cat	gcg	act	gat	gag	aat	gtg	aac	acc	ctt	gat	gtc	691
Leu	Asn	Glu	Ala	His	Ala	Thr	Asp	Glu	Asn	Val	Asn	Thr	Leu	Asp	Val	
			185					190					195			
gaa	gac	att	atg	agc	aat	ctt	ggc	gat	tcc	acc	tat	tca	ctc	acc	aca	739
Glu	Asp	Ile	Met	Ser	Asn	Leu	Gly	Asp	Ser	Thr	Tyr	Ser	Leu	Thr	Thr	
		200					205					210				
gtt	gat	gcc	aat	ttg	ggg	gcc	cgc	atg	gaa	cag	gat	cta	gcg	ggg	att	787
Val	Asp	Ala	Asn	Leu	Gly	Ala	Arg	Met	Glu	Gln	Asp	Leu	Ala	Gly	Ile	
	215					220					225					
ccg	ggg	ctg	acg	ttc	aat	gag	gaa	gca	tcc	atg	gta	gcc	acc	gac	cca	835
Pro	Gly	Leu	Thr	Phe	Asn	Glu	Glu	Ala	Ser	Met	Val	Ala	Thr	Asp	Pro	
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ggg	ttt	gct	ccg	gat	att	gtg	tct	cgc	gtt	gcg	cgc	att	gtg	gaa	gat	883
Gly	Phe	Ala	Pro	Asp	Ile	Val	Ser	Arg	Val	Ala	Arg	Ile	Val	Glu	Asp	
				250					255					260		
gaa	tta	gaa	gga	tcc	aat	ggg	tgg	cgc	gcc	tcc	att	gtc	act	tcc	aat	931
Glu	Leu	Glu	Gly	Ser	Asn	Gly	Trp	Arg	Ala	Ser	Ile	Val	Thr	Ser	Asn	
			265					270					275			
ggg	gcg	gtg	att	gat	gat	atc	gcc	tac	gac	gcc	cca	gag	ctt	gcc	ccc	979
Gly	Ala	Val	Ile	Asp	Asp	Ile	Ala	Tyr	Asp	Ala	Pro	Glu	Leu	Ala	Pro	
		280					285					290				
agc	gtg	agg	atc	agc	ctg	gat	cac	aac	gtt	caa	cga	gca	gcg	gaa	gaa	1027
Ser	Val	Arg	Ile	Ser	Leu	Asp	His	Asn	Val	Gln	Arg	Ala	Ala	Glu	Glu	
	295					300					305					
gcc	gta	gac	ctg	cgc	gct	gag	atg	aaa	gcc	atg	atg	gtg	gtc	atg	agg	1075
Ala	Val	Asp	Leu	Arg	Ala	Glu	Met	Lys	Ala	Met	Met	Val	Val	Met	Arg	
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cca	tcc	act	ggg	gaa	atc	ctc	gca	gtg	gcc	caa	aca	gat	gaa	gct	gac	1123
Pro	Ser	Thr	Gly	Glu	Ile	Leu	Ala	Val	Ala	Gln	Thr	Asp	Glu	Ala	Asp	
				330					335					340		
aaa	gac	ggc	gat	gtt	gcg	ctg	atg	gga	caa	tac	cca	ccg	gga	tgc	aca	1171
Lys	Asp	Gly	Asp	Val	Ala	Leu	Met	Gly	Gln	Tyr	Pro	Pro	Gly	Ser	Thr	
			345					350					355			
ttc	aag	atc	atc	act	gca	gcc	gcg	ggg	ttg	gcg	cat	gaa	gga	tta	act	1219
Phe	Lys	Ile	Ile	Thr	Ala	Ala	Ala	Gly	Leu	Ala	His	Glu	Gly	Leu	Thr	
		360					365					370				
cca	gac	agc	att	gtg	cca	tgc	cct	ggc	acc	atg	aat	atc	tac	ggc	cga	1267
Pro	Asp	Ser	Ile	Val	Pro	Cys	Pro	Gly	Thr	Met	Asn	Ile	Tyr	Gly	Arg	
	375					380					385					
att	gtc	acc	aac	tac	aac	agc	ttc	tcc	ttg	ggc	aac	acc	tca	ttg	gat	1315
Ile	Val	Thr	Asn	Tyr	Asn	Ser	Phe	Ser	Leu	Gly	Asn	Thr	Ser	Leu	Asp	
390					395					400					405	
gat	gct	ttt	gcc	aat	tca	tgc	aac	acc	act	ttc	gcg	gat	att	ttc	cac	1363
Asp	Ala	Phe	Ala	Asn	Ser	Cys	Asn	Thr	Thr	Phe	Ala	Asp	Ile	Phe	His	

410										415					420					
cac	ttg	gag	cca	ggc	caa	ctg	aaa	aat	gtg	gct	aag	cag	ttt	ggc	ctc	1411				
His	Leu	Glu	Pro	Gly	Gln	Leu	Lys	Asn	Val	Ala	Lys	Gln	Phe	Gly	Leu					
			425					430					435							
gga	att	gat	tat	caa	atc	cca	ggc	ctt	gac	acc	atg	acg	gga	tcg	gtg	1459				
Gly	Ile	Asp	Tyr	Gln	Ile	Pro	Gly	Leu	Asp	Thr	Met	Thr	Gly	Ser	Val					
		440					445					450								
cct	gaa	ggt	gac	atc	gtg	ttg	gac	cgt	acc	gaa	tct	ggt	tac	ggc	cag	1507				
Pro	Glu	Gly	Asp	Ile	Val	Leu	Asp	Arg	Thr	Glu	Ser	Gly	Tyr	Gly	Gln					
	455					460					465									
ggt	ctt	gac	cta	gca	agt	ccc	ttt	ggc	atg	gcg	ttg	gtc	gcc	tcc	act	1555				
Gly	Leu	Asp	Leu	Ala	Ser	Pro	Phe	Gly	Met	Ala	Leu	Val	Ala	Ser	Thr					
470					475					480					485					
gca	gcc	acc	ggt	tca	gtt	ccc	acg	cca	acg	ctg	att	tct	gga	cat	gaa	1603				
Ala	Ala	Thr	Gly	Ser	Val	Pro	Thr	Pro	Thr	Leu	Ile	Ser	Gly	His	Glu					
			490					495						500						
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Thr	Val	Ala	Ser	Glu	Glu	Val	Leu	Ala	Leu	Asp	Pro	Glu	Val	Leu	Ala					
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aat	gtg	cag	cgg	atg	atg	aaa	tcc	gtg	gtc	aat	gac	ggt	acc	gct	cgt	1699				
Asn	Val	Gln	Arg	Met	Met	Lys	Ser	Val	Val	Asn	Asp	Gly	Thr	Ala	Arg					
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ggc	atg	cgc	caa	acc	ggt	ggc	cag	atc	tac	gca	aag	aca	ggt	gaa	gcc	1747				
Gly	Met	Arg	Gln	Thr	Gly	Gly	Gln	Ile	Tyr	Ala	Lys	Thr	Gly	Glu	Ala					
	535					540					545									
gaa	atc	aac	gaa	ggc	tcc	cat	gcg	tgg	ttc	acc	ggc	tac	cgc	gaa	gat	1795				
Glu	Ile	Asn	Glu	Gly	Ser	His	Ala	Trp	Phe	Thr	Gly	Tyr	Arg	Glu	Asp					
550					555					560					565					
gac	atc	gct	ttt	gcc	acc	ctc	gtg	gtg	ttg	ggc	gga	ggc	tcc	gaa	gcg	1843				
Asp	Ile	Ala	Phe	Ala	Thr	Leu	Val	Val	Leu	Gly	Gly	Gly	Ser	Glu	Ala					
			570						575					580						
gct	gcc	gct	gtg	aca	gat	cag	ttc	ttt	gtg	aaa	ctc	gat	gag	ctt	cgc	1891				
Ala	Ala	Ala	Val	Thr	Asp	Gln	Phe	Phe	Val	Lys	Leu	Asp	Glu	Leu	Arg					
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Ala	Gly	Gly	Glu	Val	Ala	Val	Ser	Glu	Ala	Glu	Glu	Gln	Pro	Val	Gly					
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<212> PRT

<213> Corynebacterium glutamicum

<400> 60

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 Gln Ala Trp Ala Ser Gln Asp Phe Asp Thr Ile Ala Asp Ile Thr Asp
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 Gln Ala Asp Leu Ala Thr Glu Met Leu Ser Thr Ser Phe Asp Gly Leu
 50 55 60
 Gln Ala Asp Ser Val Glu Leu Thr Leu Asp Ser Val Asp Ser Arg Asp
 65 70 75 80
 Thr Ile Ala Thr Ala Asn Phe Ser Val Val Trp Lys Leu Pro Arg Asp
 85 90 95
 Arg Glu Val Ser Tyr Asp Ser Ser Met Thr Leu Thr Lys Met Arg Asn
 100 105 110
 Glu Trp Thr Val Arg Trp Glu Pro Ser Leu Val His Pro Lys Leu Gly
 115 120 125
 Ala Asn Gln His Leu Glu Leu Arg Ala Ile Glu Ala Gln Arg Ala Asn
 130 135 140
 Val Ile Ser Ser Asp Gly Ala Pro Val Leu Ala Pro Gly Ser Ile Tyr
 145 150 155 160
 Arg Val Leu Val Asp Pro Ser Ala Gly Asp Ala Asp Val Val Val Lys
 165 170 175
 Arg Val Ala Asp Tyr Leu Asn Glu Ala His Ala Thr Asp Glu Asn Val
 180 185 190
 Asn Thr Leu Asp Val Glu Asp Ile Met Ser Asn Leu Gly Asp Ser Thr
 195 200 205
 Tyr Ser Leu Thr Thr Val Asp Ala Asn Leu Gly Ala Arg Met Glu Gln
 210 215 220
 Asp Leu Ala Gly Ile Pro Gly Leu Thr Phe Asn Glu Glu Ala Ser Met
 225 230 235 240
 Val Ala Thr Asp Pro Gly Phe Ala Pro Asp Ile Val Ser Arg Val Ala
 245 250 255
 Arg Ile Val Glu Asp Glu Leu Glu Gly Ser Asn Gly Trp Arg Ala Ser
 260 265 270
 Ile Val Thr Ser Asn Gly Ala Val Ile Asp Asp Ile Ala Tyr Asp Ala
 275 280 285
 Pro Glu Leu Ala Pro Ser Val Arg Ile Ser Leu Asp His Asn Val Gln
 290 295 300
 Arg Ala Ala Glu Glu Ala Val Asp Leu Arg Ala Glu Met Lys Ala Met
 305 310 315 320
 Met Val Val Met Arg Pro Ser Thr Gly Glu Ile Leu Ala Val Ala Gln
 325 330 335

Thr Asp Glu Ala Asp Lys Asp Gly Asp Val Ala Leu Met Gly Gln Tyr
 340 345 350
 Pro Pro Gly Ser Thr Phe Lys Ile Ile Thr Ala Ala Ala Gly Leu Ala
 355 360 365
 His Glu Gly Leu Thr Pro Asp Ser Ile Val Pro Cys Pro Gly Thr Met
 370 375 380
 Asn Ile Tyr Gly Arg Ile Val Thr Asn Tyr Asn Ser Phe Ser Leu Gly
 385 390 395 400
 Asn Thr Ser Leu Asp Asp Ala Phe Ala Asn Ser Cys Asn Thr Thr Phe
 405 410 415
 Ala Asp Ile Phe His His Leu Glu Pro Gly Gln Leu Lys Asn Val Ala
 420 425 430
 Lys Gln Phe Gly Leu Gly Ile Asp Tyr Gln Ile Pro Gly Leu Asp Thr
 435 440 445
 Met Thr Gly Ser Val Pro Glu Gly Asp Ile Val Leu Asp Arg Thr Glu
 450 455 460
 Ser Gly Tyr Gly Gln Gly Leu Asp Leu Ala Ser Pro Phe Gly Met Ala
 465 470 475 480
 Leu Val Ala Ser Thr Ala Ala Thr Gly Ser Val Pro Thr Pro Thr Leu
 485 490 495
 Ile Ser Gly His Glu Thr Val Ala Ser Glu Glu Val Leu Ala Leu Asp
 500 505 510
 Pro Glu Val Leu Ala Asn Val Gln Arg Met Met Lys Ser Val Val Asn
 515 520 525
 Asp Gly Thr Ala Arg Gly Met Arg Gln Thr Gly Gly Gln Ile Tyr Ala
 530 535 540
 Lys Thr Gly Glu Ala Glu Ile Asn Glu Gly Ser His Ala Trp Phe Thr
 545 550 555 560
 Gly Tyr Arg Glu Asp Asp Ile Ala Phe Ala Thr Leu Val Val Leu Gly
 565 570 575
 Gly Gly Ser Glu Ala Ala Ala Ala Val Thr Asp Gln Phe Phe Val Lys
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 Glu Gln Pro Val Gly
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<210> 61

<211> 1962

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1939)

<223> FRXA01608

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Thr	Val	Ala	Phe	Ala	Gly	Gly	Ser	Leu	Thr	Ala	Cys	Thr	Pro	Arg	Pro	
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gat	acc	gca	gac	ccc	atc	gca	gag	gaa	ttc	ctt	caa	gct	tgg	gca	tcg	211
Asp	Thr	Ala	Asp	Pro	Ile	Ala	Glu	Glu	Phe	Leu	Gln	Ala	Trp	Ala	Ser	
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caa	gat	ttc	gac	act	att	gcg	gac	atc	acc	gac	caa	gct	gac	ctt	gcc	259
Gln	Asp	Phe	Asp	Thr	Ile	Ala	Asp	Ile	Thr	Asp	Gln	Ala	Asp	Leu	Ala	
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aca	gaa	atg	ctc	agc	acc	agt	ttc	gat	ggc	ctg	caa	gca	gac	agc	gtt	307
Thr	Glu	Met	Leu	Ser	Thr	Ser	Phe	Asp	Gly	Leu	Gln	Ala	Asp	Ser	Val	
	55					60					65					

gaa	ctg	act	ttg	gat	tcc	gtg	gat	tcc	cgg	gac	acc	atc	gcc	acc	gcc	355
Glu	Leu	Thr	Leu	Asp	Ser	Val	Asp	Ser	Arg	Asp	Thr	Ile	Ala	Thr	Ala	
	70					75				80					85	

aat	ttc	tcc	gtg	gtg	tgg	aag	ctt	ccc	cga	gac	aga	gaa	gtt	tcc	tac	403
Asn	Phe	Ser	Val	Val	Trp	Lys	Leu	Pro	Arg	Asp	Arg	Glu	Val	Ser	Tyr	
				90					95					100		

gac	tca	tcg	atg	acg	ctg	acc	aag	atg	cgc	aac	gaa	tgg	aca	gtg	cgt	451
Asp	Ser	Ser	Met	Thr	Leu	Thr	Lys	Met	Arg	Asn	Glu	Trp	Thr	Val	Arg	
			105					110					115			

tgg	gaa	cct	tcc	ctc	gtg	cac	ccc	aaa	ctg	ggc	gcc	aac	cag	cac	ctg	499
Trp	Glu	Pro	Ser	Leu	Val	His	Pro	Lys	Leu	Gly	Ala	Asn	Gln	His	Leu	
		120					125					130				

gaa	ttg	cgc	gcc	att	gaa	gcg	cag	cga	gcc	aac	gta	att	tcc	tcc	gat	547
Glu	Leu	Arg	Ala	Ile	Glu	Ala	Gln	Arg	Ala	Asn	Val	Ile	Ser	Ser	Asp	
	135					140					145					

gga	gct	ccg	gtt	ctc	gcg	ccg	gga	agt	atc	tac	cga	gtt	ttg	gtt	gat	595
Gly	Ala	Pro	Val	Leu	Ala	Pro	Gly	Ser	Ile	Tyr	Arg	Val	Leu	Val	Asp	
	150				155				160						165	

ccc	agc	gca	ggg	gat	gcc	gat	gtg	gtg	gtc	aag	agg	gtg	gca	gat	tat	643
Pro	Ser	Ala	Gly	Asp	Ala	Asp	Val	Val	Val	Lys	Arg	Val	Ala	Asp	Tyr	
				170					175					180		

ttg	aat	gaa	gcc	cat	gcg	act	gat	gag	aat	gtg	aac	acc	ctt	gat	gtc	691
Leu	Asn	Glu	Ala	His	Ala	Thr	Asp	Glu	Asn	Val	Asn	Thr	Leu	Asp	Val	
			185					190					195			

gaa	gac	att	atg	agc	aat	ctt	ggc	gat	tcc	acc	tat	tca	ctc	acc	aca	739
Glu	Asp	Ile	Met	Ser	Asn	Leu	Gly	Asp	Ser	Thr	Tyr	Ser	Leu	Thr	Thr	

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Val	Asp	Ala	Asn	Leu	Gly	Ala	Arg	Met	Glu	Gln	Asp	Leu	Ala	Gly	Ile	
215					220					225						
ccg	ggg	ctg	acg	ttc	aat	gag	gaa	gca	tcc	atg	gta	gcc	acc	gac	cca	835
Pro	Gly	Leu	Thr	Phe	Asn	Glu	Glu	Ala	Ser	Met	Val	Ala	Thr	Asp	Pro	
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Gly	Phe	Ala	Pro	Asp	Ile	Val	Ser	Arg	Val	Ala	Arg	Ile	Val	Glu	Asp	
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gaa	tta	gaa	gga	tcc	aat	ggt	tgg	cgc	gcc	tcc	att	gtc	act	tcc	aat	931
Glu	Leu	Glu	Gly	Ser	Asn	Gly	Trp	Arg	Ala	Ser	Ile	Val	Thr	Ser	Asn	
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ggt	gcg	gtg	att	gat	gat	atc	gcc	tac	gac	gcc	cca	gag	ctt	gcc	ccc	979
Gly	Ala	Val	Ile	Asp	Asp	Ile	Ala	Tyr	Asp	Ala	Pro	Glu	Leu	Ala	Pro	
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agc	gtg	agg	atc	agc	ctg	gat	cac	aac	gtt	caa	cga	gca	gcg	gaa	gaa	1027
Ser	Val	Arg	Ile	Ser	Leu	Asp	His	Asn	Val	Gln	Arg	Ala	Ala	Glu	Glu	
295					300					305						
gcc	gta	gac	ctg	cgc	gct	gag	atg	aaa	gcc	atg	atg	gtg	gtc	atg	agg	1075
Ala	Val	Asp	Leu	Arg	Ala	Glu	Met	Lys	Ala	Met	Met	Val	Val	Met	Arg	
310					315					320					325	
cca	tcc	act	ggt	gaa	atc	ctc	gca	gtg	gcc	caa	aca	gat	gaa	gct	gac	1123
Pro	Ser	Thr	Gly	Glu	Ile	Leu	Ala	Val	Ala	Gln	Thr	Asp	Glu	Ala	Asp	
330					335					340						
aaa	gac	ggc	gat	gtt	gcg	ctg	atg	gga	caa	tac	cca	ccg	gga	tcg	aca	1171
Lys	Asp	Gly	Asp	Val	Ala	Leu	Met	Gly	Gln	Tyr	Pro	Pro	Gly	Ser	Thr	
345					350					355						
ttc	aag	atc	atc	act	gca	gcc	gcg	ggg	ttg	gcg	cat	gaa	gga	tta	act	1219
Phe	Lys	Ile	Ile	Thr	Ala	Ala	Ala	Gly	Leu	Ala	His	Glu	Gly	Leu	Thr	
360					365					370						
cca	gac	agc	att	gtg	cca	tgc	cct	ggc	acc	atg	aat	atc	tac	ggc	cga	1267
Pro	Asp	Ser	Ile	Val	Pro	Cys	Pro	Gly	Thr	Met	Asn	Ile	Tyr	Gly	Arg	
375					380					385						
att	gtc	acc	aac	tac	aac	agc	ttc	tcc	ttg	ggc	aac	acc	tca	ttg	gat	1315
Ile	Val	Thr	Asn	Tyr	Asn	Ser	Phe	Ser	Leu	Gly	Asn	Thr	Ser	Leu	Asp	
390					395					400					405	
gat	gct	ttt	gcc	aat	tca	tgc	aac	acc	act	ttc	gcg	gat	att	ttc	cac	1363
Asp	Ala	Phe	Ala	Asn	Ser	Cys	Asn	Thr	Thr	Phe	Ala	Asp	Ile	Phe	His	
410					415					420						
cac	ttg	gag	cca	ggc	caa	ctg	aaa	aat	gtg	gct	aag	cag	ttt	ggc	ctc	1411
His	Leu	Glu	Pro	Gly	Gln	Leu	Lys	Asn	Val	Ala	Lys	Gln	Phe	Gly	Leu	
425					430					435						
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Gly	Ile	Asp	Tyr	Gln	Ile	Pro	Gly	Leu	Asp	Thr	Met	Thr	Gly	Ser	Val	
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cct gaa ggt gac atc gtg ttg gac cgt acc gaa tct ggt tac ggc cag 1507
 Pro Glu Gly Asp Ile Val Leu Asp Arg Thr Glu Ser Gly Tyr Gly Gln
 455 460 465

ggt ctt gac cta gca agt ccc ttt ggc atg gcg ttg gtc gcc tcc act 1555
 Gly Leu Asp Leu Ala Ser Pro Phe Gly Met Ala Leu Val Ala Ser Thr
 470 475 480 485

gca gcc acc ggt tca gtt ccc acg cca acg ctg att tct gga cat gaa 1603
 Ala Ala Thr Gly Ser Val Pro Thr Pro Thr Leu Ile Ser Gly His Glu
 490 495 500

act gtt gcc agt gaa gaa gtt ctg gcg ctt gat cca gaa gtc ctt gcc 1651
 Thr Val Ala Ser Glu Glu Val Leu Ala Leu Asp Pro Glu Val Leu Ala
 505 510 515

aat gtg cag cgg atg atg aaa tcc gtg gtc aat gac ggt acc gct cgt 1699
 Asn Val Gln Arg Met Met Lys Ser Val Val Asn Asp Gly Thr Ala Arg
 520 525 530

ggc atg cgc caa acc ggt ggc cag atc tac gca aag aca ggt gaa gcc 1747
 Gly Met Arg Gln Thr Gly Gly Gln Ile Tyr Ala Lys Thr Gly Glu Ala
 535 540 545

gaa atc aac gaa ggc tcc cat gcg tgg ttc acc ggc tac cgc gaa gat 1795
 Glu Ile Asn Glu Gly Ser His Ala Trp Phe Thr Gly Tyr Arg Glu Asp
 550 555 560 565

gac atc gct ttt gcc acc ctc gtg gtg ttg ggc gga ggc tcc gaa gcg 1843
 Asp Ile Ala Phe Ala Thr Leu Val Val Leu Gly Gly Gly Ser Glu Ala
 570 575 580

gct gcc gct gtg aca gat cag ttc ttt gtg aaa ctc gat gag ctt cgc 1891
 Ala Ala Ala Val Thr Asp Gln Phe Phe Val Lys Leu Asp Glu Leu Arg
 585 590 595

gca ggg gga gaa gtt gca gtc agt gaa gct gaa gag cag cca gtc ggc 1939
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<211> 613

<212> PRT

<213> *Corynebacterium glutamicum*

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 35 40 45

Gln Ala Asp Leu Ala Thr Glu Met Leu Ser Thr Ser Phe Asp Gly Leu
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Gln	Ala	Asp	Ser	Val	Glu	Leu	Thr	Leu	Asp	Ser	Val	Asp	Ser	Arg	Asp	
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Thr	Ile	Ala	Thr	Ala	Asn	Phe	Ser	Val	Val	Trp	Lys	Leu	Pro	Arg	Asp	
				85					90					95		
Arg	Glu	Val	Ser	Tyr	Asp	Ser	Ser	Met	Thr	Leu	Thr	Lys	Met	Arg	Asn	
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Glu	Trp	Thr	Val	Arg	Trp	Glu	Pro	Ser	Leu	Val	His	Pro	Lys	Leu	Gly	
		115					120					125				
Ala	Asn	Gln	His	Leu	Glu	Leu	Arg	Ala	Ile	Glu	Ala	Gln	Arg	Ala	Asn	
		130				135					140					
Val	Ile	Ser	Ser	Asp	Gly	Ala	Pro	Val	Leu	Ala	Pro	Gly	Ser	Ile	Tyr	
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Arg	Val	Leu	Val	Asp	Pro	Ser	Ala	Gly	Asp	Ala	Asp	Val	Val	Val	Lys	
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Arg	Val	Ala	Asp	Tyr	Leu	Asn	Glu	Ala	His	Ala	Thr	Asp	Glu	Asn	Val	
			180					185					190			
Asn	Thr	Leu	Asp	Val	Glu	Asp	Ile	Met	Ser	Asn	Leu	Gly	Asp	Ser	Thr	
		195					200					205				
Tyr	Ser	Leu	Thr	Thr	Val	Asp	Ala	Asn	Leu	Gly	Ala	Arg	Met	Glu	Gln	
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Asp	Leu	Ala	Gly	Ile	Pro	Gly	Leu	Thr	Phe	Asn	Glu	Glu	Ala	Ser	Met	
225					230					235					240	
Val	Ala	Thr	Asp	Pro	Gly	Phe	Ala	Pro	Asp	Ile	Val	Ser	Arg	Val	Ala	
				245					250					255		
Arg	Ile	Val	Glu	Asp	Glu	Leu	Glu	Gly	Ser	Asn	Gly	Trp	Arg	Ala	Ser	
			260					265					270			
Ile	Val	Thr	Ser	Asn	Gly	Ala	Val	Ile	Asp	Asp	Ile	Ala	Tyr	Asp	Ala	
		275					280					285				
Pro	Glu	Leu	Ala	Pro	Ser	Val	Arg	Ile	Ser	Leu	Asp	His	Asn	Val	Gln	
	290					295					300					
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Met	Val	Val	Met	Arg	Pro	Ser	Thr	Gly	Glu	Ile	Leu	Ala	Val	Ala	Gln	
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Thr	Asp	Glu	Ala	Asp	Lys	Asp	Gly	Asp	Val	Ala	Leu	Met	Gly	Gln	Tyr	
			340					345					350			
Pro	Pro	Gly	Ser	Thr	Phe	Lys	Ile	Ile	Thr	Ala	Ala	Ala	Gly	Leu	Ala	
		355					360					365				
His	Glu	Gly	Leu	Thr	Pro	Asp	Ser	Ile	Val	Pro	Cys	Pro	Gly	Thr	Met	
	370					375					380					

Asn Ile Tyr Gly Arg Ile Val Thr Asn Tyr Asn Ser Phe Ser Leu Gly
 385 390 395 400
 Asn Thr Ser Leu Asp Asp Ala Phe Ala Asn Ser Cys Asn Thr Thr Phe
 405 410 415
 Ala Asp Ile Phe His His Leu Glu Pro Gly Gln Leu Lys Asn Val Ala
 420 425 430
 Lys Gln Phe Gly Leu Gly Ile Asp Tyr Gln Ile Pro Gly Leu Asp Thr
 435 440 445
 Met Thr Gly Ser Val Pro Glu Gly Asp Ile Val Leu Asp Arg Thr Glu
 450 455 460
 Ser Gly Tyr Gly Gln Gly Leu Asp Leu Ala Ser Pro Phe Gly Met Ala
 465 470 475 480
 Leu Val Ala Ser Thr Ala Ala Thr Gly Ser Val Pro Thr Pro Thr Leu
 485 490 495
 Ile Ser Gly His Glu Thr Val Ala Ser Glu Glu Val Leu Ala Leu Asp
 500 505 510
 Pro Glu Val Leu Ala Asn Val Gln Arg Met Met Lys Ser Val Val Asn
 515 520 525
 Asp Gly Thr Ala Arg Gly Met Arg Gln Thr Gly Gly Gln Ile Tyr Ala
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 Lys Thr Gly Glu Ala Glu Ile Asn Glu Gly Ser His Ala Trp Phe Thr
 545 550 555 560
 Gly Tyr Arg Glu Asp Asp Ile Ala Phe Ala Thr Leu Val Val Leu Gly
 565 570 575
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<210> 63
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1255)
 <223> RXA01270

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 Met Thr Asn Glu Arg

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Ile Phe Leu Ser Ser Pro Asp Val Thr Gln Leu Glu Glu Asp Ala Leu															
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gta cgc gca atc cga tca gga tgg att gca ccg ctt ggt cca gaa gtt	211														
Val Arg Ala Ile Arg Ser Gly Trp Ile Ala Pro Leu Gly Pro Glu Val															
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Asp Ala Phe Glu Gln Glu Leu Ala Glu Tyr Cys Gly Arg Lys Tyr Val															
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gtt gca ctt tca tgc ggt act gca gcc ctc cac tta ggt cta tta gca	307														
Val Ala Leu Ser Ser Gly Thr Ala Ala Leu His Leu Gly Leu Leu Ala															
	55					60				65					
cta ggc gtt gga gaa gga gac ttg gtt ctt aca tca tca atg act ttt	355														
Leu Gly Val Gly Glu Gly Asp Leu Val Leu Thr Ser Ser Met Thr Phe															
	70				75			80						85	
gca gcg acc acc aac gca att gtt tat acg ggt gct gag cca att ttc	403														
Ala Ala Thr Thr Asn Ala Ile Val Tyr Thr Gly Ala Glu Pro Ile Phe															
				90				95					100		
gtg gac tgc gat gaa tct gga aat atg gat cca gat ctt tta gaa aaa	451														
Val Asp Cys Asp Glu Ser Gly Asn Met Asp Pro Asp Leu Leu Glu Lys															
		105					110					115			
gcc ttt gct gag cta aag agt gaa gga aag gaa gta aag gct gta gta	499														
Ala Phe Ala Glu Leu Lys Ser Glu Gly Lys Glu Val Lys Ala Val Val															
		120				125				130					
cct gtc gat cta ctt ggc aaa gtt gtt cag cac gag aag att aaa aag	547														
Pro Val Asp Leu Leu Gly Lys Val Val Gln His Glu Lys Ile Lys Lys															
	135				140					145					
att gct gat gaa tac ggg gca gta gtg ctt tct gat gcc gct gaa tcc	595														
Ile Ala Asp Glu Tyr Gly Ala Val Val Leu Ser Asp Ala Ala Glu Ser															
	150				155			160					165		
ttg ggc gcc att cgc aat gga aag tct gct gca gca tat gga gtg gcg	643														
Leu Gly Ala Ile Arg Asn Gly Lys Ser Ala Ala Ala Tyr Gly Val Ala															
			170				175					180			
gca gcg gtt tcc ttc aac gga aac aaa att atg act acc agc ggt ggt	691														
Ala Ala Val Ser Phe Asn Gly Asn Lys Ile Met Thr Thr Ser Gly Gly															
		185					190					195			
gga gct ttg tta act gat gac aag gat att gca gac aac gtc cgc tat	739														
Gly Ala Leu Leu Thr Asp Asp Lys Asp Ile Ala Asp Asn Val Arg Tyr															
		200				205				210					
ctt gcg aca caa gct cgc caa cct gta gtt cat tac gaa cac acc gat	787														
Leu Ala Thr Gln Ala Arg Gln Pro Val Val His Tyr Glu His Thr Asp															
	215					220				225					
gtt ggg tat aac tat cgc ctt tca aat atc ctc gct gca ctg gga cga	835														
Val Gly Tyr Asn Tyr Arg Leu Ser Asn Ile Leu Ala Ala Leu Gly Arg															
	230			235				240				245			

Ser Ser Met Thr Phe Ala Ala Thr Thr Asn Ala Ile Val Tyr Thr Gly
 85 90 95
 Ala Glu Pro Ile Phe Val Asp Cys Asp Glu Ser Gly Asn Met Asp Pro
 100 105 110
 Asp Leu Leu Glu Lys Ala Phe Ala Glu Leu Lys Ser Glu Gly Lys Glu
 115 120 125
 Val Lys Ala Val Val Pro Val Asp Leu Leu Gly Lys Val Val Gln His
 130 135 140
 Glu Lys Ile Lys Lys Ile Ala Asp Glu Tyr Gly Ala Val Val Leu Ser
 145 150 155 160
 Asp Ala Ala Glu Ser Leu Gly Ala Ile Arg Asn Gly Lys Ser Ala Ala
 165 170 175
 Ala Tyr Gly Val Ala Ala Ala Val Ser Phe Asn Gly Asn Lys Ile Met
 180 185 190
 Thr Thr Ser Gly Gly Gly Ala Leu Leu Thr Asp Asp Lys Asp Ile Ala
 195 200 205
 Asp Asn Val Arg Tyr Leu Ala Thr Gln Ala Arg Gln Pro Val Val His
 210 215 220
 Tyr Glu His Thr Asp Val Gly Tyr Asn Tyr Arg Leu Ser Asn Ile Leu
 225 230 235 240
 Ala Ala Leu Gly Arg Ala Gln Leu Ser Arg Leu Asp Lys Met Ile Glu
 245 250 255
 Arg Arg Arg Gln His Arg Ala Phe Tyr Arg Glu Leu Phe Ala Gly Val
 260 265 270
 Ser Gly Val Glu Ile Phe Gly Glu Pro Ser Gly Val Asp Gly Gly Asp
 275 280 285
 Thr Ile Asp Asn Phe Trp Leu Thr Ser Ile Leu Ile Asp Lys Glu Val
 290 295 300
 Ala Gly Phe Ser Ser Glu Asp Leu Arg Ser Val Leu Asn Gln Ala Asn
 305 310 315 320
 Ile Glu Ser Arg Pro Leu Trp Lys Pro Met His Leu Gln Pro Val Phe
 325 330 335
 Lys Lys Tyr Arg Ser Phe Thr Asn Glu Glu Gly Gln Arg Leu Phe Asp
 340 345 350
 Ser Gly Leu Ser Leu Pro Ser Gly Ser Val Leu Asp Asn Ala Ser Met
 355 360 365
 Asn Arg Val Glu Thr Thr Ile Gly Gln Phe Leu Glu Ser Gln His Ala
 370 375 380

Ile
 385

cca gta gaa gag ctc acg gct gct gag ggc gca gtg ctg gcg gcc agt 643
Pro Val Glu Glu Leu Thr Ala Ala Glu Gly Ala Val Leu Ala Ala Ser
170 175 180

att cag ctg cca agc cag ttg gat cct tgg aca aat cca gtt gag gcg Ile Gln Leu Pro Ser Gln Leu Asp Pro Trp Thr Asn Pro Val Glu Ala 185 190 195	691
gaa acg cgt tgg aac tat gtc atg gac ggc ctg gtg gaa att ggc gct Glu Thr Arg Trp Asn Tyr Val Met Asp Gly Leu Val Glu Ile Gly Ala 200 205 210	739
atc tcg gca gag gag cgc gca gtt gct acc tac cct gaa acc act gac Ile Ser Ala Glu Glu Arg Ala Val Ala Thr Tyr Pro Glu Thr Thr Asp 215 220 225	787
cct gcg tcc aac agt gcg tac acc gaa gcc acc ggc act aat ggt ttg Pro Ala Ser Asn Ser Ala Tyr Thr Glu Ala Thr Gly Thr Asn Gly Leu 230 235 240 245	835
att aag aac caa gtg atg gcg gag ttg tct gag ctt ggt atc act gag Ile Lys Asn Gln Val Met Ala Glu Leu Ser Glu Leu Gly Ile Thr Glu 250 255 260	883
gat gat gtg caa acc tgt ggt ttg cag gtc acc acc acc att gat cca Asp Asp Val Gln Thr Cys Gly Leu Gln Val Thr Thr Thr Ile Asp Pro 265 270 275	931
aag act cag gaa ggt gcc gtt gaa gcg gta caa aac cag ttg gat ctt Lys Thr Gln Glu Gly Ala Val Glu Ala Val Gln Asn Gln Leu Asp Leu 280 285 290	979
ctg tct gag aac aac cgt gca gcg gta gtc tcc att gat cct tct aat Leu Ser Glu Asn Asn Arg Ala Ala Val Val Ser Ile Asp Pro Ser Asn 295 300 305	1027
ggt gcg gtt cgt gct tat tac ggc ggc gag aat gcg act ggt tgg gac Gly Ala Val Arg Ala Tyr Tyr Gly Gly Glu Asn Ala Thr Gly Trp Asp 310 315 320 325	1075
ttt gca aac gct ccg ctt cag acc ggt tct aca ttc aag atc ttt ggt Phe Ala Asn Ala Pro Leu Gln Thr Gly Ser Thr Phe Lys Ile Phe Gly 330 335 340	1123
ctg gca gca gca ctt cag caa ggt att cca ctg tct cag cca tac agc Leu Ala Ala Ala Leu Gln Gln Gly Ile Pro Leu Ser Gln Pro Tyr Ser 345 350 355	1171
tct gcg ccg gtg act gtg ggt gat gct caa atc gga aac gtc ggt ggc Ser Ala Pro Val Thr Val Gly Asp Ala Gln Ile Gly Asn Val Gly Gly 360 365 370	1219
agc ggt tgt ggt tcc tgt tcc atc gag cag gcg ttg ttg cat tct tac Ser Gly Cys Gly Ser Cys Ser Ile Glu Gln Ala Leu Leu His Ser Tyr 375 380 385	1267
aac acc agc ttc att cgt ttg cag cag gat ctg gaa aat ggt tca cag Asn Thr Ser Phe Ile Arg Leu Gln Gln Asp Leu Glu Asn Gly Ser Gln 390 395 400 405	1315
gat act gcg gac atg gcg cat gct ttg ggt atc gcg aag tct ttg cca Asp Thr Ala Asp Met Ala His Ala Leu Gly Ile Ala Lys Ser Leu Pro 410 415 420	1363
act atc cct gag aca ctg act gaa aac gga gag acc cct tat gag ggc	1411

Thr Ile Pro Glu Thr Leu Thr Glu Asn Gly Glu Thr Pro Tyr Glu Gly
 425 430 435
 atc atc ttg ggt cag tat gag tcc cgc cca ctt gat atg gct tct gcg 1459
 Ile Ile Leu Gly Gln Tyr Glu Ser Arg Pro Leu Asp Met Ala Ser Ala
 440 445 450
 atg gca act atc gct aat gaa ggt gtc tgg cac cgc ccg cac ttc gtg 1507
 Met Ala Thr Ile Ala Asn Glu Gly Val Trp His Arg Pro His Phe Val
 455 460 465
 tcc aag gtg gag act gtc agc ggt gag gtt ctc tac gag ttc gag gat 1555
 Ser Lys Val Glu Thr Val Ser Gly Glu Val Leu Tyr Glu Phe Glu Asp
 470 475 480 485
 ggc gac ggc gag cgt cgt gtt tct gaa aag gtt gca ctg aat ctg ctc 1603
 Gly Asp Gly Glu Arg Arg Val Ser Glu Lys Val Ala Leu Asn Leu Leu
 490 495 500
 aag gcc atg ggg cca atc gct gca tac tcc aac gga aac gct ctg gct 1651
 Lys Ala Met Gly Pro Ile Ala Ala Tyr Ser Asn Gly Asn Ala Leu Ala
 505 510 515
 gat ggc cag gtt tct gca tcc aag act ggt acc act cag ctt ggt gat 1699
 Asp Gly Gln Val Ser Ala Ser Lys Thr Gly Thr Thr Gln Leu Gly Asp
 520 525 530
 acc ggt gca aac aag gat gcg tgg atg ttg ggt gcg gca cct cag cta 1747
 Thr Gly Ala Asn Lys Asp Ala Trp Met Leu Gly Ala Ala Pro Gln Leu
 535 540 545
 gct act gcg gtg tgg gtc gga act gct tgataacact gcattgtata aca 1797
 Ala Thr Ala Val Trp Val Gly Thr Ala
 550 555

<210> 66

<211> 558

<212> PRT

<213> Corynebacterium glutamicum

<400> 66

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 20 25 30
 Thr Glu Leu Ala Arg Ile Val Pro Pro Glu Gly Asn Arg Gln Met Val
 35 40 45
 Thr Ile Asp Gln Val Pro Asp Thr Val Lys Asn Ala Val Val Ala Ala
 50 55 60
 Glu Asp Arg Glu Phe Tyr Thr Asn Pro Gly Phe Ser Ile Thr Gly Tyr
 65 70 75 80
 Ala Arg Ala Ala Leu Gly Val Ile Thr Gly Asp Ser Ser Ala Gly Gly
 85 90 95
 Gly Ser Thr Ile Thr Gln Gln Tyr Val Lys Lys Ala Val Val Gly Asp

100					105					110					
Glu	Arg	Ser	Leu	Ile	Arg	Lys	Ala	Lys	Glu	Leu	Val	Tyr	Ser	Ala	Lys
		115					120					125			
Met	Ala	Asn	Glu	Trp	Ser	Lys	Asp	Glu	Val	Leu	Glu	Ala	Tyr	Leu	Asn
	130					135					140				
Thr	Val	Tyr	Phe	Gly	Arg	Asn	Ala	Tyr	Gly	Val	Gln	Ala	Ala	Ala	His
145					150					155					160
Ala	Phe	Phe	Asp	Lys	Pro	Val	Glu	Glu	Leu	Thr	Ala	Ala	Glu	Gly	Ala
				165					170					175	
Val	Leu	Ala	Ala	Ser	Ile	Gln	Leu	Pro	Ser	Gln	Leu	Asp	Pro	Trp	Thr
			180					185					190		
Asn	Pro	Val	Glu	Ala	Glu	Thr	Arg	Trp	Asn	Tyr	Val	Met	Asp	Gly	Leu
		195					200					205			
Val	Glu	Ile	Gly	Ala	Ile	Ser	Ala	Glu	Glu	Arg	Ala	Val	Ala	Thr	Tyr
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Pro	Glu	Thr	Thr	Asp	Pro	Ala	Ser	Asn	Ser	Ala	Tyr	Thr	Glu	Ala	Thr
225					230					235					240
Gly	Thr	Asn	Gly	Leu	Ile	Lys	Asn	Gln	Val	Met	Ala	Glu	Leu	Ser	Glu
				245					250					255	
Leu	Gly	Ile	Thr	Glu	Asp	Asp	Val	Gln	Thr	Cys	Gly	Leu	Gln	Val	Thr
			260					265					270		
Thr	Thr	Ile	Asp	Pro	Lys	Thr	Gln	Glu	Gly	Ala	Val	Glu	Ala	Val	Gln
		275					280					285			
Asn	Gln	Leu	Asp	Leu	Leu	Ser	Glu	Asn	Asn	Arg	Ala	Ala	Val	Val	Ser
	290					295				300					
Ile	Asp	Pro	Ser	Asn	Gly	Ala	Val	Arg	Ala	Tyr	Tyr	Gly	Gly	Glu	Asn
305					310					315					320
Ala	Thr	Gly	Trp	Asp	Phe	Ala	Asn	Ala	Pro	Leu	Gln	Thr	Gly	Ser	Thr
				325					330					335	
Phe	Lys	Ile	Phe	Gly	Leu	Ala	Ala	Ala	Leu	Gln	Gln	Gly	Ile	Pro	Leu
			340					345					350		
Ser	Gln	Pro	Tyr	Ser	Ser	Ala	Pro	Val	Thr	Val	Gly	Asp	Ala	Gln	Ile
		355					360					365			
Gly	Asn	Val	Gly	Gly	Ser	Gly	Cys	Gly	Ser	Cys	Ser	Ile	Glu	Gln	Ala
	370					375					380				
Leu	Leu	His	Ser	Tyr	Asn	Thr	Ser	Phe	Ile	Arg	Leu	Gln	Gln	Asp	Leu
385					390					395					400
Glu	Asn	Gly	Ser	Gln	Asp	Thr	Ala	Asp	Met	Ala	His	Ala	Leu	Gly	Ile
				405					410					415	
Ala	Lys	Ser	Leu	Pro	Thr	Ile	Pro	Glu	Thr	Leu	Thr	Glu	Asn	Gly	Glu
			420					425					430		

Thr Pro Tyr Glu Gly Ile Ile Leu Gly Gln Tyr Glu Ser Arg Pro Leu
 435 440 445
 Asp Met Ala Ser Ala Met Ala Thr Ile Ala Asn Glu Gly Val Trp His
 450 455 460
 Arg Pro His Phe Val Ser Lys Val Glu Thr Val Ser Gly Glu Val Leu
 465 470 475 480
 Tyr Glu Phe Glu Asp Gly Asp Gly Glu Arg Arg Val Ser Glu Lys Val
 485 490 495
 Ala Leu Asn Leu Leu Lys Ala Met Gly Pro Ile Ala Ala Tyr Ser Asn
 500 505 510
 Gly Asn Ala Leu Ala Asp Gly Gln Val Ser Ala Ser Lys Thr Gly Thr
 515 520 525
 Thr Gln Leu Gly Asp Thr Gly Ala Asn Lys Asp Ala Trp Met Leu Gly
 530 535 540
 Ala Ala Pro Gln Leu Ala Thr Ala Val Trp Val Gly Thr Ala
 545 550 555

<210> 67
 <211> 444
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(421)
 <223> RXN00550

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 Met Tyr Gly Ser Asn
 1 5
 tcc cct gcc acg atc tgg aag cag acc atg gat aac gcc ctc gag aac 163
 Ser Pro Ala Thr Ile Trp Lys Gln Thr Met Asp Asn Ala Leu Glu Asn
 10 15 20
 tcc cct ctc gaa act tgg gat atc gct cca gca ttg ggg tac ggt aac 211
 Ser Pro Leu Glu Thr Trp Asp Ile Ala Pro Ala Leu Gly Tyr Gly Asn
 25 30 35
 cca cca gtt ccg gaa tat gtg tgg act cca agt cca aac atc gcg act 259
 Pro Pro Val Pro Glu Tyr Val Trp Thr Pro Ser Pro Asn Ile Ala Thr
 40 45 50
 aat gat cca gaa gga gca acc gag gaa gct cca gtg gag gat cca aat 307
 Asn Asp Pro Glu Gly Ala Thr Glu Glu Ala Pro Val Glu Asp Pro Asn
 55 60 65
 gca gta atc gat acc cct gct gta gat ccc act gca cct gca gag gag 355
 Ala Val Ile Asp Thr Pro Ala Val Asp Pro Thr Ala Pro Ala Glu Glu

gat ctc tta ggg atc ggc taaaatccgg tcgtagccta aac 444
Asp Leu Leu Gly Ile Gly
105

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<400> 68
Met Tyr Gly Ser Asn Ser Pro Ala Thr Ile Trp Lys Gln Thr Met Asp
  1                               10                      15

Asn Ala Leu Glu Asn Ser Pro Leu Glu Thr Trp Asp Ile Ala Pro Ala
  20                               25                      30

Leu Gly Tyr Gly Asn Pro Pro Val Pro Glu Tyr Val Trp Thr Pro Ser
  35                               40                      45

Pro Asn Ile Ala Thr Asn Asp Pro Glu Gly Ala Thr Glu Glu Ala Pro
  50                               55                      60

Val Glu Asp Pro Asn Ala Val Ile Asp Thr Pro Ala Val Asp Pro Thr
  65                               70                      75                      80

Ala Pro Ala Glu Glu Thr Gly Asn Gly Gln Val Glu Ile Leu Pro Gly
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Leu Thr Ile Pro Gly Asp Leu Leu Gly Ile Gly
  100                               105

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<222> (101)..(646)
<223> RXN03091
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Ser Tyr Thr Ile Lys Leu Thr Leu Asp Pro Asp Val Gln Asp Ala Ala
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cac aat gcg gtg tcc tcc cac gtt gat cca acc acc cca ggt gtc gct 211


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His Asn Ala Val Ser Ser His Val Asp Pro Thr Thr Pro Gly Val Ala
      25                      30                      35

gaa gtt gtg aac gtc att gag cct ggc gag aac tcc cgc gat att ttg 259
Glu Val Val Asn Val Ile Glu Pro Gly Glu Asn Ser Arg Asp Ile Leu
      40                      45                      50

gct att act tct tcc cgc aac tac ggc ctt gac ctg gat gct ggt gaa 307
Ala Ile Thr Ser Ser Arg Asn Tyr Gly Leu Asp Leu Asp Ala Gly Glu
      55                      60                      65

acg atg ctg cct cag gca acg tcc cgt gtg ggt aat ggt gcc ggt tcc 355
Thr Met Leu Pro Gln Ala Thr Ser Arg Val Gly Asn Gly Ala Gly Ser
      70                      75                      80                      85

att ttc aag atc ttt acc gcc gct gca gcc att cag cag ggc gct ggc 403
Ile Phe Lys Ile Phe Thr Ala Ala Ala Ile Gln Gln Gly Ala Gly
      90                      95                      100

cta gac acc atg ttg gat gtt cct tct cga tat gag gtc aag ggc atg 451
Leu Asp Thr Met Leu Asp Val Pro Ser Arg Tyr Glu Val Lys Gly Met
      105                      110                      115

ggc tcc ggc ggt gcc gcg aac tgt ccc gca aat act tac tgc gtg gaa 499
Gly Ser Gly Gly Ala Ala Asn Cys Pro Ala Asn Thr Tyr Cys Val Glu
      120                      125                      130

aac gca gga tcc tac gcg cct cgc atg act ctg cag gac gct ctc gcg 547
Asn Ala Gly Ser Tyr Ala Pro Arg Met Thr Leu Gln Asp Ala Leu Ala
      135                      140                      145

cag tcc ccc aac act gca ttc gtt gaa atg atc gag cag gtt ggc gtg 595
Gln Ser Pro Asn Thr Ala Phe Val Glu Met Ile Glu Gln Val Gly Val
      150                      155                      160                      165

gac acc cgt tgt gga tct ttc agt aaa gct ggg cct gcg aag cta cac 643
Asp Thr Arg Cys Gly Ser Phe Ser Lys Ala Gly Pro Ala Lys Leu His
      170                      175                      180

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Arg

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<210> 70

<211> 182

<212> PRT

<213> Corynebacterium glutamicum

<400> 70

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Met Leu Ala Lys Asp Ser Tyr Thr Ile Lys Leu Thr Leu Asp Pro Asp
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Val Gln Asp Ala Ala His Asn Ala Val Ser Ser His Val Asp Pro Thr
      20                      25                      30

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Thr Pro Gly Val Ala Glu Val Val Asn Val Ile Glu Pro Gly Glu Asn
      35                      40                      45

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Ser Arg Asp Ile Leu Ala Ile Thr Ser Ser Arg Asn Tyr Gly Leu Asp
      50                      55                      60

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Leu Asp Ala Gly Glu Thr Met Leu Pro Gln Ala Thr Ser Arg Val Gly
 65 70 75 80
 Asn Gly Ala Gly Ser Ile Phe Lys Ile Phe Thr Ala Ala Ala Ile
 85 90 95
 Gln Gln Gly Ala Gly Leu Asp Thr Met Leu Asp Val Pro Ser Arg Tyr
 100 105 110
 Glu Val Lys Gly Met Gly Ser Gly Gly Ala Ala Asn Cys Pro Ala Asn
 115 120 125
 Thr Tyr Cys Val Glu Asn Ala Gly Ser Tyr Ala Pro Arg Met Thr Leu
 130 135 140
 Gln Asp Ala Leu Ala Gln Ser Pro Asn Thr Ala Phe Val Glu Met Ile
 145 150 155 160
 Glu Gln Val Gly Val Asp Thr Arg Cys Gly Ser Phe Ser Lys Ala Gly
 165 170 175
 Pro Ala Lys Leu His Arg
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<210> 71
 <211> 824
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(801)
 <223> RXN03178

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 Ser Arg Val Gly Val Gly Glu Ala Gly Gln Tyr Thr Val Asp Gln Leu
 20 25 30
 ctg cac ggt ctt ctt tta gcc agc ggt aac gat gcg gcg tat atg ttg 144
 Leu His Gly Leu Leu Leu Ala Ser Gly Asn Asp Ala Ala Tyr Met Leu
 35 40 45
 gct cag gaa ctt ggt ggg gat caa gca acc ctg gag aaa gta aac gcg 192
 Ala Gln Glu Leu Gly Gly Asp Gln Ala Thr Leu Glu Lys Val Asn Ala
 50 55 60
 ctg gcc aag gag ttg ggc act caa gac acc ttc gtt gcc act tat tcc 240
 Leu Ala Lys Glu Leu Gly Thr Gln Asp Thr Phe Val Ala Thr Tyr Ser
 65 70 75 80
 ggt ttg gat gcg ccg gga atg tcg acc tcc gca tac gac atg tca ttg 288
 Gly Leu Asp Ala Pro Gly Met Ser Thr Ser Ala Tyr Asp Met Ser Leu
 85 90 95

att tat cag cat gcg tgg cag aac ccg gtt ttc gag tcg att atc tcc 336
 Ile Tyr Gln His Ala Trp Gln Asn Pro Val Phe Glu Ser Ile Ile Ser
 100 105 110
 acc gat cac att gat ttc cct ggt tgg ggc gac aat gag ggt ttc caa 384
 Thr Asp His Ile Asp Phe Pro Gly Trp Gly Asp Asn Glu Gly Phe Gln
 115 120 125
 gtc tgg aac gat aac gcc ttg ttc atg aac gat cct gat ggc atc ggc 432
 Val Trp Asn Asp Asn Ala Leu Phe Met Asn Asp Pro Asp Gly Ile Gly
 130 135 140
 ggc aag acc ggc tac acc gac gac gcg aac cac acc ttt gtc ggc ggt 480
 Gly Lys Thr Gly Tyr Thr Asp Asp Ala Asn His Thr Phe Val Gly Gly
 145 150 155 160
 ctc gat cgg ggt ggt cgc cgc ctc gcc gcc gta ctc ttg gat tcc acc 528
 Leu Asp Arg Gly Gly Arg Arg Leu Ala Ala Val Leu Leu Asp Ser Thr
 165 170 175
 gtc agc gac att cgt ccg tgg gaa caa gca cga ttg ctt atc gac gcc 576
 Val Ser Asp Ile Arg Pro Trp Glu Gln Ala Arg Leu Leu Ile Asp Ala
 180 185 190
 tcc ctc ccc atc acg ccg ggg tcc ggc gtg ggc cag ctg ggc tcc ggc 624
 Ser Leu Pro Ile Thr Pro Gly Ser Gly Val Gly Gln Leu Gly Ser Gly
 195 200 205
 agc gcg aac gat gtg gca ccg gcg acc cca gaa tta cca gaa ccc acc 672
 Ser Ala Asn Asp Val Ala Pro Ala Thr Pro Glu Leu Pro Glu Pro Thr
 210 215 220
 gac aac ctg act tca ggt gag ggt ggg tcg cag aac acg ctt ctt aag 720
 Asp Asn Leu Thr Ser Gly Glu Gly Gly Ser Gln Asn Thr Leu Leu Lys
 225 230 235 240
 ctc gtg gtg ccc atc gga atc atc gtg ctg ttg cta atc gcc gca cta 768
 Leu Val Val Pro Ile Gly Ile Ile Val Leu Leu Leu Ile Ala Ala Leu
 245 250 255
 gcg tgg aca ttc aga tct ccc aag aaa aag aac taggtgttct tcttcacgac 821
 Ala Trp Thr Phe Arg Ser Pro Lys Lys Lys Asn
 260 265

ctc 824

<210> 72

<211> 267

<212> PRT

<213> Corynebacterium glutamicum

<400> 72

Pro Thr Thr Val Val Thr Gly Thr Met Glu Ala Ala Asn Ile Glu Gly
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Ser Arg Val Gly Val Gly Glu Ala Gly Gln Tyr Thr Val Asp Gln Leu
 20 25 30

Leu His Gly Leu Leu Leu Ala Ser Gly Asn Asp Ala Ala Tyr Met Leu
 35 40 45

Ala Gln Glu Leu Gly Gly Asp Gln Ala Thr Leu Glu Lys Val Asn Ala
50 55 60

Leu Ala Lys Glu Leu Gly Thr Gln Asp Thr Phe Val Ala Thr Tyr Ser
65 70 75 80

Gly Leu Asp Ala Pro Gly Met Ser Thr Ser Ala Tyr Asp Met Ser Leu
85 90 95

Ile Tyr Gln His Ala Trp Gln Asn Pro Val Phe Glu Ser Ile Ile Ser
100 105 110

Thr Asp His Ile Asp Phe Pro Gly Trp Gly Asp Asn Glu Gly Phe Gln
115 120 125

Val Trp Asn Asp Asn Ala Leu Phe Met Asn Asp Pro Asp Gly Ile Gly
130 135 140

Gly Lys Thr Gly Tyr Thr Asp Asp Ala Asn His Thr Phe Val Gly Gly
145 150 155 160

Leu Asp Arg Gly Gly Arg Arg Leu Ala Ala Val Leu Leu Asp Ser Thr
165 170 175

Val Ser Asp Ile Arg Pro Trp Glu Gln Ala Arg Leu Leu Ile Asp Ala
180 185 190

Ser Leu Pro Ile Thr Pro Gly Ser Gly Val Gly Gln Leu Gly Ser Gly
195 200 205

Ser Ala Asn Asp Val Ala Pro Ala Thr Pro Glu Leu Pro Glu Pro Thr
210 215 220

Asp Asn Leu Thr Ser Gly Glu Gly Gly Ser Gln Asn Thr Leu Leu Lys
225 230 235 240

Leu Val Val Pro Ile Gly Ile Ile Val Leu Leu Leu Ile Ala Ala Leu
245 250 255

Ala Trp Thr Phe Arg Ser Pro Lys Lys Lys Asn
260 265

<210> 73

<211> 749

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(726)

<223> FRXA02859

<400> 73

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5

10

15

aac gat gcg gcg tat ctg ttg gct cag gaa ctt ggt ggg gat caa gca 96

Asn Asp Ala Ala Tyr Leu Leu Ala Gln Glu Leu Gly Gly Asp Gln Ala

20										25										30									
acc	ctg	gag	aaa	gta	aac	gcg	ctg	gcc	aag	gag	ttg	ggc	act	caa	gac														
Thr	Leu	Glu	Lys	Val	Asn	Ala	Leu	Ala	Lys	Glu	Leu	Gly	Thr	Gln	Asp														
		35						40				45																	144
acc	ttc	gtt	gcc	act	tat	tcc	ggt	ttg	gat	gcg	ccg	gga	atg	tcg	acc														
Thr	Phe	Val	Ala	Thr	Tyr	Ser	Gly	Leu	Asp	Ala	Pro	Gly	Met	Ser	Thr														
		50				55					60																		192
tcc	gca	tac	gac	atg	tca	ttg	att	tat	cag	cat	gcg	tg	cag	aac	ccg														
Ser	Ala	Tyr	Asp	Met	Ser	Leu	Ile	Tyr	Gln	His	Ala	Trp	Gln	Asn	Pro														
		65			70					75					80														240
gtt	ttc	gag	tcg	att	atc	tcc	acc	gat	cac	att	gat	ttc	cct	ggt	tg														
Val	Phe	Glu	Ser	Ile	Ile	Ser	Thr	Asp	His	Ile	Asp	Phe	Pro	Gly	Trp														
				85					90					95															288
ggc	gac	aac	gag	ggt	ttc	caa	gtc	tg	aac	gat	aac	gcc	ttg	ttc	atg														
Gly	Asp	Asn	Glu	Gly	Phe	Gln	Val	Trp	Asn	Asp	Asn	Ala	Leu	Phe	Met														
		100					105					110																	336
aac	gat	cct	gat	ggc	atc	ggc	ggc	aag	acc	ggc	tac	acc	gac	gac	gcg														
Asn	Asp	Pro	Asp	Gly	Ile	Gly	Gly	Lys	Thr	Gly	Tyr	Thr	Asp	Asp	Ala														
		115					120				125																		384
aac	cac	acc	ttt	gtc	ggc	ggt	ctc	gat	cgg	ggt	ggt	cgc	cgc	ctc	gcc														
Asn	His	Thr	Phe	Val	Gly	Gly	Leu	Asp	Arg	Gly	Gly	Arg	Arg	Leu	Ala														
		130				135					140																		432
gcc	gta	ctc	ttg	gat	tcc	acc	gtc	agc	gac	att	cgt	ccg	tg	gaa	caa														
Ala	Val	Leu	Leu	Asp	Ser	Thr	Val	Ser	Asp	Ile	Arg	Pro	Trp	Glu	Gln														
		145			150				155					160															480
gca	cga	ttg	ctt	atc	gac	gcc	tcc	ctc	ccc	atc	acg	ccg	ggg	tcc	ggc														
Ala	Arg	Leu	Leu	Ile	Asp	Ala	Ser	Leu	Pro	Ile	Thr	Pro	Gly	Ser	Gly														
				165					170				175																528
gtg	ggc	cag	ctg	ggc	tcc	ggc	agc	gcg	aac	gat	gtg	gca	ccg	gcg	acc														
Val	Gly	Gln	Leu	Gly	Ser	Gly	Ser	Ala	Asn	Asp	Val	Ala	Pro	Ala	Thr														
			180				185					190																	576
cca	gaa	tta	cca	gaa	ccc	acc	gac	aac	ctg	act	tca	ggt	gag	ggt	ggg														
Pro	Glu	Leu	Pro	Glu	Pro	Thr	Asp	Asn	Leu	Thr	Ser	Gly	Glu	Gly	Gly														
		195					200					205																	624
tcg	cag	aac	acg	ctg	ctt	aag	ctc	gtg	gtg	ccc	atc	gga	atc	atc	gtg														
Ser	Gln	Asn	Thr	Leu	Leu	Lys	Leu	Val	Val	Pro	Ile	Gly	Ile	Ile	Val														
		210				215					220																		672
ctg	ttg	cta	atc	gcc	gca	cta	gcg	tg	aca	ttc	aga	tct	ccc	aag	aaa														
Leu	Leu	Leu	Ile	Ala	Ala	Leu	Ala	Trp	Thr	Phe	Arg	Ser	Pro	Lys	Lys														
		225			230					235					240														720
aag	aac	taggtgttct	tcttcacgac	ctc																									
Lys	Asn																												749

<210> 74

<211> 242

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 74

Gln Tyr Thr Val Asp Gln Leu Leu His Gly Leu Leu Leu Ala Ser Gly
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Asn Asp Ala Ala Tyr Leu Leu Ala Gln Glu Leu Gly Gly Asp Gln Ala
 20 25 30

Thr Leu Glu Lys Val Asn Ala Leu Ala Lys Glu Leu Gly Thr Gln Asp
 35 40 45

Thr Phe Val Ala Thr Tyr Ser Gly Leu Asp Ala Pro Gly Met Ser Thr
 50 55 60

Ser Ala Tyr Asp Met Ser Leu Ile Tyr Gln His Ala Trp Gln Asn Pro
 65 70 75 80

Val Phe Glu Ser Ile Ile Ser Thr Asp His Ile Asp Phe Pro Gly Trp
 85 90 95

Gly Asp Asn Glu Gly Phe Gln Val Trp Asn Asp Asn Ala Leu Phe Met
 100 105 110

Asn Asp Pro Asp Gly Ile Gly Gly Lys Thr Gly Tyr Thr Asp Asp Ala
 115 120 125

Asn His Thr Phe Val Gly Gly Leu Asp Arg Gly Gly Arg Arg Leu Ala
 130 135 140

Ala Val Leu Leu Asp Ser Thr Val Ser Asp Ile Arg Pro Trp Glu Gln
 145 150 155 160

Ala Arg Leu Leu Ile Asp Ala Ser Leu Pro Ile Thr Pro Gly Ser Gly
 165 170 175

Val Gly Gln Leu Gly Ser Gly Ser Ala Asn Asp Val Ala Pro Ala Thr
 180 185 190

Pro Glu Leu Pro Glu Pro Thr Asp Asn Leu Thr Ser Gly Glu Gly Gly
 195 200 205

Ser Gln Asn Thr Leu Leu Lys Leu Val Val Pro Ile Gly Ile Ile Val
 210 215 220

Leu Leu Leu Ile Ala Ala Leu Ala Trp Thr Phe Arg Ser Pro Lys Lys
 225 230 235 240

Lys Asn

<210> 75

<211> 1437

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1414)

<223> RXN01267

<400> 75

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gatttttcga attgaagatg tttctgaaag gtatttagat atg tat gca gaa att 115
                                         Met Tyr Ala Glu Ile
                                         1 5

aat ggc ggt ttt att cca gag ggc acc gtg cgg gta agc ggc gca aaa 163
Asn Gly Gly Phe Ile Pro Glu Gly Thr Val Arg Val Ser Gly Ala Lys
          10          15          20

aac tct gct act aga ctt ctc gcg gcg gca ctg cta acc gat gag gtg 211
Asn Ser Ala Thr Arg Leu Leu Ala Ala Leu Leu Thr Asp Glu Val
          25          30          35

gtg cat ctt ggt aat ttc cca acc aag ctt gtg gat gtt gaa cat aaa 259
Val His Leu Gly Asn Phe Pro Thr Lys Leu Val Asp Val Glu His Lys
          40          45          50

att cgc ttt att gaa gag ctt ggc gga aaa gtg cat gtc gac cat gat 307
Ile Arg Phe Ile Glu Glu Leu Gly Gly Lys Val His Val Asp His Asp
          55          60          65

gag caa att tta gta gtt gat gct aag gat ctt gca gcg cga gaa atg 355
Glu Gln Ile Leu Val Val Asp Ala Lys Asp Leu Ala Ala Arg Glu Met
          70          75          80          85

act act gat gaa ctg aat att ccg att cga act act tat ctc cta gca 403
Thr Thr Asp Glu Leu Asn Ile Pro Ile Arg Thr Thr Tyr Leu Leu Ala
          90          95          100

gca gcg cag att ggg cgt ggg gaa att gct cga gtt cct ttt cct ggg 451
Ala Ala Gln Ile Gly Arg Gly Glu Ile Ala Arg Val Pro Phe Pro Gly
          105          110          115

ggg tgt gct att gga gga ggt cct gct ggc gga cga gga tat gat ctt 499
Gly Cys Ala Ile Gly Gly Gly Pro Ala Gly Gly Arg Gly Tyr Asp Leu
          120          125          130

cat ctt atg gtc tgg gaa cag cta ggt tgt aaa att ctt gaa aaa gat 547
His Leu Met Val Trp Glu Gln Leu Gly Cys Lys Ile Leu Glu Lys Asp
          135          140          145

gat cac att gaa gta act gca ccc cag ggc ttt atc ggg gga gtt att 595
Asp His Ile Glu Val Thr Ala Pro Gln Gly Phe Ile Gly Gly Val Ile
          150          155          160          165

gac ttt cct att tct act gtg gga ggc act gaa aac gcg tta cta tgc 643
Asp Phe Pro Ile Ser Thr Val Gly Gly Thr Glu Asn Ala Leu Leu Cys
          170          175          180

gca agt att gct tca ggg gat act aaa att gcc aat gct tat att acc 691
Ala Ser Ile Ala Ser Gly Asp Thr Lys Ile Ala Asn Ala Tyr Ile Thr
          185          190          195

cct gag ata act gat ctt att gaa ctt ctg cga cgt atg ggt gcg gag 739
Pro Glu Ile Thr Asp Leu Ile Glu Leu Leu Arg Arg Met Gly Ala Glu
          200          205          210

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[illegible]

<210> 76
 <211> 438
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 76

Met	Tyr	Ala	Glu	Ile	Asn	Gly	Gly	Phe	Ile	Pro	Glu	Gly	Thr	Val	Arg	1	5	10	15
Val	Ser	Gly	Ala	Lys	Asn	Ser	Ala	Thr	Arg	Leu	Leu	Ala	Ala	Ala	Leu	20	25	30	
Leu	Thr	Asp	Glu	Val	Val	His	Leu	Gly	Asn	Phe	Pro	Thr	Lys	Leu	Val	35	40	45	
Asp	Val	Glu	His	Lys	Ile	Arg	Phe	Ile	Glu	Glu	Leu	Gly	Gly	Lys	Val	50	55	60	
His	Val	Asp	His	Asp	Glu	Gln	Ile	Leu	Val	Val	Asp	Ala	Lys	Asp	Leu	65	70	75	80
Ala	Ala	Arg	Glu	Met	Thr	Thr	Asp	Glu	Leu	Asn	Ile	Pro	Ile	Arg	Thr	85	90	95	
Thr	Tyr	Leu	Leu	Ala	Ala	Ala	Gln	Ile	Gly	Arg	Gly	Glu	Ile	Ala	Arg	100	105	110	
Val	Pro	Phe	Pro	Gly	Gly	Cys	Ala	Ile	Gly	Gly	Gly	Pro	Ala	Gly	Gly	115	120	125	
Arg	Gly	Tyr	Asp	Leu	His	Leu	Met	Val	Trp	Glu	Gln	Leu	Gly	Cys	Lys	130	135	140	
Ile	Leu	Glu	Lys	Asp	Asp	His	Ile	Glu	Val	Thr	Ala	Pro	Gln	Gly	Phe	145	150	155	160
Ile	Gly	Gly	Val	Ile	Asp	Phe	Pro	Ile	Ser	Thr	Val	Gly	Gly	Thr	Glu	165	170	175	
Asn	Ala	Leu	Leu	Cys	Ala	Ser	Ile	Ala	Ser	Gly	Asp	Thr	Lys	Ile	Ala	180	185	190	
Asn	Ala	Tyr	Ile	Thr	Pro	Glu	Ile	Thr	Asp	Leu	Ile	Glu	Leu	Leu	Arg	195	200	205	
Arg	Met	Gly	Ala	Glu	Ile	Thr	Val	Tyr	Gly	Thr	Ser	Arg	Ile	His	Val	210	215	220	
Lys	Gly	Arg	Ala	Gly	Leu	Leu	Gln	Gly	Ala	Tyr	Met	Asp	Val	Met	Pro	225	230	235	240
Asp	Arg	Ile	Glu	Ala	Leu	Thr	Trp	Ile	Val	Tyr	Gly	Ile	Ile	Ser	Gly	245	250	255	
Gly	Arg	Ile	Thr	Val	Glu	Gly	Val	Pro	Phe	Ser	Ser	Met	Glu	Val	Pro	260	265	270	

Phe	Ile	His	Leu	Glu	Lys	Ala	Gly	Val	Asp	Leu	Phe	Arg	Asn	Ser	Ser	275	280	285
Ser	Val	Tyr	Ile	Thr	Pro	Glu	Cys	Leu	Pro	Ser	Gly	Ser	Val	Gln	Pro			

290	295	300
Phe Glu Leu Ala Cys Gly Thr His Pro Gly Val Ile Ser Asp Met Gln 305 310 315 320		
Ala Leu Phe Val Leu Leu Gly Leu Lys Gly Ala Gly Thr Ser Arg Val 325 330 335		
Tyr Asp Tyr Arg Tyr Pro Glu Arg Ile Ala Phe Val Glu Glu Leu Thr 340 345 350		
Asn Leu Val Ser Gly Asp Lys Leu Ser Ala Glu Ala Gly Lys Ile Thr 355 360 365		
Ile Gln Gly Asp Ala Thr Phe Arg Pro Gly Tyr Ala Asn Ser Thr Asp 370 375 380		
Leu Arg Gly Ser Met Ala Val Val Leu Ala Ala Leu Cys Ala Asp Gly 385 390 395 400		
Lys Ser Thr Ile Asn Asn Val His Met Ala Leu Arg Gly Tyr Asn Glu 405 410 415		
Leu Asp Lys Lys Leu Arg Leu Leu Gly Ala Asp Leu Thr Ile Arg Glu 420 425 430		
Gly Glu Val Pro Ser Pro 435		

<210> 77
 <211> 1032
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1009)
 <223> RXN00045

<400> 77
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tggtgatgaa ttctgtaca ccgcttaagg cccacacctc atg act gat ccc act 115
 Met Thr Asp Pro Thr
 1 5

tgc acc ctt gcc ctt gat att ggt gcc aca aag att gcc tac gca cta 163
 Cys Thr Leu Ala Leu Asp Ile Gly Ala Thr Lys Ile Ala Tyr Ala Leu
 10 15 20

gtc ccc gat aac acc ccg acg aca aca ttg tcc acg gga cgc ttg gga 211
 Val Pro Asp Asn Thr Pro Thr Thr Thr Leu Ser Thr Gly Arg Leu Gly
 25 30 35

aca aaa gaa ggc gac agc cct atc gag cag atc cgg ctg gtt ctt ctg 259
 Thr Lys Glu Gly Asp Ser Pro Ile Glu Gln Ile Arg Leu Val Leu Leu
 40 45 50

gca ggc tta aaa gct gcc gag gaa cac ggt ctc agt gtc gcc cgc atc 307
 Ala Gly Leu Lys Ala Ala Glu Glu His Gly Leu Ser Val Ala Arg Ile

55	60	65	
ggc atg ggc gct cct ggt gta att ctg gga cca gag gga acc atc gtg Gly Met Gly Ala Pro Gly Val Ile Leu Gly Pro Glu Gly Thr Ile Val 70 75 80 85			355
tac aac ggt gaa acc ctc aca gag tgg gca ggc act gac ctg cga gga Tyr Asn Gly Glu Thr Leu Thr Glu Trp Ala Gly Thr Asp Leu Arg Gly 90 95 100			403
tta tcc cga gaa gtc ctc aac gtt cca ttc gcg gca cac aat gat gtc Leu Ser Arg Glu Val Leu Asn Val Pro Phe Ala Ala His Asn Asp Val 105 110 115			451
cgc gta tgg gcc tac ggt gag cac cac tta ggc acc ggc aaa gac ctc Arg Val Trp Ala Tyr Gly Glu His His Leu Gly Thr Gly Lys Asp Leu 120 125 130			499
acc ggc agg gta ctc tac gtg tcc ctc ggc act gga gtc ggc gga gca Thr Gly Arg Val Leu Tyr Val Ser Leu Gly Thr Gly Val Gly Gly Ala 135 140 145			547
atc atc gaa gac gga atc atg atg agt agc ccc act gga act gcg gga Ile Ile Glu Asp Gly Ile Met Met Ser Ser Pro Thr Gly Thr Ala Gly 150 155 160 165			595
gaa ttc gca gaa gtt gtg tgc tct gac cat gca gga tta gcc gtt cgg Glu Phe Ala Glu Val Val Cys Ser Asp His Ala Gly Leu Ala Val Arg 170 175 180			643
tgc gaa aat gta gca agt ggc acc ggc cta acc agg tac tac aac gag Cys Glu Asn Val Ala Ser Gly Thr Gly Leu Thr Arg Tyr Tyr Asn Glu 185 190 195			691
gcc gcc gca act caa ctt gac ctt ccc gcc atc atg gag cgc ttc cac Ala Ala Ala Thr Gln Leu Asp Leu Pro Ala Ile Met Glu Arg Phe His 200 205 210			739
caa ggt gac ggc ctg gca cag caa atc att act gga aat ctc cga ggc Gln Gly Asp Gly Leu Ala Gln Gln Ile Ile Thr Gly Asn Leu Arg Gly 215 220 225			787
ttt ggc caa gcg cta ggc gca tta gtc aca gtg ctg gac ctt tcc gca Phe Gly Gln Ala Leu Gly Ala Leu Val Thr Val Leu Asp Leu Ser Ala 230 235 240 245			835
gta gta gtt gga ggc gga gtc gca ggc atc ggc gca ccc gtc atg gat Val Val Val Gly Gly Gly Val Ala Gly Ile Gly Ala Pro Val Met Asp 250 255 260			883
ccc atc acc gca ggg att ttc gat cga gtg tta acc ccc aac aaa tcc Pro Ile Thr Ala Gly Ile Phe Asp Arg Val Leu Thr Pro Asn Lys Ser 265 270 275			931
gta caa gtt tta agc acg tcc ctt ggt gcc caa gca gcc gtc atc gca Val Gln Val Leu Ser Thr Ser Leu Gly Ala Gln Ala Ala Val Ile Ala 280 285 290			979
gca gca aaa tat gcc cgc gat aac gcc ttt taagcaccta aaacgctggt Ala Ala Lys Tyr Ala Arg Asp Asn Ala Phe 295 300			1029

ctc

1032

<210> 78

<211> 303

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 78

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Ile Ala Tyr Ala Leu Val Pro Asp Asn Thr Pro Thr Thr Thr Leu Ser
 20 25 30

Thr Gly Arg Leu Gly Thr Lys Glu Gly Asp Ser Pro Ile Glu Gln Ile
 35 40 45

Arg Leu Val Leu Leu Ala Gly Leu Lys Ala Ala Glu Glu His Gly Leu
 50 55 60

Ser Val Ala Arg Ile Gly Met Gly Ala Pro Gly Val Ile Leu Gly Pro
 65 70 75 80

Glu Gly Thr Ile Val Tyr Asn Gly Glu Thr Leu Thr Glu Trp Ala Gly
 85 90 95

Thr Asp Leu Arg Gly Leu Ser Arg Glu Val Leu Asn Val Pro Phe Ala
 100 105 110

Ala His Asn Asp Val Arg Val Trp Ala Tyr Gly Glu His His Leu Gly
 115 120 125

Thr Gly Lys Asp Leu Thr Gly Arg Val Leu Tyr Val Ser Leu Gly Thr
 130 135 140

Gly Val Gly Gly Ala Ile Ile Glu Asp Gly Ile Met Met Ser Ser Pro
 145 150 155 160

Thr Gly Thr Ala Gly Glu Phe Ala Glu Val Val Cys Ser Asp His Ala
 165 170 175

Gly Leu Ala Val Arg Cys Glu Asn Val Ala Ser Gly Thr Gly Leu Thr
 180 185 190

Arg Tyr Tyr Asn Glu Ala Ala Ala Thr Gln Leu Asp Leu Pro Ala Ile
 195 200 205

Met Glu Arg Phe His Gln Gly Asp Gly Leu Ala Gln Gln Ile Ile Thr
 210 215 220

Gly Asn Leu Arg Gly Phe Gly Gln Ala Leu Gly Ala Leu Val Thr Val
 225 230 235 240

Leu Asp Leu Ser Ala Val Val Val Gly Gly Gly Val Ala Gly Ile Gly
 245 250 255

Ala Pro Val Met Asp Pro Ile Thr Ala Gly Ile Phe Asp Arg Val Leu
 260 265 270

Thr Pro Asn Lys Ser Val Gln Val Leu Ser Thr Ser Leu Gly Ala Gln
 275 280 285

Ala Ala Val Ile Ala Ala Ala Lys Tyr Ala Arg Asp Asn Ala Phe
 290 295 300

<210> 79
 <211> 1812
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1789)
 <223> RXN02704

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 Met Thr Thr Gly Ala
 1 5

tca aaa aaa ccc gca cgt ccg aac act ggc gct aaa acc aga acg ggg 163
 Ser Lys Lys Pro Ala Arg Pro Asn Thr Gly Ala Lys Thr Arg Thr Gly
 10 15 20

ctg gga att agg gag cgt att tcc ggt gca tgg aat gat ctt ctc gcg 211
 Leu Gly Ile Arg Glu Arg Ile Ser Gly Ala Trp Asn Asp Leu Leu Ala
 25 30 35

cgc cct tta act gac tac atc atg atc ttg tgc atc gtg gtc att ttg 259
 Arg Pro Leu Thr Asp Tyr Ile Met Ile Leu Cys Ile Val Val Ile Leu
 40 45 50

tcg tgc ctc ggt gta gtc atg gtg tat tcc tcc tca atg aca tgg tcg 307
 Ser Cys Leu Gly Val Val Met Val Tyr Ser Ser Ser Met Thr Trp Ser
 55 60 65

ttg agg gaa ggt ggc tcc gtg tgg ggt act gcc gtg cgc cag ggc atc 355
 Leu Arg Glu Gly Gly Ser Val Trp Gly Thr Ala Val Arg Gln Gly Ile
 70 75 80 85

atg atc gtg ttg ggt ttc ttt gcc atg tgg gtg gcg ttg atg acg cgc 403
 Met Ile Val Leu Gly Phe Phe Ala Met Trp Val Ala Leu Met Thr Arg
 90 95 100

ccg caa acc att aga aac cta tcc aac ctg ata ttg att gtg tct att 451
 Pro Gln Thr Ile Arg Asn Leu Ser Asn Leu Ile Leu Ile Val Ser Ile
 105 110 115

gtc ttg ctg ctt gcc gtg cag att cct ggc att ggt aca ggt aaa gaa 499
 Val Leu Leu Leu Ala Val Gln Ile Pro Gly Ile Gly Thr Gly Lys Glu
 120 125 130

gag gtc ggg tcg cag tcg tgg att gct ctt gga cct att cag ttt cag 547
 Glu Val Gly Ser Gln Ser Trp Ile Ala Leu Gly Pro Ile Gln Phe Gln
 135 140 145

cct tcg gag atc gcc aaa gtg gcc att gcc gtg tgg gga gcg cac tac 595

Pro	Ser	Glu	Ile	Ala	Lys	Val	Ala	Ile	Ala	Val	Trp	Gly	Ala	His	Tyr			
150					155					160					165			
ctc	gca	ggc	aag	ggc	cct	gtg	cag	cac	tgg	ttc	aat	aat	cac	ttg	atg		643	
Leu	Ala	Gly	Lys	Gly	Pro	Val	Gln	His	Trp	Phe	Asn	Asn	His	Leu	Met			
				170					175					180				
cgt	ttt	ggt	ggc	gtc	ggg	gca	ttc	atg	gcg	ttt	ttg	atc	ttc	atg	gaa		691	
Arg	Phe	Gly	Gly	Val	Gly	Ala	Phe	Met	Ala	Phe	Leu	Ile	Phe	Met	Glu			
			185					190					195					
ggc	gac	gcc	ggc	atg	gcg	atg	tct	ttc	gtg	ctg	gtt	gta	ttg	ttc	atg		739	
Gly	Asp	Ala	Gly	Met	Ala	Met	Ser	Phe	Val	Leu	Val	Val	Leu	Phe	Met			
		200					205					210						
ctg	ttt	ttt	gcg	ggc	atc	gcc	atg	ggg	tgg	atc	gcg	att	gcc	ggc	gta		787	
Leu	Phe	Phe	Ala	Gly	Ile	Ala	Met	Gly	Trp	Ile	Ala	Ile	Ala	Gly	Val			
	215					220					225							
ctg	att	atc	gca	gcc	ctc	gca	gtc	ctg	gca	ttg	ggc	gga	ggc	ttc	cgt		835	
Leu	Ile	Ile	Ala	Ala	Leu	Ala	Val	Leu	Ala	Leu	Gly	Gly	Gly	Phe	Arg			
230					235				240						245			
tca	agc	cga	ttc	gag	gtg	tat	ttc	gat	gcg	ctg	ttt	ggc	aat	ttc	cac		883	
Ser	Ser	Arg	Phe	Glu	Val	Tyr	Phe	Asp	Ala	Leu	Phe	Gly	Asn	Phe	His			
				250					255					260				
gat	gtg	cga	ggc	att	gcc	ttc	cag	tcc	tat	cag	ggc	ttc	ctc	tct	ctt		931	
Asp	Val	Arg	Gly	Ile	Ala	Phe	Gln	Ser	Tyr	Gln	Gly	Phe	Leu	Ser	Leu			
			265					270					275					
gca	gat	ggt	tcc	ggc	ttg	gga	gtt	ggg	ttg	ggc	caa	tca	agg	gcg	aag		979	
Ala	Asp	Gly	Ser	Gly	Leu	Gly	Val	Gly	Leu	Gly	Gln	Ser	Arg	Ala	Lys			
		280					285					290						
tgg	ttc	tac	ctg	ccc	gaa	gct	aaa	aat	gac	ttc	atc	ttt	gcc	atc	att		1027	
Trp	Phe	Tyr	Leu	Pro	Glu	Ala	Lys	Asn	Asp	Phe	Ile	Phe	Ala	Ile	Ile			
	295					300					305							
ggg	gag	gag	ctg	ggg	ctg	tgg	ggg	ggc	gct	ctg	gtc	atc	gca	ctt	ttc		1075	
Gly	Glu	Glu	Leu	Gly	Leu	Trp	Gly	Gly	Ala	Leu	Val	Ile	Ala	Leu	Phe			
310					315					320					325			
gcg	ggg	ctg	ctg	tac	ttc	ggg	ctg	cgc	aca	gcc	aag	aag	agc	cac	gat		1123	
Ala	Gly	Leu	Leu	Tyr	Phe	Gly	Leu	Arg	Thr	Ala	Lys	Lys	Ser	His	Asp			
				330					335					340				
cca	ttc	ttg	ggc	ttg	atg	gct	gca	acc	ttg	acg	gca	tcc	gtg	gtg	tcg		1171	
Pro	Phe	Leu	Gly	Leu	Met	Ala	Ala	Thr	Leu	Thr	Ala	Ser	Val	Val	Ser			
			345					350					355					
cag	gcg	ttc	atc	aac	att	ggc	tac	gtg	gtt	ggg	ctg	ctg	cca	gtt	acc		1219	
Gln	Ala	Phe	Ile	Asn	Ile	Gly	Tyr	Val	Val	Gly	Leu	Leu	Pro	Val	Thr			
		360					365					370						
ggg	att	cag	ctg	ccc	atg	att	tcc	ggc	ggg	ggg	acc	tcc	gcg	atc	att		1267	
Gly	Ile	Gln	Leu	Pro	Met	Ile	Ser	Ala	Gly	Gly	Thr	Ser	Ala	Ile	Ile			
	375					380					385							
acc	ttg	gct	tcc	atg	ggc	ttg	ctc	att	agc	tgt	gca	cgc	cac	gaa	cca		1315	
Thr	Leu	Ala	Ser	Met	Gly	Leu	Leu	Ile	Ser	Cys	Ala	Arg	His	Glu	Pro			

390	395	400	405	
gag aca gtt tct	gcg atg gct tcc tat	gga cgc ccc gca atc gat cga	1363	
Glu Thr Val Ser	Ala Met Ala Ser Tyr	Gly Arg Pro Ala Ile Asp Arg		
	410	415 420		
ctt ctg gga ttg	cgt gag cct tca agt act ttg acc acc agt aat gca	1411		
Leu Leu Gly Leu	Arg Glu Pro Ser Ser Thr Leu Thr Thr Ser Asn Ala			
	425 430	435		
tcc ttg cgt tcc aac aaa acc aag gcc gct aaa caa aag ccg agt cct	1459			
Ser Leu Arg Ser Asn Lys Thr Lys Ala Ala Lys Gln Lys Pro Ser Pro				
	440 445	450		
cag aaa gag tct cgg gac cgc ttc ggc gag cct gtg acc gca cgc cga	1507			
Gln Lys Glu Ser Arg Asp Arg Phe Gly Glu Pro Val Thr Ala Arg Arg				
	455 460	465		
gcg cag gcg cca cga agt ggg cga gct gga gta caa tcg gaa gct ccg	1555			
Ala Gln Ala Pro Arg Ser Gly Arg Ala Gly Val Gln Ser Glu Ala Pro				
	470 475	480 485		
cga cgc tcg act ggt agc gtc aaa ggt cga agc agt ggt cag gac aac	1603			
Arg Arg Ser Thr Gly Ser Val Lys Gly Arg Ser Ser Gly Gln Asp Asn				
	490 495	500		
ggt cga agc aac gaa ggt acg gcg cgt agc caa tca act act ggt ggg	1651			
Gly Arg Ser Asn Glu Gly Thr Ala Arg Ser Gln Ser Thr Thr Gly Gly				
	505 510	515		
cgc gca gcc gat cgc agc gtt gat cga agt cgt caa agc agg cct acc	1699			
Arg Ala Ala Asp Arg Ser Val Asp Arg Ser Arg Gln Ser Arg Pro Thr				
	520 525	530		
gag cgc cgt tcc gag agt cgc gcg atg att ggc gtg aca acc gca acc	1747			
Glu Arg Arg Ser Glu Ser Arg Ala Met Ile Gly Val Thr Thr Ala Thr				
	535 540	545		
gca gat aaa tgt gaa atc agg aga act acg aat aaa gat ggc	1789			
Ala Asp Lys Cys Glu Ile Arg Arg Thr Thr Asn Lys Asp Gly				
	550 555	560		
taactcccca aaacccatgc ggg	1812			

<210> 80

<211> 563

<212> PRT

<213> Corynebacterium glutamicum

<400> 80

Met Thr Thr Gly Ala Ser Lys Lys Pro Ala Arg Pro Asn Thr Gly Ala
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Lys Thr Arg Thr Gly Leu Gly Ile Arg Glu Arg Ile Ser Gly Ala Trp
20 25 30

Asn Asp Leu Leu Ala Arg Pro Leu Thr Asp Tyr Ile Met Ile Leu Cys
35 40 45

Ile Val Val Ile Leu Ser Cys Leu Gly Val Val Met Val Tyr Ser Ser

50					55					60					
Ser 65	Met	Thr	Trp	Ser	Leu 70	Arg	Glu	Gly	Gly	Ser 75	Val	Trp	Gly	Thr	Ala 80
Val	Arg	Gln	Gly	Ile 85	Met	Ile	Val	Leu	Gly 90	Phe	Phe	Ala	Met	Trp	Val 95
Ala	Leu	Met	Thr 100	Arg	Pro	Gln	Thr	Ile 105	Arg	Asn	Leu	Ser	Asn	Leu	Ile 110
Leu	Ile	Val 115	Ser	Ile	Val	Leu	Leu	Leu 120	Ala	Val	Gln	Ile	Pro	Gly	Ile 125
Gly	Thr 130	Gly	Lys	Glu	Glu	Val 135	Gly	Ser	Gln	Ser	Trp 140	Ile	Ala	Leu	Gly
Pro	Ile	Gln	Phe	Gln	Pro	Ser 150	Glu	Ile	Ala	Lys	Val	Ala	Ile	Ala	Val 160
Trp	Gly	Ala	His	Tyr 165	Leu	Ala	Gly	Lys	Gly 170	Pro	Val	Gln	His	Trp	Phe 175
Asn	Asn	His	Leu 180	Met	Arg	Phe	Gly	Gly 185	Val	Gly	Ala	Phe	Met	Ala	Phe 190
Leu	Ile	Phe 195	Met	Glu	Gly	Asp	Ala 200	Gly	Met	Ala	Met	Ser	Phe	Val	Leu 205
Val	Val	Leu	Phe	Met	Leu	Phe 215	Phe	Ala	Gly	Ile	Ala 220	Met	Gly	Trp	Ile 225
Ala	Ile	Ala	Gly	Val	Leu	Ile 230	Ile	Ala	Ala	Leu	Ala 235	Val	Leu	Ala	Leu 240
Gly	Gly	Gly	Phe	Arg	Ser	Ser	Arg	Phe	Glu 250	Val	Tyr	Phe	Asp	Ala	Leu 255
Phe	Gly	Asn	Phe 260	His	Asp	Val	Arg	Gly 265	Ile	Ala	Phe	Gln	Ser	Tyr	Gln 270
Gly	Phe	Leu	Ser	Leu	Ala	Asp	Gly 280	Ser	Gly	Leu	Gly 285	Val	Gly	Leu	Gly 290
Gln	Ser	Arg	Ala	Lys	Trp	Phe	Tyr	Leu	Pro	Glu	Ala 300	Lys	Asn	Asp	Phe 305
Ile	Phe	Ala	Ile	Ile	Gly	Glu	Glu	Leu	Gly	Leu	Trp	Gly	Gly	Ala	Leu 320
Val	Ile	Ala	Leu	Phe	Ala	Gly	Leu	Leu	Tyr	Phe	Gly	Leu	Arg	Thr	Ala 335
Lys	Lys	Ser	His	Asp	Pro	Phe	Leu	Gly	Leu	Met	Ala	Ala	Thr	Leu	Thr 350
Ala	Ser	Val	Val	Ser	Gln	Ala	Phe	Ile	Asn	Ile	Gly	Tyr	Val	Val	Gly 365
Leu	Leu	Pro	Val	Thr	Gly	Ile	Gln	Leu	Pro	Met	Ile	Ser	Ala	Gly	Gly 380

Thr Ser Ala Ile Ile Thr Leu Ala Ser Met Gly Leu Leu Ile Ser Cys
 385 390 395 400
 Ala Arg His Glu Pro Glu Thr Val Ser Ala Met Ala Ser Tyr Gly Arg
 405 410 415
 Pro Ala Ile Asp Arg Leu Leu Gly Leu Arg Glu Pro Ser Ser Thr Leu
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 Thr Thr Ser Asn Ala Ser Leu Arg Ser Asn Lys Thr Lys Ala Ala Lys
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 Gln Lys Pro Ser Pro Gln Lys Glu Ser Arg Asp Arg Phe Gly Glu Pro
 450 455 460
 Val Thr Ala Arg Arg Ala Gln Ala Pro Arg Ser Gly Arg Ala Gly Val
 465 470 475 480
 Gln Ser Glu Ala Pro Arg Arg Ser Thr Gly Ser Val Lys Gly Arg Ser
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 Ser Gly Gln Asp Asn Gly Arg Ser Asn Glu Gly Thr Ala Arg Ser Gln
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 Ser Thr Thr Gly Gly Arg Ala Ala Asp Arg Ser Val Asp Arg Ser Arg
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 Lys Asp Gly

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 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1789)
 <223> FRXA02704

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 Met Thr Thr Gly Ala
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 tca aaa aaa ccc gca cgt ccg aac act ggc gct aaa acc aga acg ggg 163
 Ser Lys Lys Pro Ala Arg Pro Asn Thr Gly Ala Lys Thr Arg Thr Gly
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 ctg gga att agg gag cgt att tcc ggt gca tgg aat gat ctt ctc gcg 211
 Leu Gly Ile Arg Glu Arg Ile Ser Gly Ala Trp Asn Asp Leu Leu Ala

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cgc	cct	tta	act	gac	tac	atc	atg	atc	ttg	tgc	atc	gtg	gtc	att	ttg	259
Arg	Pro	Leu	Thr	Asp	Tyr	Ile	Met	Ile	Leu	Cys	Ile	Val	Val	Ile	Leu	
		40					45					50				
tcg	tgc	ctc	ggg	gta	gtc	atg	gtg	tat	tcc	tcc	tca	atg	aca	tgg	tcg	307
Ser	Cys	Leu	Gly	Val	Val	Met	Val	Tyr	Ser	Ser	Ser	Met	Thr	Trp	Ser	
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ttg	agg	gaa	ggg	ggc	tcc	gtg	tgg	ggg	act	gcc	gtg	cgc	cag	ggc	atc	355
Leu	Arg	Glu	Gly	Gly	Ser	Val	Trp	Gly	Thr	Ala	Val	Arg	Gln	Gly	Ile	
70					75					80					85	
atg	atc	gtg	ttg	ggg	ttc	ttt	gcc	atg	tgg	gtg	gcg	ttg	atg	acg	cgc	403
Met	Ile	Val	Leu	Gly	Phe	Phe	Ala	Met	Trp	Val	Ala	Leu	Met	Thr	Arg	
				90					95					100		
ccg	caa	acc	att	aga	aac	cta	tcc	aac	ctg	ata	ttg	att	gtg	tct	att	451
Pro	Gln	Thr	Ile	Arg	Asn	Leu	Ser	Asn	Leu	Ile	Leu	Ile	Val	Ser	Ile	
			105					110					115			
gtc	ttg	ctg	ctt	gcc	gtg	cag	att	cct	ggc	att	ggg	aca	ggg	aaa	gaa	499
Val	Leu	Leu	Leu	Ala	Val	Gln	Ile	Pro	Gly	Ile	Gly	Thr	Gly	Lys	Glu	
	120					125					130					
gag	gtc	ggg	tcg	cag	tcg	tgg	att	gct	ctt	gga	cct	att	cag	ttt	cag	547
Glu	Val	Gly	Ser	Gln	Ser	Trp	Ile	Ala	Leu	Gly	Pro	Ile	Gln	Phe	Gln	
	135					140					145					
cct	tcg	gag	atc	gcc	aaa	gtg	gcc	att	gcc	gtg	tgg	gga	gcg	cac	tac	595
Pro	Ser	Glu	Ile	Ala	Lys	Val	Ala	Ile	Ala	Val	Trp	Gly	Ala	His	Tyr	
150					155					160					165	
ctc	gca	ggc	aag	ggc	cct	gtg	cag	cac	tgg	ttc	aat	aat	cac	ttg	atg	643
Leu	Ala	Gly	Lys	Gly	Pro	Val	Gln	His	Trp	Phe	Asn	Asn	His	Leu	Met	
				170					175					180		
cgt	ttt	ggg	ggc	gtc	ggg	gca	ttc	atg	gcg	ttt	ttg	atc	ttc	atg	gaa	691
Arg	Phe	Gly	Gly	Val	Gly	Ala	Phe	Met	Ala	Phe	Leu	Ile	Phe	Met	Glu	
			185					190					195			
ggc	gac	gcc	ggc	atg	gcg	atg	tct	ttc	gtg	ctg	gtt	gta	ttg	ttc	atg	739
Gly	Asp	Ala	Gly	Met	Ala	Met	Ser	Phe	Val	Leu	Val	Val	Leu	Phe	Met	
		200					205					210				
ctg	ttt	ttt	gcg	ggc	atc	gcc	atg	ggg	tgg	atc	gcg	att	gcc	ggc	gta	787
Leu	Phe	Phe	Ala	Gly	Ile	Ala	Met	Gly	Trp	Ile	Ala	Ile	Ala	Gly	Val	
	215					220					225					
ctg	att	atc	gca	ggc	ctc	gca	gtc	ctg	gca	ttg	ggc	gga	ggc	ttc	cgt	835
Leu	Ile	Ile	Ala	Ala	Leu	Ala	Val	Leu	Ala	Leu	Gly	Gly	Gly	Phe	Arg	
230					235					240					245	
tca	agc	cga	ttc	gag	gtg	tat	ttc	gat	gcg	ctg	ttt	ggc	aat	ttc	cac	883
Ser	Ser	Arg	Phe	Glu	Val	Tyr	Phe	Asp	Ala	Leu	Phe	Gly	Asn	Phe	His	
				250					255					260		
gat	gtg	cga	ggc	att	gcc	ttc	cag	tcc	tat	cag	ggc	ttc	ctc	tct	ctt	931
Asp	Val	Arg	Gly	Ile	Ala	Phe	Gln	Ser	Tyr	Gln	Gly	Phe	Leu	Ser	Leu	
			265					270					275			

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Ala Asp Gly Ser Gly Leu Gly Val Gly Leu Gly Gln Ser Arg Ala Lys	
280 285 290	
tgg ttc tac ctg ccc gaa gct aaa aat gac ttc atc ttt gcc atc att	1027
Trp Phe Tyr Leu Pro Glu Ala Lys Asn Asp Phe Ile Phe Ala Ile Ile	
295 300 305	
ggt gag gag ctg ggg ctg tgg ggt ggc gct ctg gtc atc gca ctt ttc	1075
Gly Glu Glu Leu Gly Leu Trp Gly Gly Ala Leu Val Ile Ala Leu Phe	
310 315 320 325	
gcg ggg ctg ctg tac ttc ggt ctg cgc aca gcc aag aag agc cac gat	1123
Ala Gly Leu Leu Tyr Phe Gly Leu Arg Thr Ala Lys Lys Ser His Asp	
330 335 340	
cca ttc ttg ggc ttg atg gct gca acc ttg acg gca tcc gtg gtg tcg	1171
Pro Phe Leu Gly Leu Met Ala Ala Thr Leu Thr Ala Ser Val Val Ser	
345 350 355	
cag gcg ttc atc aac att ggc tac gtg gtt ggt ctg ctg cca gtt acc	1219
Gln Ala Phe Ile Asn Ile Gly Tyr Val Val Gly Leu Leu Pro Val Thr	
360 365 370	
ggt att cag ctg ccc atg att tcc gcc ggt ggt acc tcc gcg atc att	1267
Gly Ile Gln Leu Pro Met Ile Ser Ala Gly Gly Thr Ser Ala Ile Ile	
375 380 385	
acc ttg gct tcc atg ggc ttg ctc att agc tgt gca cgc cac gaa cca	1315
Thr Leu Ala Ser Met Gly Leu Leu Ile Ser Cys Ala Arg His Glu Pro	
390 395 400 405	
gag aca gtt tct gcg atg gct tcc tat gga cgc ccc gca atc gat cga	1363
Glu Thr Val Ser Ala Met Ala Ser Tyr Gly Arg Pro Ala Ile Asp Arg	
410 415 420	
ctt ctg gga ttg cgt gag cct tca agt act ttg acc acc agt aat gca	1411
Leu Leu Gly Leu Arg Glu Pro Ser Ser Thr Leu Thr Thr Ser Asn Ala	
425 430 435	
tcc ttg cgt tcc aac aaa acc aag gcc gct aaa caa aag ccg agt cct	1459
Ser Leu Arg Ser Asn Lys Thr Lys Ala Ala Lys Gln Lys Pro Ser Pro	
440 445 450	
cag aaa gag tct cgg gac cgc ttc ggc gag cct gtg acc gca cgc cga	1507
Gln Lys Glu Ser Arg Asp Arg Phe Gly Glu Pro Val Thr Ala Arg Arg	
455 460 465	
gcg cag gcg cca cga agt ggg cga gct gga gta caa tcg gaa gct ccg	1555
Ala Gln Ala Pro Arg Ser Gly Arg Ala Gly Val Gln Ser Glu Ala Pro	
470 475 480 485	
cga cgc tcg act ggt agc gtc aaa ggt cga agc agt ggt cag gac aac	1603
Arg Arg Ser Thr Gly Ser Val Lys Gly Arg Ser Ser Gly Gln Asp Asn	
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ggt cga agc aac gaa ggt acg gcg cgt agc caa tca act act ggt ggg	1651
Gly Arg Ser Asn Glu Gly Thr Ala Arg Ser Gln Ser Thr Thr Gly Gly	
505 510 515	

cgc gca gcc gat cgc agc gtt gat cga agt cgt caa agc agg cct acc 1699
 Arg Ala Ala Asp Arg Ser Val Asp Arg Ser Arg Gln Ser Arg Pro Thr
 520 525 530

gag cgc cgt tcc gag agt cgc gcg atg att ggc gtg aca acc gca acc 1747
 Glu Arg Arg Ser Glu Ser Arg Ala Met Ile Gly Val Thr Thr Ala Thr
 535 540 545

gca gat aaa tgt gaa atc agg aga act acg aat aaa gat ggc 1789
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taactcccca aaacccatgc ggg 1812

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<211> 563

<212> PRT

<213> Corynebacterium glutamicum

<400> 82

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Asn Asp Leu Leu Ala Arg Pro Leu Thr Asp Tyr Ile Met Ile Leu Cys
 35 40 45

Ile Val Val Ile Leu Ser Cys Leu Gly Val Val Met Val Tyr Ser Ser
 50 55 60

Ser Met Thr Trp Ser Leu Arg Glu Gly Gly Ser Val Trp Gly Thr Ala
 65 70 75 80

Val Arg Gln Gly Ile Met Ile Val Leu Gly Phe Phe Ala Met Trp Val
 85 90 95

Ala Leu Met Thr Arg Pro Gln Thr Ile Arg Asn Leu Ser Asn Leu Ile
 100 105 110

Leu Ile Val Ser Ile Val Leu Leu Leu Ala Val Gln Ile Pro Gly Ile
 115 120 125

Gly Thr Gly Lys Glu Glu Val Gly Ser Gln Ser Trp Ile Ala Leu Gly
 130 135 140

Pro Ile Gln Phe Gln Pro Ser Glu Ile Ala Lys Val Ala Ile Ala Val
 145 150 155 160

Trp Gly Ala His Tyr Leu Ala Gly Lys Gly Pro Val Gln His Trp Phe
 165 170 175

Asn Asn His Leu Met Arg Phe Gly Gly Val Gly Ala Phe Met Ala Phe
 180 185 190

Leu Ile Phe Met Glu Gly Asp Ala Gly Met Ala Met Ser Phe Val Leu
 195 200 205

Val Val Leu Phe Met Leu Phe Phe Ala Gly Ile Ala Met Gly Trp Ile

210	215	220
Ala Ile Ala Gly Val Leu Ile Ile Ala Ala Leu Ala Val Leu Ala Leu 225 230 235 240		
Gly Gly Gly Phe Arg Ser Ser Arg Phe Glu Val Tyr Phe Asp Ala Leu 245 250 255		
Phe Gly Asn Phe His Asp Val Arg Gly Ile Ala Phe Gln Ser Tyr Gln 260 265 270		
Gly Phe Leu Ser Leu Ala Asp Gly Ser Gly Leu Gly Val Gly Leu Gly 275 280 285		
Gln Ser Arg Ala Lys Trp Phe Tyr Leu Pro Glu Ala Lys Asn Asp Phe 290 295 300		
Ile Phe Ala Ile Ile Gly Glu Glu Leu Gly Leu Trp Gly Gly Ala Leu 305 310 315 320		
Val Ile Ala Leu Phe Ala Gly Leu Leu Tyr Phe Gly Leu Arg Thr Ala 325 330 335		
Lys Lys Ser His Asp Pro Phe Leu Gly Leu Met Ala Ala Thr Leu Thr 340 345 350		
Ala Ser Val Val Ser Gln Ala Phe Ile Asn Ile Gly Tyr Val Val Gly 355 360 365		
Leu Leu Pro Val Thr Gly Ile Gln Leu Pro Met Ile Ser Ala Gly Gly 370 375 380		
Thr Ser Ala Ile Ile Thr Leu Ala Ser Met Gly Leu Leu Ile Ser Cys 385 390 395 400		
Ala Arg His Glu Pro Glu Thr Val Ser Ala Met Ala Ser Tyr Gly Arg 405 410 415		
Pro Ala Ile Asp Arg Leu Leu Gly Leu Arg Glu Pro Ser Ser Thr Leu 420 425 430		
Thr Thr Ser Asn Ala Ser Leu Arg Ser Asn Lys Thr Lys Ala Ala Lys 435 440 445		
Gln Lys Pro Ser Pro Gln Lys Glu Ser Arg Asp Arg Phe Gly Glu Pro 450 455 460		
Val Thr Ala Arg Arg Ala Gln Ala Pro Arg Ser Gly Arg Ala Gly Val 465 470 475 480		
Gln Ser Glu Ala Pro Arg Arg Ser Thr Gly Ser Val Lys Gly Arg Ser 485 490 495		
Ser Gly Gln Asp Asn Gly Arg Ser Asn Glu Gly Thr Ala Arg Ser Gln 500 505 510		
Ser Thr Thr Gly Gly Arg Ala Ala Asp Arg Ser Val Asp Arg Ser Arg 515 520 525		
Gln Ser Arg Pro Thr Glu Arg Arg Ser Glu Ser Arg Ala Met Ile Gly 530 535 540		

Val Thr Thr Ala Thr Ala Asp Lys Cys Glu Ile Arg Arg Thr Thr Asn
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Lys Asp Gly

<210> 83

<211> 1449

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1426)

<223> RXA02722

<400> 83

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Met Thr Ser Pro Asn
1 5

aac tac ctc gcc aag att aag gtc gtc ggc gtg ggc ggc ggc gga gtc 163
Asn Tyr Leu Ala Lys Ile Lys Val Val Gly Val Gly Gly Gly Gly Val
10 15 20

aac gcc gtc aac cgc atg att gaa gaa ggc ctc aaa ggc gtg gag ttc 211
Asn Ala Val Asn Arg Met Ile Glu Glu Gly Leu Lys Gly Val Glu Phe
25 30 35

atc gcg gtg aac acc gac tcg cag gct ctc atg ttc tct gat gcc gac 259
Ile Ala Val Asn Thr Asp Ser Gln Ala Leu Met Phe Ser Asp Ala Asp
40 45 50

gta aag ctc gat atc gga cgt gaa gct acc cgt ggt ctt ggt gcc ggc 307
Val Lys Leu Asp Ile Gly Arg Glu Ala Thr Arg Gly Leu Gly Ala Gly
55 60 65

gcg aac cca gaa gtt gga cgt gcc tcg gca gag gat cac aag aac gaa 355
Ala Asn Pro Glu Val Gly Arg Ala Ser Ala Glu Asp His Lys Asn Glu
70 75 80 85

atc gaa gaa acc atc aag ggc gcc gac atg gtc ttc gtt acc gcc ggc 403
Ile Glu Glu Thr Ile Lys Gly Ala Asp Met Val Phe Val Thr Ala Gly
90 95 100

gaa ggt ggt ggc acc gga act ggt gct gca cca gtc gtg gca ggg atc 451
Glu Gly Gly Gly Thr Gly Thr Gly Ala Ala Pro Val Val Ala Gly Ile
105 110 115

gcc aag aag atg ggc gca ctg acc att ggt gtt gtg acc aag cct ttc 499
Ala Lys Lys Met Gly Ala Leu Thr Ile Gly Val Val Thr Lys Pro Phe
120 125 130

gag ttc gaa ggc cgt cgc cgt act cgc cag gca gaa gaa ggc atc gca 547
Glu Phe Glu Gly Arg Arg Arg Thr Arg Gln Ala Glu Glu Gly Ile Ala
135 140 145

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				170					175					180		
gca	gcc	gat	gaa	gtt	ctc	cac	aat	ggt	gtt	cag	ggt	att	acc	aac	ctg	691
Ala	Ala	Asp	Glu	Val	Leu	His	Asn	Gly	Val	Gln	Gly	Ile	Thr	Asn	Leu	
			185					190					195			
atc	acc	atc	cct	ggt	gtg	atc	aac	gtg	gac	ttc	gcg	gac	gtt	cgc	tcc	739
Ile	Thr	Ile	Pro	Gly	Val	Ile	Asn	Val	Asp	Phe	Ala	Asp	Val	Arg	Ser	
		200					205					210				
gtc	atg	tcc	gaa	gct	ggt	tcc	gca	ctc	atg	ggt	gtg	ggc	tct	gca	cgt	787
Val	Met	Ser	Glu	Ala	Gly	Ser	Ala	Leu	Met	Gly	Val	Gly	Ser	Ala	Arg	
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ggg	gac	aac	cgc	gtt	gtc	tct	gca	acc	gag	cag	gcc	atc	aac	tct	cca	835
Gly	Asp	Asn	Arg	Val	Val	Ser	Ala	Thr	Glu	Gln	Ala	Ile	Asn	Ser	Pro	
230					235					240					245	
ctt	ctc	gaa	gca	aca	atg	gac	ggc	gca	act	ggc	gtc	ctg	ctg	tcc	ttt	883
Leu	Leu	Glu	Ala	Thr	Met	Asp	Gly	Ala	Thr	Gly	Val	Leu	Leu	Ser	Phe	
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gct	ggt	gga	tcc	gac	ctg	ggc	ctc	atg	gaa	gtc	aac	gca	gct	gca	tcc	931
Ala	Gly	Gly	Ser	Asp	Leu	Gly	Leu	Met	Glu	Val	Asn	Ala	Ala	Ala	Ser	
			265					270					275			
atg	gtc	cgt	gag	cgt	tcc	gat	gaa	gat	gtc	aac	ctc	atc	ttc	ggt	acc	979
Met	Val	Arg	Glu	Arg	Ser	Asp	Glu	Asp	Val	Asn	Leu	Ile	Phe	Gly	Thr	
		280					285					290				
atc	atc	gac	gac	aac	ctg	ggc	gac	gaa	gtc	cgc	gta	acc	gtc	atc	gcg	1027
Ile	Ile	Asp	Asp	Asn	Leu	Gly	Asp	Glu	Val	Arg	Val	Thr	Val	Ile	Ala	
		295				300					305					
acc	ggt	ttt	gac	gca	gct	cgc	gca	agc	gcc	gct	gag	aac	cgc	cgc	gca	1075
Thr	Gly	Phe	Asp	Ala	Ala	Arg	Ala	Ser	Ala	Ala	Glu	Asn	Arg	Arg	Ala	
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ggc	atc	tca	gct	gca	cct	gca	gct	gag	cca	gtc	cag	cag	cag	gtc	cca	1123
Gly	Ile	Ser	Ala	Ala	Pro	Ala	Ala	Glu	Pro	Val	Gln	Gln	Gln	Val	Pro	
				330					335					340		
acc	acc	aac	gca	acc	ctt	cca	cca	gag	aag	gaa	agc	atc	ttc	ggt	ggt	1171
Thr	Thr	Asn	Ala	Thr	Leu	Pro	Pro	Glu	Lys	Glu	Ser	Ile	Phe	Gly	Gly	
			345					350					355			
gca	cgt	gag	gag	aac	gat	cct	tac	ctg	tcc	cgc	tct	gct	ggt	gca	cgt	1219
Ala	Arg	Glu	Glu	Asn	Asp	Pro	Tyr	Leu	Ser	Arg	Ser	Ala	Gly	Ala	Arg	
		360					365					370				
cat	cgc	att	gag	gag	acc	cgc	tcc	ggc	ggt	gga	ctc	ttc	acc	acc	ggc	1267
His	Arg	Ile	Glu	Glu	Thr	Arg	Ser	Gly	Gly	Gly	Leu	Phe	Thr	Thr	Gly	
	375					380					385					
aat	gat	cgc	gat	tac	cgt	cgt	gat	gag	cgc	cgc	gaa	gat	cac	cgt	gac	1315

Asn Asp Arg Asp Tyr Arg Arg Asp Glu Arg Arg Glu Asp His Arg Asp
 390 395 400 405
 gag cgc cgc gat gag cgc cgc gat gac cgt tcc tac gac cgc cgt gat 1363
 Glu Arg Arg Asp Glu Arg Arg Asp Asp Arg Ser Tyr Asp Arg Arg Asp
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 gat cgt cgt gac gat cgc cgc gat gac cgc gga gac gac ctg gat gta 1411
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 Pro Ser Phe Leu Gln
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<210> 84
 <211> 442
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 84
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 35 40 45
 Phe Ser Asp Ala Asp Val Lys Leu Asp Ile Gly Arg Glu Ala Thr Arg
 50 55 60
 Gly Leu Gly Ala Gly Ala Asn Pro Glu Val Gly Arg Ala Ser Ala Glu
 65 70 75 80
 Asp His Lys Asn Glu Ile Glu Glu Thr Ile Lys Gly Ala Asp Met Val
 85 90 95
 Phe Val Thr Ala Gly Glu Gly Gly Gly Thr Gly Thr Gly Ala Ala Pro
 100 105 110
 Val Val Ala Gly Ile Ala Lys Lys Met Gly Ala Leu Thr Ile Gly Val
 115 120 125
 Val Thr Lys Pro Phe Glu Phe Glu Gly Arg Arg Arg Thr Arg Gln Ala
 130 135 140
 Glu Glu Gly Ile Ala Ala Leu Lys Glu Val Cys Asp Thr Leu Ile Val
 145 150 155 160
 Ile Pro Asn Asp Arg Leu Leu Glu Leu Gly Asp Ala Asn Leu Ser Ile
 165 170 175
 Met Glu Ala Phe Arg Ala Ala Asp Glu Val Leu His Asn Gly Val Gln
 180 185 190
 Gly Ile Thr Asn Leu Ile Thr Ile Pro Gly Val Ile Asn Val Asp Phe
 195 200 205

Ala Asp Val Arg Ser Val Met Ser Glu Ala Gly Ser Ala Leu Met Gly
 210 215 220
 Val Gly Ser Ala Arg Gly Asp Asn Arg Val Val Ser Ala Thr Glu Gln
 225 230 235 240
 Ala Ile Asn Ser Pro Leu Leu Glu Ala Thr Met Asp Gly Ala Thr Gly
 245 250 255
 Val Leu Leu Ser Phe Ala Gly Gly Ser Asp Leu Gly Leu Met Glu Val
 260 265 270
 Asn Ala Ala Ala Ser Met Val Arg Glu Arg Ser Asp Glu Asp Val Asn
 275 280 285
 Leu Ile Phe Gly Thr Ile Ile Asp Asp Asn Leu Gly Asp Glu Val Arg
 290 295 300
 Val Thr Val Ile Ala Thr Gly Phe Asp Ala Ala Arg Ala Ser Ala Ala
 305 310 315 320
 Glu Asn Arg Arg Ala Gly Ile Ser Ala Ala Pro Ala Ala Glu Pro Val
 325 330 335
 Gln Gln Gln Val Pro Thr Thr Asn Ala Thr Leu Pro Pro Glu Lys Glu
 340 345 350
 Ser Ile Phe Gly Gly Ala Arg Glu Glu Asn Asp Pro Tyr Leu Ser Arg
 355 360 365
 Ser Ala Gly Ala Arg His Arg Ile Glu Glu Thr Arg Ser Gly Gly Gly
 370 375 380
 Leu Phe Thr Thr Gly Asn Asp Arg Asp Tyr Arg Arg Asp Glu Arg Arg
 385 390 395 400
 Glu Asp His Arg Asp Glu Arg Arg Asp Glu Arg Arg Asp Asp Arg Ser
 405 410 415
 Tyr Asp Arg Arg Asp Asp Arg Arg Asp Asp Arg Arg Asp Asp Arg Gly
 420 425 430
 Asp Asp Leu Asp Val Pro Ser Phe Leu Gln
 435 440

<210> 85
 <211> 1023
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1000)
 <223> RXA00009

<400> 85
 gacgacatgc gcaggcgagt aatcgaactg caattgggca aactagtccg cgatgatgcc 60
 cacggcgtct acggcgaaat gcgatagggg agtacttcac atg gct ttt gga tat 115
 Met Ala Phe Gly Tyr

	1	5	
gta ctg cgt gaa gct gtt cgc ggc atg ggc cgc aac gtc acc atg acc			163
Val Leu Arg Glu Ala Val Arg Gly Met Gly Arg Asn Val Thr Met Thr			
	10	15	20
atc gcg ctc atc atc acc acc tct att tcc ttg gca ctt ctt gcc act			211
Ile Ala Leu Ile Ile Thr Thr Ser Ile Ser Leu Ala Leu Leu Ala Thr			
	25	30	35
gga ttt ttg gtg acc aac atg acc gac cgc acc aag gac atc tac ctg			259
Gly Phe Leu Val Thr Asn Met Thr Asp Arg Thr Lys Asp Ile Tyr Leu			
	40	45	50
gat cgc gtc gaa gtg atg atc caa ctc gat gag gac acc tct gcc aac			307
Asp Arg Val Glu Val Met Ile Gln Leu Asp Glu Asp Thr Ser Ala Asn			
	55	60	65
gat ccc gaa tgc acc gcg gag tcc tgc acc gaa gtt cgt gat gtc tta			355
Asp Pro Glu Cys Thr Ala Glu Ser Cys Thr Glu Val Arg Asp Val Leu			
	70	75	85
gaa gga ctc gac ggc atc gat tcc atc acc tac cgt tcc cgc gag gcc			403
Glu Gly Leu Asp Gly Ile Asp Ser Ile Thr Tyr Arg Ser Arg Glu Ala			
	90	95	100
tcc tac gaa cga ttc gta gaa gtt ttc aaa gat act gac cca gtt ctc			451
Ser Tyr Glu Arg Phe Val Glu Val Phe Lys Asp Thr Asp Pro Val Leu			
	105	110	115
gtc gct gaa acc tct ccc gac gca ttg cca gca gcg ttc cac gtc cga			499
Val Ala Glu Thr Ser Pro Asp Ala Leu Pro Ala Ala Phe His Val Arg			
	120	125	130
ctt gaa gat cca ctt gcc gtt gag att ctc gat ccg gtc cgc gat ctt			547
Leu Glu Asp Pro Leu Ala Val Glu Ile Leu Asp Pro Val Arg Asp Leu			
	135	140	145
cct caa gta agc aac gtg atc gac cag gtg gat gat ctg cgc gga gca			595
Pro Gln Val Ser Asn Val Ile Asp Gln Val Asp Asp Leu Arg Gly Ala			
	150	155	160
acc gaa aac ctt gac tcc atc cgc aac gcc acc ttc ctc atc gcg gct			643
Thr Glu Asn Leu Asp Ser Ile Arg Asn Ala Thr Phe Leu Ile Ala Ala			
	170	175	180
gtg caa gtt ttg gca tcg atc ttc ctg att gcc aac atg gtg caa atc			691
Val Gln Val Leu Ala Ser Ile Phe Leu Ile Ala Asn Met Val Gln Ile			
	185	190	195
gct gca ttc aat cgt cgt gaa gaa act gaa atc atg cgc atc gtc ggc			739
Ala Ala Phe Asn Arg Arg Glu Glu Thr Glu Ile Met Arg Ile Val Gly			
	200	205	210
gca tcg cgg ttc tac act cag gga cca ttc gtc ttc gaa gcg att cta			787
Ala Ser Arg Phe Tyr Thr Gln Gly Pro Phe Val Phe Glu Ala Ile Leu			
	215	220	225
tcc acc ctc att ggt gcg gtt ttc gcc gtc ggc gcg ctc ttc ttg ggt			835
Ser Thr Leu Ile Gly Ala Val Phe Ala Val Gly Ala Leu Phe Leu Gly			
	230	235	240
			245

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aaa gaa ctc gtc att gat aaa gca ctc cgc gga ctc tac gat tcc cag 883
Lys Glu Leu Val Ile Asp Lys Ala Leu Arg Gly Leu Tyr Asp Ser Gln
                250                255                260

ctc atc gca cca gtt acc acc aca gat att tgg ctg gtc gca ccg ata 931
Leu Ile Ala Pro Val Thr Thr Thr Asp Ile Trp Leu Val Ala Pro Ile
                265                270                275

att tcc ggc att ggc gtg gtg atc gcc ggc att atc gca caa ctc acc 979
Ile Ser Gly Ile Gly Val Val Ile Ala Gly Ile Ile Ala Gln Leu Thr
                280                285                290

ctg cgc ttc tac gtg agg aaa taagactatt gaactccttg ccg 1023
Leu Arg Phe Tyr Val Arg Lys
                295                300

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<210> 86

<211> 300

<212> PRT

<213> Corynebacterium glutamicum

<400> 86

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Met Ala Phe Gly Tyr Val Leu Arg Glu Ala Val Arg Gly Met Gly Arg
 1              5              10              15

Asn Val Thr Met Thr Ile Ala Leu Ile Ile Thr Thr Ser Ile Ser Leu
                20                25                30

Ala Leu Leu Ala Thr Gly Phe Leu Val Thr Asn Met Thr Asp Arg Thr
                35                40                45

Lys Asp Ile Tyr Leu Asp Arg Val Glu Val Met Ile Gln Leu Asp Glu
                50                55                60

Asp Thr Ser Ala Asn Asp Pro Glu Cys Thr Ala Glu Ser Cys Thr Glu
                65                70                75                80

Val Arg Asp Val Leu Glu Gly Leu Asp Gly Ile Asp Ser Ile Thr Tyr
                85                90                95

Arg Ser Arg Glu Ala Ser Tyr Glu Arg Phe Val Glu Val Phe Lys Asp
                100                105                110

Thr Asp Pro Val Leu Val Ala Glu Thr Ser Pro Asp Ala Leu Pro Ala
                115                120                125

Ala Phe His Val Arg Leu Glu Asp Pro Leu Ala Val Glu Ile Leu Asp
                130                135                140

Pro Val Arg Asp Leu Pro Gln Val Ser Asn Val Ile Asp Gln Val Asp
                145                150                155                160

Asp Leu Arg Gly Ala Thr Glu Asn Leu Asp Ser Ile Arg Asn Ala Thr
                165                170                175

Phe Leu Ile Ala Ala Val Gln Val Leu Ala Ser Ile Phe Leu Ile Ala
                180                185                190

Asn Met Val Gln Ile Ala Ala Phe Asn Arg Arg Glu Glu Thr Glu Ile

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195	200	205
Met Arg Ile Val Gly Ala Ser Arg Phe Tyr Thr Gln Gly Pro Phe Val		
210	215	220
Phe Glu Ala Ile Leu Ser Thr Leu Ile Gly Ala Val Phe Ala Val Gly		
225	230	235
Ala Leu Phe Leu Gly Lys Glu Leu Val Ile Asp Lys Ala Leu Arg Gly		
245	250	255
Leu Tyr Asp Ser Gln Leu Ile Ala Pro Val Thr Thr Thr Asp Ile Trp		
260	265	270
Leu Val Ala Pro Ile Ile Ser Gly Ile Gly Val Val Ile Ala Gly Ile		
275	280	285
Ile Ala Gln Leu Thr Leu Arg Phe Tyr Val Arg Lys		
290	295	300

<210> 87
 <211> 810
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(787)
 <223> RXA00010

<400> 87
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ccgtttcttt agccacagga gtttcgctaa agtgtgaccc gtg atc acc ttc gag 115
 Val Ile Thr Phe Glu
 1 5

aac gtc acc aag aac tac aag aca tca acc cgc cct gca tta gac aat 163
 Asn Val Thr Lys Asn Tyr Lys Thr Ser Thr Arg Pro Ala Leu Asp Asn
 10 15 20

gtg tcc cta cac att gaa aaa ggc gag ttc gtg ttc ctc atc ggc cca 211
 Val Ser Leu His Ile Glu Lys Gly Glu Phe Val Phe Leu Ile Gly Pro
 25 30 35

tcc ggc tcc gga aaa tca acc ttc ctg cgc ctg atg acg cgg gag gaa 259
 Ser Gly Ser Gly Lys Ser Thr Phe Leu Arg Leu Met Thr Arg Glu Glu
 40 45 50

aac gtc agc tcc gga tcg ctg aca ctg gct gat ttt cag gtg aac aaa 307
 Asn Val Ser Ser Gly Ser Leu Thr Leu Ala Asp Phe Gln Val Asn Lys
 55 60 65

ctt cgc ggc acg caa gta aac aaa ctg cgc caa cgc atc gga tat gtg 355
 Leu Arg Gly Thr Gln Val Asn Lys Leu Arg Gln Arg Ile Gly Tyr Val
 70 75 80 85

ttc caa gat ttc cga ctc tta aaa aac aag aat gtc tac gac aac gtc 403
 Phe Gln Asp Phe Arg Leu Leu Lys Asn Lys Asn Val Tyr Asp Asn Val
 90 95 100

gca ttc gca ttg gag gtc atc ggg aag aag aag gac aag att caa gaa 451
 Ala Phe Ala Leu Glu Val Ile Gly Lys Lys Lys Asp Lys Ile Gln Glu
 105 110 115
 ctt gtc ccc gaa act ctg gaa atg gtt ggc ctt gcc gga aaa gcc aac 499
 Leu Val Pro Glu Thr Leu Glu Met Val Gly Leu Ala Gly Lys Ala Asn
 120 125 130
 cgc atg ccc aac gaa cta tcc ggt ggt gag cag cag cgc gtg gcc atc 547
 Arg Met Pro Asn Glu Leu Ser Gly Gly Glu Gln Gln Arg Val Ala Ile
 135 140 145
 gcc cga gct ttc gtg aac cgc cca ctc gtc ttg ctt gct gat gaa cca 595
 Ala Arg Ala Phe Val Asn Arg Pro Leu Val Leu Leu Ala Asp Glu Pro
 150 155 160 165
 acc ggc aac ctc gac ccc gat acc tcc gat gag atc atg att ttg ctc 643
 Thr Gly Asn Leu Asp Pro Asp Thr Ser Asp Glu Ile Met Ile Leu Leu
 170 175 180
 aac cgc atc aat cgc ctc ggc acc acg gtg gtc atg tcc acc cac aac 691
 Asn Arg Ile Asn Arg Leu Gly Thr Thr Val Val Met Ser Thr His Asn
 185 190 195
 gcc cga act gtc gac gac atg cgc agg cga gta atc gaa ctg caa ttg 739
 Ala Arg Thr Val Asp Asp Met Arg Arg Arg Val Ile Glu Leu Gln Leu
 200 205 210
 ggc aaa cta gtc cgc gat gat gcc cac ggc gtc tac ggc gaa atg cga 787
 Gly Lys Leu Val Arg Asp Asp Ala His Gly Val Tyr Gly Glu Met Arg
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 taggggagta cttcacatgg ctt 810

<210> 88

<211> 229

<212> PRT

<213> Corynebacterium glutamicum

<400> 88

Val Ile Thr Phe Glu Asn Val Thr Lys Asn Tyr Lys Thr Ser Thr Arg
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Pro Ala Leu Asp Asn Val Ser Leu His Ile Glu Lys Gly Glu Phe Val
 20 25 30

Phe Leu Ile Gly Pro Ser Gly Ser Gly Lys Ser Thr Phe Leu Arg Leu
 35 40 45

Met Thr Arg Glu Glu Asn Val Ser Ser Gly Ser Leu Thr Leu Ala Asp
 50 55 60

Phe Gln Val Asn Lys Leu Arg Gly Thr Gln Val Asn Lys Leu Arg Gln
 65 70 75 80

Arg Ile Gly Tyr Val Phe Gln Asp Phe Arg Leu Leu Lys Asn Lys Asn
 85 90 95

Val Tyr Asp Asn Val Ala Phe Ala Leu Glu Val Ile Gly Lys Lys Lys

100	105	110
Asp Lys Ile Gln Glu Leu Val	Pro Glu Thr Leu Glu Met Val Gly Leu	
115	120	125
Ala Gly Lys Ala Asn Arg Met	Pro Asn Glu Leu Ser Gly Gly Glu Gln	
130	135	140
Gln Arg Val Ala Ile Ala Arg Ala Phe Val Asn Arg Pro Leu Val Leu		
145	150	155
Leu Ala Asp Glu Pro Thr Gly Asn Leu Asp Pro Asp Thr Ser Asp Glu		
165	170	175
Ile Met Ile Leu Leu Asn Arg Ile Asn Arg Leu Gly Thr Thr Val Val		
180	185	190
Met Ser Thr His Asn Ala Arg Thr Val Asp Asp Met Arg Arg Arg Val		
195	200	205
Ile Glu Leu Gln Leu Gly Lys Leu Val Arg Asp Asp Ala His Gly Val		
210	215	220
Tyr Gly Glu Met Arg		
225		

<210> 89

<211> 1605

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1582)

<223> RXA00143

<400> 89

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gagtcctgacc	acaagccatt	ttattccttt	tccccgagaa	atg gtc tgg gat tgg	115
				Met Val Trp Asp Trp	
				1 5	

cat acc cgc aag ggc gct gtc gca cgt ctg act ccc cca ttc atc cca	163
His Thr Arg Lys Gly Ala Val Ala Arg Leu Thr Pro Pro Phe Ile Pro	
10 15 20	

ctt aac ccc att acg cag gca gaa cgc ctc gcc gac ggc acc acc atc	211
Leu Asn Pro Ile Thr Gln Ala Glu Arg Leu Ala Asp Gly Thr Thr Ile	
25 30 35	

ttc agt ctc ccc gcg gga ctt aaa tgg gtg gca cgc cac gat tta tcc	259
Phe Ser Leu Pro Ala Gly Leu Lys Trp Val Ala Arg His Asp Leu Ser	
40 45 50	

ggg ttt ttg aac ggg tca cgc ttc acc gac gtc tgc ctc acc gcc cct	307
Gly Phe Leu Asn Gly Ser Arg Phe Thr Asp Val Cys Leu Thr Ala Pro	
55 60 65	

gtg aag gcc ctc gca aac tgg cgc cac gtg cat aat ttc gtc gac caa	355
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Val	Lys	Ala	Leu	Ala	Asn	Trp	Arg	His	Val	His	Asn	Phe	Val	Asp	Gln		
70					75					80					85		
gac	ggc	ggc	aca	ctc	atc	aca	gat	tcc	gtg	agc	acc	cgc	cta	ccg	gca	403	
Asp	Gly	Gly	Thr	Leu	Ile	Thr	Asp	Ser	Val	Ser	Thr	Arg	Leu	Pro	Ala		
				90					95					100			
tcc	aca	ctc	acg	ggc	atg	ttc	gcc	tat	cgc	caa	act	cag	ctc	atc	gaa	451	
Ser	Thr	Leu	Thr	Gly	Met	Phe	Ala	Tyr	Arg	Gln	Thr	Gln	Leu	Ile	Glu		
			105					110					115				
gac	cta	aaa	ttc	tta	agt	aga	aca	agc	acg	ctt	ttc	gac	ggc	tcc	ccc	499	
Asp	Leu	Lys	Phe	Leu	Ser	Arg	Thr	Ser	Thr	Leu	Phe	Asp	Gly	Ser	Pro		
		120					125					130					
ctc	acc	gta	gcc	atc	acc	ggc	tcc	agg	ggg	ctc	gtc	ggc	cgc	gcg	ctg	547	
Leu	Thr	Val	Ala	Ile	Thr	Gly	Ser	Arg	Gly	Leu	Val	Gly	Arg	Ala	Leu		
	135					140					145						
aca	gcg	cag	ctg	caa	acc	ggc	ggc	cac	gaa	gtc	atc	caa	ctc	gtg	cgc	595	
Thr	Ala	Gln	Leu	Gln	Thr	Gly	Gly	His	Glu	Val	Ile	Gln	Leu	Val	Arg		
150					155				160					165			
aaa	gaa	ccc	aaa	cct	ggc	caa	cgt	ttc	tgg	gat	cca	ctc	aac	cca	gca	643	
Lys	Glu	Pro	Lys	Pro	Gly	Gln	Arg	Phe	Trp	Asp	Pro	Leu	Asn	Pro	Ala		
				170					175					180			
tcc	gat	ctc	ctc	gac	ggc	gcg	gat	gtt	ttg	gtt	cac	ctt	gcc	ggc	gaa	691	
Ser	Asp	Leu	Leu	Asp	Gly	Ala	Asp	Val	Leu	Val	His	Leu	Ala	Gly	Glu		
			185					190					195				
ccg	atc	ttc	ggg	cga	ttc	aac	gac	tcc	cac	aaa	gaa	gcc	atc	cgc	gag	739	
Pro	Ile	Phe	Gly	Arg	Phe	Asn	Asp	Ser	His	Lys	Glu	Ala	Ile	Arg	Glu		
		200					205					210					
tcc	cgc	gta	ctt	ccc	acc	aaa	ttc	ctc	gca	gaa	tta	gtt	gcc	gaa	tcc	787	
Ser	Arg	Val	Leu	Pro	Thr	Lys	Phe	Leu	Ala	Glu	Leu	Val	Ala	Glu	Ser		
		215				220					225						
acc	cag	tgc	acc	acc	atg	att	tcc	gcc	tct	gca	gtt	gga	ttc	tat	ggc	835	
Thr	Gln	Cys	Thr	Thr	Met	Ile	Ser	Ala	Ser	Ala	Val	Gly	Phe	Tyr	Gly		
230					235				240					245			
cac	gac	cgc	ggc	gac	gag	atc	ctg	acc	gaa	gaa	tcc	gaa	tcc	ggc	gat	883	
His	Asp	Arg	Gly	Asp	Glu	Ile	Leu	Thr	Glu	Glu	Ser	Glu	Ser	Gly	Asp		
				250					255					260			
gat	ttc	ctc	gcc	gag	gtc	tgt	agg	gat	tgg	gaa	cac	gcc	act	gct	cct	931	
Asp	Phe	Leu	Ala	Glu	Val	Cys	Arg	Asp	Trp	Glu	His	Ala	Thr	Ala	Pro		
			265					270					275				
gcc	tca	gat	gca	gga	aag	cgc	gta	gcc	ttc	att	cgc	acc	ggc	gtg	gcc	979	
Ala	Ser	Asp	Ala	Gly	Lys	Arg	Val	Ala	Phe	Ile	Arg	Thr	Gly	Val	Ala		
		280					285					290					
ctc	agt	gga	cgc	ggc	atg	ctt	ccc	ctg	ctg	aaa	acc	ctg	ttc	tcc		1027	
Leu	Ser	Gly	Arg	Gly	Gly	Met	Leu	Pro	Leu	Leu	Lys	Thr	Leu	Phe	Ser		
		295				300					305						
acc	gga	cta	ggc	gga	aaa	ttc	ggc	gat	ggc	acc	tcc	tgg	ttc	agc	tgg	1075	
Thr	Gly	Leu	Gly	Gly	Lys	Phe	Gly	Asp	Gly	Thr	Ser	Trp	Phe	Ser	Trp		

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310          315          320          325
atc gcc atc gat gac ctc acc gac atc tac tac cgc gcc atc gtg gac 1123
Ile Ala Ile Asp Asp Leu Thr Asp Ile Tyr Tyr Arg Ala Ile Val Asp
          330          335          340

gcc cag atc tcc ggc ccc atc aac gcg gta gcc ccc aat cca gtc tcc 1171
Ala Gln Ile Ser Gly Pro Ile Asn Ala Val Ala Pro Asn Pro Val Ser
          345          350          355

aat gcg gac atg acc aag att ctg gcc acc agc atg cac cgt ccc gca 1219
Asn Ala Asp Met Thr Lys Ile Leu Ala Thr Ser Met His Arg Pro Ala
          360          365          370

ttc atc caa att cct tcc ctc ggc ccc aaa att ctg ctc gga agc caa 1267
Phe Ile Gln Ile Pro Ser Leu Gly Pro Lys Ile Leu Leu Gly Ser Gln
          375          380          385

ggc gct gaa gag cta gcc ctg gcg tcc caa cgc acc gcc cca gca gca 1315
Gly Ala Glu Glu Leu Ala Leu Ala Ser Gln Arg Thr Ala Pro Ala Ala
          390          395          400

ctg gaa aac ctc agc cac acc ttc cgc tac acc gac atc ggg gcc gcc 1363
Leu Glu Asn Leu Ser His Thr Phe Arg Tyr Thr Asp Ile Gly Ala Ala
          410          415          420

atc gca cac gaa ctt ggc tac gaa caa ctc gca gat ttc gcc caa cag 1411
Ile Ala His Glu Leu Gly Tyr Glu Gln Leu Ala Asp Phe Ala Gln Gln
          425          430          435

caa gaa atc gaa gcc gaa cgc aaa cag gaa cga gcc gaa ctc aaa gcc 1459
Gln Glu Ile Glu Ala Glu Arg Lys Gln Glu Arg Ala Glu Leu Lys Ala
          440          445          450

gcc aag aag atc gcc aag aaa gcc cca gtc cta gag gaa tcc ccc acc 1507
Ala Lys Lys Ile Ala Lys Lys Ala Pro Val Leu Glu Glu Ser Pro Thr
          455          460          465

aac ctg gaa gat ccc gaa gaa gta gag caa agt atc ctt tca tca atc 1555
Asn Leu Glu Asp Pro Glu Glu Val Glu Gln Ser Ile Leu Ser Ser Ile
          470          475          480          485

ctc aat ttc cgc cgt aag cgc aac gac taaaaccacc atctgtagtg tgg 1605
Leu Asn Phe Arg Arg Lys Arg Asn Asp
          490

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<210> 90

<211> 494

<212> PRT

<213> Corynebacterium glutamicum

<400> 90

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Met Val Trp Asp Trp His Thr Arg Lys Gly Ala Val Ala Arg Leu Thr
  1           5           10           15

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Pro Pro Phe Ile Pro Leu Asn Pro Ile Thr Gln Ala Glu Arg Leu Ala
          20           25           30

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Asp Gly Thr Thr Ile Phe Ser Leu Pro Ala Gly Leu Lys Trp Val Ala
          35           40           45

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Arg	His	Asp	Leu	Ser	Gly	Phe	Leu	Asn	Gly	Ser	Arg	Phe	Thr	Asp	Val	50	55	60
Cys	Leu	Thr	Ala	Pro	Val	Lys	Ala	Leu	Ala	Asn	Trp	Arg	His	Val	His	65	70	75
Asn	Phe	Val	Asp	Gln	Asp	Gly	Gly	Thr	Leu	Ile	Thr	Asp	Ser	Val	Ser	85	90	95
Thr	Arg	Leu	Pro	Ala	Ser	Thr	Leu	Thr	Gly	Met	Phe	Ala	Tyr	Arg	Gln	100	105	110
Thr	Gln	Leu	Ile	Glu	Asp	Leu	Lys	Phe	Leu	Ser	Arg	Thr	Ser	Thr	Leu	115	120	125
Phe	Asp	Gly	Ser	Pro	Leu	Thr	Val	Ala	Ile	Thr	Gly	Ser	Arg	Gly	Leu	130	135	140
Val	Gly	Arg	Ala	Leu	Thr	Ala	Gln	Leu	Gln	Thr	Gly	Gly	His	Glu	Val	145	150	155
Ile	Gln	Leu	Val	Arg	Lys	Glu	Pro	Lys	Pro	Gly	Gln	Arg	Phe	Trp	Asp	165	170	175
Pro	Leu	Asn	Pro	Ala	Ser	Asp	Leu	Leu	Asp	Gly	Ala	Asp	Val	Leu	Val	180	185	190
His	Leu	Ala	Gly	Glu	Pro	Ile	Phe	Gly	Arg	Phe	Asn	Asp	Ser	His	Lys	195	200	205
Glu	Ala	Ile	Arg	Glu	Ser	Arg	Val	Leu	Pro	Thr	Lys	Phe	Leu	Ala	Glu	210	215	220
Leu	Val	Ala	Glu	Ser	Thr	Gln	Cys	Thr	Thr	Met	Ile	Ser	Ala	Ser	Ala	225	230	235
Val	Gly	Phe	Tyr	Gly	His	Asp	Arg	Gly	Asp	Glu	Ile	Leu	Thr	Glu	Glu	245	250	255
Ser	Glu	Ser	Gly	Asp	Asp	Phe	Leu	Ala	Glu	Val	Cys	Arg	Asp	Trp	Glu	260	265	270
His	Ala	Thr	Ala	Pro	Ala	Ser	Asp	Ala	Gly	Lys	Arg	Val	Ala	Phe	Ile	275	280	285
Arg	Thr	Gly	Val	Ala	Leu	Ser	Gly	Arg	Gly	Gly	Met	Leu	Pro	Leu	Leu	290	295	300
Lys	Thr	Leu	Phe	Ser	Thr	Gly	Leu	Gly	Gly	Lys	Phe	Gly	Asp	Gly	Thr	305	310	315
Ser	Trp	Phe	Ser	Trp	Ile	Ala	Ile	Asp	Asp	Leu	Thr	Asp	Ile	Tyr	Tyr	325	330	335
Arg	Ala	Ile	Val	Asp	Ala	Gln	Ile	Ser	Gly	Pro	Ile	Asn	Ala	Val	Ala	340	345	350
Pro	Asn	Pro	Val	Ser	Asn	Ala	Asp	Met	Thr	Lys	Ile	Leu	Ala	Thr	Ser	355	360	365

Met His Arg Pro Ala Phe Ile Gln Ile Pro Ser Leu Gly Pro Lys Ile
 370 375 380

Leu Leu Gly Ser Gln Gly Ala Glu Glu Leu Ala Leu Ala Ser Gln Arg
 385 390 395 400

Thr Ala Pro Ala Ala Leu Glu Asn Leu Ser His Thr Phe Arg Tyr Thr
 405 410 415

Asp Ile Gly Ala Ala Ile Ala His Glu Leu Gly Tyr Glu Gln Leu Ala
 420 425 430

Asp Phe Ala Gln Gln Gln Glu Ile Glu Ala Glu Arg Lys Gln Glu Arg
 435 440 445

Ala Glu Leu Lys Ala Ala Lys Lys Ile Ala Lys Lys Ala Pro Val Leu
 450 455 460

Glu Glu Ser Pro Thr Asn Leu Glu Asp Pro Glu Glu Val Glu Gln Ser
 465 470 475 480

Ile Leu Ser Ser Ile Leu Asn Phe Arg Arg Lys Arg Asn Asp
 485 490

<210> 91

<211> 1684

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1684)

<223> RXA00277

<400> 91

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cagctgcagt acatgccaga ggaagaaggg acagaaaacg atg aag gat aat gaa 115
 Met Lys Asp Asn Glu
 1 5

gat ttc gat cca gat tca cca gca acc gaa gct gtt gcc ttc aac cct 163
 Asp Phe Asp Pro Asp Ser Pro Ala Thr Glu Ala Val Ala Phe Asn Pro
 10 15 20

ttc gac gat gac gat gag gat gat tcc ccc gct acc tca gcc gtt gcc 211
 Phe Asp Asp Asp Asp Glu Asp Asp Ser Pro Ala Thr Ser Ala Val Ala
 25 30 35

ttt aac cct ttt gaa gat gac gat gac gac gat gag ttc caa ggc gaa 259
 Phe Asn Pro Phe Glu Asp Asp Asp Asp Asp Asp Glu Phe Gln Gly Glu
 40 45 50

ggc cta gaa ttc ctg ctg cgc gac ctc gac aat ctg cga gcc acc caa 307
 Gly Leu Glu Phe Leu Leu Arg Asp Leu Asp Asn Leu Arg Ala Thr Gln
 55 60 65

ggt caa atg gtg gtg gaa caa cca gca gtt gaa gac agc ctc ggg tca 355
 Gly Gln Met Val Val Glu Gln Pro Ala Val Glu Asp Ser Leu Gly Ser
 70 75 80 85

gca tct gcg cat acg gag aca act gcg gcc tca ctg cgt ccc cgc cca	403
Ala Ser Ala His Thr Glu Thr Thr Ala Ala Ser Leu Arg Pro Arg Pro	
90 95 100	
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Glu Val Asp Pro Ser Glu Arg Ser Arg Arg Gln Ala Ile Ser Leu Phe	
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cgc gaa cgg cgc cgc gta agg cgc caa tcc cgc cca gtt gct gat ggc	499
Arg Glu Arg Arg Arg Val Arg Arg Gln Ser Arg Pro Val Ala Asp Gly	
120 125 130	
atg gtg gaa ttg ccg ttc atc acc ccc aaa ccg gaa gat gag ctg ctc	547
Met Val Glu Leu Pro Phe Ile Thr Pro Lys Pro Glu Asp Glu Leu Leu	
135 140 145	
atc gac ccg gaa aag aag cgc aaa cct ggt gtg gca gcg ccg caa ctt	595
Ile Asp Pro Glu Lys Lys Arg Lys Pro Gly Val Ala Ala Pro Gln Leu	
150 155 160 165	
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Val Ala Gly Asp Ile Val Ala Glu Gln Tyr Glu Val Leu Gly Val Ile	
170 175 180	
gcg cac ggc ggc atg ggt tgg att tac ctc gcc aac gac cgc aat gtg	691
Ala His Gly Gly Met Gly Trp Ile Tyr Leu Ala Asn Asp Arg Asn Val	
185 190 195	
tcc ggc cgc atc gtg gtg ctc aaa ggc atg atg gcg caa tct tcc gtt	739
Ser Gly Arg Ile Val Val Leu Lys Gly Met Met Ala Gln Ser Ser Val	
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caa gac caa ggc acc gct gaa gcc gaa cgc gaa ttc ctc gcc gac atc	787
Gln Asp Gln Gly Thr Ala Glu Ala Glu Arg Glu Phe Leu Ala Asp Ile	
215 220 225	
acc cac ccc ggc atc gtg aag gcc tac aac ttc atc gac gac ccc cgc	835
Thr His Pro Gly Ile Val Lys Ala Tyr Asn Phe Ile Asp Asp Pro Arg	
230 235 240 245	
gtc ccc ggc gga ttc atc gtc atg gaa tac gtc aac ggc ccc tcc ctg	883
Val Pro Gly Gly Phe Ile Val Met Glu Tyr Val Asn Gly Pro Ser Leu	
250 255 260	
aaa gac cgc tgc aaa gcc caa ccc gac ggc gtg ctc cgc gtc gac ctc	931
Lys Asp Arg Cys Lys Ala Gln Pro Asp Gly Val Leu Arg Val Asp Leu	
265 270 275	
gcc atc ggc tac atc ctc gaa ctc ctc ccc gcc atg gac tac ctg cac	979
Ala Ile Gly Tyr Ile Leu Glu Leu Leu Pro Ala Met Asp Tyr Leu His	
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Gln Arg Gly Val Val Tyr Asn Asp Leu Lys Pro Glu Asn Val Ile Ala	
295 300 305	
acc gaa gac caa gtt aaa ctc atc gac ctc ggc gcg gtt acc ggc atc	1075
Thr Glu Asp Gln Val Lys Leu Ile Asp Leu Gly Ala Val Thr Gly Ile	
310 315 320 325	

ggc gca ttc ggc tac att tac ggc acc aaa gga ttc caa gca ccc gaa 1123
 Gly Ala Phe Gly Tyr Ile Tyr Gly Thr Lys Gly Phe Gln Ala Pro Glu
 330 335 340

gta gcc acc cat ggc ccc tca atc tcc tcc gat att ttc acc atc gga 1171
 Val Ala Thr His Gly Pro Ser Ile Ser Ser Asp Ile Phe Thr Ile Gly
 345 350 355

cgc acc ctc gca gca ctc acc atg ccc ctc ccc gtt gaa gac ggt gtc 1219
 Arg Thr Leu Ala Ala Leu Thr Met Pro Leu Pro Val Glu Asp Gly Val
 360 365 370

ctc gca ccg ggc atc ccc tcg ccc aaa aat tca cct ctt ctg cgc agg 1267
 Leu Ala Pro Gly Ile Pro Ser Pro Lys Asn Ser Pro Leu Leu Arg Arg
 375 380 385

cat ttg tcg ttc tac cgc ctc ctg caa cgc gcc acc gcc gac gac ccc 1315
 His Leu Ser Phe Tyr Arg Leu Leu Gln Arg Ala Thr Ala Asp Asp Pro
 390 395 400 405

caa cac cga ttc cgc aac gtc agc gaa cta cgc acc caa ctc tac ggc 1363
 Gln His Arg Phe Arg Asn Val Ser Glu Leu Arg Thr Gln Leu Tyr Gly
 410 415 420

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 Val Leu Arg Glu Ile Leu Ala Val Arg Asp Gly Lys Gln Tyr Pro Pro
 425 430 435

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 440 445 450

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 Leu Val Phe Arg Thr Asp Arg Ile Ile Asp Gly Ile Glu Arg Gln Ala
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 Arg Ile Thr Ala Pro Glu Ile Val Ser Ala Leu Pro Val Pro Leu Ile
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gac cgc acc gac ccc ggc gcc cgt atg ctc tcc gga tcc tcc tat gca 1603
 Asp Arg Thr Asp Pro Gly Ala Arg Met Leu Ser Gly Ser Ser Tyr Ala
 490 495 500

gaa ccc tcc gaa acc ctg gaa act ctg cgc aac tcc atg gaa gac gag 1651
 Glu Pro Ser Glu Thr Leu Glu Thr Leu Arg Asn Ser Met Glu Asp Glu
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<212> PRT

<213> *Corynebacterium glutamicum*

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 Thr Ser Ala Val Ala Phe Asn Pro Phe Glu Asp Asp Asp Asp Asp Asp
 35 40 45
 Glu Phe Gln Gly Glu Gly Leu Glu Phe Leu Leu Arg Asp Leu Asp Asn
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 Leu Arg Ala Thr Gln Gly Gln Met Val Val Glu Gln Pro Ala Val Glu
 65 70 75 80
 Asp Ser Leu Gly Ser Ala Ser Ala His Thr Glu Thr Thr Ala Ala Ser
 85 90 95
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 100 105 110
 Ala Ile Ser Leu Phe Arg Glu Arg Arg Arg Val Arg Arg Gln Ser Arg
 115 120 125
 Pro Val Ala Asp Gly Met Val Glu Leu Pro Phe Ile Thr Pro Lys Pro
 130 135 140
 Glu Asp Glu Leu Leu Ile Asp Pro Glu Lys Lys Arg Lys Pro Gly Val
 145 150 155 160
 Ala Ala Pro Gln Leu Val Ala Gly Asp Ile Val Ala Glu Gln Tyr Glu
 165 170 175
 Val Leu Gly Val Ile Ala His Gly Gly Met Gly Trp Ile Tyr Leu Ala
 180 185 190
 Asn Asp Arg Asn Val Ser Gly Arg Ile Val Val Leu Lys Gly Met Met
 195 200 205
 Ala Gln Ser Ser Val Gln Asp Gln Gly Thr Ala Glu Ala Glu Arg Glu
 210 215 220
 Phe Leu Ala Asp Ile Thr His Pro Gly Ile Val Lys Ala Tyr Asn Phe
 225 230 235 240
 Ile Asp Asp Pro Arg Val Pro Gly Gly Phe Ile Val Met Glu Tyr Val
 245 250 255
 Asn Gly Pro Ser Leu Lys Asp Arg Cys Lys Ala Gln Pro Asp Gly Val
 260 265 270
 Leu Arg Val Asp Leu Ala Ile Gly Tyr Ile Leu Glu Leu Leu Pro Ala
 275 280 285
 Met Asp Tyr Leu His Gln Arg Gly Val Val Tyr Asn Asp Leu Lys Pro
 290 295 300
 Glu Asn Val Ile Ala Thr Glu Asp Gln Val Lys Leu Ile Asp Leu Gly
 305 310 315 320
 Ala Val Thr Gly Ile Gly Ala Phe Gly Tyr Ile Tyr Gly Thr Lys Gly
 325 330 335

Phe Gln Ala Pro Glu Val Ala Thr His Gly Pro Ser Ile Ser Ser Asp
 340 345 350
 Ile Phe Thr Ile Gly Arg Thr Leu Ala Ala Leu Thr Met Pro Leu Pro
 355 360 365
 Val Glu Asp Gly Val Leu Ala Pro Gly Ile Pro Ser Pro Lys Asn Ser
 370 375 380
 Pro Leu Leu Arg Arg His Leu Ser Phe Tyr Arg Leu Leu Gln Arg Ala
 385 390 395 400
 Thr Ala Asp Asp Pro Gln His Arg Phe Arg Asn Val Ser Glu Leu Arg
 405 410 415
 Thr Gln Leu Tyr Gly Val Leu Arg Glu Ile Leu Ala Val Arg Asp Gly
 420 425 430
 Lys Gln Tyr Pro Pro Gln His Ser Leu Phe Ser Pro Gln Arg Ser Thr
 435 440 445
 Phe Gly Thr Lys His Leu Val Phe Arg Thr Asp Arg Ile Ile Asp Gly
 450 455 460
 Ile Glu Arg Gln Ala Arg Ile Thr Ala Pro Glu Ile Val Ser Ala Leu
 465 470 475 480
 Pro Val Pro Leu Ile Asp Arg Thr Asp Pro Gly Ala Arg Met Leu Ser
 485 490 495
 Gly Ser Ser Tyr Ala Glu Pro Ser Glu Thr Leu Glu Thr Leu Arg Asn
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 Ser Met Glu Asp Glu Gln Tyr Arg Gln Ser Ile Glu Ile Pro Leu Gly
 515 520 525

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 <213> Corynebacterium glutamicum

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 <223> RXA00857

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 Gly Asp Val Leu Asn Ala Arg Ala Thr Val Glu Asn Lys Asp Ser Met
 20 25 30
 ctc att ggt ttg ggt aag gat att gaa ggc gac ttc gtg tcc tac tcc 144
 Leu Ile Gly Leu Gly Lys Asp Ile Glu Gly Asp Phe Val Ser Tyr Ser
 35 40 45
 gtg cag aaa atg cct cac ctt ctt gtg gct ggt tcc acc ggt tct ggt 192

Val	Gln	Lys	Met	Pro	His	Leu	Leu	Val	Ala	Gly	Ser	Thr	Gly	Ser	Gly	
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aag	tcg	gcg	ttc	gtg	aac	tcg	ctg	ctg	gtg	tca	ctg	ctc	acg	cgt	gca	240
Lys	Ser	Ala	Phe	Val	Asn	Ser	Leu	Leu	Val	Ser	Leu	Leu	Thr	Arg	Ala	
65					70					75					80	
aag	cca	gaa	gaa	gtc	cgt	ctg	att	ctg	gtg	gac	cca	aag	atg	gtg	gaa	288
Lys	Pro	Glu	Glu	Val	Arg	Leu	Ile	Leu	Val	Asp	Pro	Lys	Met	Val	Glu	
				85					90					95		
ctc	aca	cca	tac	gag	ggc	att	cca	cac	ctg	att	acg	ccg	atc	att	acc	336
Leu	Thr	Pro	Tyr	Glu	Gly	Ile	Pro	His	Leu	Ile	Thr	Pro	Ile	Ile	Thr	
			100					105					110			
caa	cca	aag	aag	gcc	gcg	gca	gca	ctg	cag	tgg	ctg	gtt	gag	gaa	atg	384
Gln	Pro	Lys	Lys	Ala	Ala	Ala	Ala	Leu	Gln	Trp	Leu	Val	Glu	Glu	Met	
		115					120					125				
gaa	cag	cgc	tac	atg	gac	atg	aaa	caa	acc	cgt	gtg	cgc	cac	atc	aag	432
Glu	Gln	Arg	Tyr	Met	Asp	Met	Lys	Gln	Thr	Arg	Val	Arg	His	Ile	Lys	
	130					135					140					
gac	ttc	aac	cgc	aag	att	aaa	tct	ggc	gaa	att	gag	acc	cct	cca	gga	480
Asp	Phe	Asn	Arg	Lys	Ile	Lys	Ser	Gly	Glu	Ile	Glu	Thr	Pro	Pro	Gly	
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tcc	aag	cgc	gaa	tac	cgt	gcg	tac	cca	tac	atc	gtg	tgt	gtg	gtc	gac	528
Ser	Lys	Arg	Glu	Tyr	Arg	Ala	Tyr	Pro	Tyr	Ile	Val	Cys	Val	Val	Asp	
				165					170					175		
gag	ctc	gct	gac	ctg	atg	atg	acc	gca	ccg	aag	gaa	atc	gaa	gag	tcc	576
Glu	Leu	Ala	Asp	Leu	Met	Met	Thr	Ala	Pro	Lys	Glu	Ile	Glu	Glu	Ser	
			180					185					190			
atc	gtg	cgc	atc	acc	cag	aag	gca	cgt	gcc	gcc	ggc	atc	cac	ctc	gtg	624
Ile	Val	Arg	Ile	Thr	Gln	Lys	Ala	Arg	Ala	Ala	Gly	Ile	His	Leu	Val	
		195					200					205				
ctg	gca	acg	cag	cgc	cca	tcc	gtg	gac	gtt	gtg	acc	ggc	ctg	atc	aag	672
Leu	Ala	Thr	Gln	Arg	Pro	Ser	Val	Asp	Val	Val	Thr	Gly	Leu	Ile	Lys	
	210					215					220					
acc	aac	gtt	cct	tca	cgt	ttg	gct	ttc	gca	acc	tca	tcg	cta	act	gac	720
Thr	Asn	Val	Pro	Ser	Arg	Leu	Ala	Phe	Ala	Thr	Ser	Ser	Leu	Thr	Asp	
225					230					235					240	
tcc	cgc	gtt	att	ttg	gac	cag	ggc	ggc	gct	gaa	aag	ctg	atc	ggc	atg	768
Ser	Arg	Val	Ile	Leu	Asp	Gln	Gly	Gly	Ala	Glu	Lys	Leu	Ile	Gly	Met	
				245				250						255		
ggc	gac	gcg	ctg	ttc	atc	cca	cag	ggc	ggc	ggc	aag	cca	caa	cgt	atc	816
Gly	Asp	Ala	Leu	Phe	Ile	Pro	Gln	Gly	Ala	Gly	Lys	Pro	Gln	Arg	Ile	
			260					265					270			
cag	ggc	gcc	ttt	gtc	acc	gat	gaa	gaa	atc	caa	gcg	gtc	gtg	gac	atg	864
Gln	Gly	Ala	Phe	Val	Thr	Asp	Glu	Glu	Ile	Gln	Ala	Val	Val	Asp	Met	
		275					280					285				
gcc	aag	gct	cag	cgc	cag	cct	gaa	tac	acc	gac	ggc	gtc	acc	gaa	gat	912
Ala	Lys	Ala	Gln	Arg	Gln	Pro	Glu	Tyr	Thr	Asp	Gly	Val	Thr	Glu	Asp	

290 295 300
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 Lys Ala Ser Glu Ala Lys Lys Ile Asp Ala Asp Ile Gly Asn Asp Leu
 305 310 315 320
 gaa gat ctc ctc gaa gca gtc gaa ctc gtg gtg acc tca caa atg gga 1008
 Glu Asp Leu Leu Glu Ala Val Glu Leu Val Val Thr Ser Gln Met Gly
 325 330 335
 tcc acc tcc atg ctg cag cgc aaa ctg cgc atc ggt ttt gcc aag gcc 1056
 Ser Thr Ser Met Leu Gln Arg Lys Leu Arg Ile Gly Phe Ala Lys Ala
 340 345 350
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 Gly Arg Leu Met Asp Leu Met Glu Thr Arg Gly Val Val Gly Pro Ser
 355 360 365
 gaa ggc tct aag gct cgt gaa gtt ttg gtc aag cca gaa gag ctg gaa 1152
 Glu Gly Ser Lys Ala Arg Glu Val Leu Val Lys Pro Glu Glu Leu Glu
 370 375 380
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 385 390 395 400
 gaa gag acc tgg gat gac gag gtg gca gcg gaa gct gaa gaa gcg gct 1248
 Glu Glu Thr Trp Asp Asp Glu Val Ala Ala Glu Ala Glu Glu Ala Ala
 405 410 415
 aac acc acc gtc gtg cag gct gat cct tcc aag gga gtg tgt 1290
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 taaggcttta ggagcctagt ggc 1313

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 <213> Corynebacterium glutamicum

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 Leu Ile Gly Leu Gly Lys Asp Ile Glu Gly Asp Phe Val Ser Tyr Ser
 35 40 45
 Val Gln Lys Met Pro His Leu Leu Val Ala Gly Ser Thr Gly Ser Gly
 50 55 60
 Lys Ser Ala Phe Val Asn Ser Leu Leu Val Ser Leu Leu Thr Arg Ala
 65 70 75 80
 Lys Pro Glu Glu Val Arg Leu Ile Leu Val Asp Pro Lys Met Val Glu
 85 90 95

Leu Thr Pro Tyr Glu Gly Ile Pro His Leu Ile Thr Pro Ile Ile Thr
 100 105 110
 Gln Pro Lys Lys Ala Ala Ala Ala Leu Gln Trp Leu Val Glu Glu Met
 115 120 125
 Glu Gln Arg Tyr Met Asp Met Lys Gln Thr Arg Val Arg His Ile Lys
 130 135 140
 Asp Phe Asn Arg Lys Ile Lys Ser Gly Glu Ile Glu Thr Pro Pro Gly
 145 150 155 160
 Ser Lys Arg Glu Tyr Arg Ala Tyr Pro Tyr Ile Val Cys Val Val Asp
 165 170 175
 Glu Leu Ala Asp Leu Met Met Thr Ala Pro Lys Glu Ile Glu Glu Ser
 180 185 190
 Ile Val Arg Ile Thr Gln Lys Ala Arg Ala Ala Gly Ile His Leu Val
 195 200 205
 Leu Ala Thr Gln Arg Pro Ser Val Asp Val Val Thr Gly Leu Ile Lys
 210 215 220
 Thr Asn Val Pro Ser Arg Leu Ala Phe Ala Thr Ser Ser Leu Thr Asp
 225 230 235 240
 Ser Arg Val Ile Leu Asp Gln Gly Gly Ala Glu Lys Leu Ile Gly Met
 245 250 255
 Gly Asp Ala Leu Phe Ile Pro Gln Gly Ala Gly Lys Pro Gln Arg Ile
 260 265 270
 Gln Gly Ala Phe Val Thr Asp Glu Glu Ile Gln Ala Val Val Asp Met
 275 280 285
 Ala Lys Ala Gln Arg Gln Pro Glu Tyr Thr Asp Gly Val Thr Glu Asp
 290 295 300
 Lys Ala Ser Glu Ala Lys Lys Ile Asp Ala Asp Ile Gly Asn Asp Leu
 305 310 315 320
 Glu Asp Leu Leu Glu Ala Val Glu Leu Val Val Thr Ser Gln Met Gly
 325 330 335
 Ser Thr Ser Met Leu Gln Arg Lys Leu Arg Ile Gly Phe Ala Lys Ala
 340 345 350
 Gly Arg Leu Met Asp Leu Met Glu Thr Arg Gly Val Val Gly Pro Ser
 355 360 365
 Glu Gly Ser Lys Ala Arg Glu Val Leu Val Lys Pro Glu Glu Leu Glu
 370 375 380
 Thr Ile Leu Trp Met Leu Lys Gly Ala Asp Pro Ala Asp Ala Pro Lys
 385 390 395 400
 Glu Glu Thr Trp Asp Asp Glu Val Ala Ala Glu Ala Glu Glu Ala Ala
 405 410 415
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420

425

430

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <223> RXA01435

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cta gag gga cgc atc ggc gac gac tgg cga cac aaa tgg ttc tcc gga 96
 Leu Glu Gly Arg Ile Gly Asp Asp Trp Arg His Lys Trp Phe Ser Gly
 20 25 30

atc acc tac ctc ctc ctc gac gac tac gcc acc gcc caa gta ttc ttc 144
 Ile Thr Tyr Leu Leu Leu Asp Asp Tyr Ala Thr Ala Gln Val Phe Phe
 35 40 45

aac cac gtc ctg acc atc ctg ccc ggc gaa gcc gct cct aaa cta gcc 192
 Asn His Val Leu Thr Ile Leu Pro Gly Glu Ala Ala Pro Lys Leu Ala
 50 55 60

ctc gca gct gtt gac gaa ctc atc ctc caa caa atc ggc gcc gaa tcc 240
 Leu Ala Ala Val Asp Glu Leu Ile Leu Gln Gln Ile Gly Ala Glu Ser
 65 70 75 80

acc gcc tat ctc acc cca gac atc gtc tct gca acc gcg acc ctc agc 288
 Thr Ala Tyr Leu Thr Pro Asp Ile Val Ser Ala Thr Ala Thr Leu Ser
 85 90 95

aaa gat ttc gaa gac ctc gac gcc tcc gcc ttc gaa tca ctc agc gac 336
 Lys Asp Phe Glu Asp Leu Asp Ala Ser Ala Phe Glu Ser Leu Ser Asp
 100 105 110

acc tgg tcc cac atc tcc agc gac cca cac gta gtc cgc ttc cat tca 384
 Thr Trp Ser His Ile Ser Ser Asp Pro His Val Val Arg Phe His Ser
 115 120 125

ctg cgc ctc tac gca ctt gtc tgg gca acc aac ccc acc acc gtg tcc 432
 Leu Arg Leu Tyr Ala Leu Val Trp Ala Thr Asn Pro Thr Thr Val Ser
 130 135 140

tcc gcg ttc ggg ctc gcc cgc caa ctc atg gcc gaa aac caa atc gaa 480
 Ser Ala Phe Gly Leu Ala Arg Gln Leu Met Ala Glu Asn Gln Ile Glu
 145 150 155 160

ctc gca gtc caa gcc cta gac aaa ctc ccc caa tca tcc acc cac tac 528
 Leu Ala Val Gln Ala Leu Asp Lys Leu Pro Gln Ser Ser Thr His Tyr
 165 170 175

cga atg gcc acc ctc acc acc atc ttg ttg ctg gtc agc tcc aat ttg 576
 Arg Met Ala Thr Leu Thr Thr Ile Leu Leu Leu Val Ser Ser Asn Leu
 180 185 190

agt gaa tcc cgc atc cga cgg gct gcc cgc cga ctc acc gaa atc ccc 624
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 195 200 205
 aca aac gaa ccc cgc ttc aac caa atc aaa att gcc atc atg tcg gca 672
 Thr Asn Glu Pro Arg Phe Asn Gln Ile Lys Ile Ala Ile Met Ser Ala
 210 215 220
 ggc ctc agc tgg ctt cga gag cga aaa ctc aaa gct tcc gcc tcc gcg 720
 Gly Leu Ser Trp Leu Arg Glu Arg Lys Leu Lys Ala Ser Ala Ser Ala
 225 230 235 240
 aac cct ttg ttt gaa tac cgc ttc tcc caa aaa ggc ctg cgc acc ggc 768
 Asn Pro Leu Phe Glu Tyr Pro Phe Ser Gln Lys Gly Leu Arg Thr Gly
 245 250 255
 atc tcc gag gca ctc cgc att cag gca cgt tct gca ccg ttc ccg cac 816
 Ile Ser Glu Ala Leu Arg Ile Gln Ala Arg Ser Ala Pro Phe Pro His
 260 265 270
 cac cgt tac gca ctt gtg gat atg gcg aat gcc gtg cgg cca ctg agt 864
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 Trp Phe
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<211> 290

<212> PRT

<213> Corynebacterium glutamicum

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 35 40 45
 Asn His Val Leu Thr Ile Leu Pro Gly Glu Ala Ala Pro Lys Leu Ala
 50 55 60
 Leu Ala Ala Val Asp Glu Leu Ile Leu Gln Gln Ile Gly Ala Glu Ser
 65 70 75 80
 Thr Ala Tyr Leu Thr Pro Asp Ile Val Ser Ala Thr Ala Thr Leu Ser
 85 90 95
 Lys Asp Phe Glu Asp Leu Asp Ala Ser Ala Phe Glu Ser Leu Ser Asp
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<223> RXA01511
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Val Ala Ser Leu Ile
1 5

ggg aat ctt gag ctg cct agg gta agc cct aat ttc ttg gaa tta cgc 163
Gly Asn Leu Glu Leu Pro Arg Val Ser Pro Asn Phe Leu Glu Leu Arg
10 15 20

aag gcg gtg cgc cct tac ctg aaa gag cat gtg cac att ggg ttg tcg 211
Lys Ala Val Arg Pro Tyr Leu Lys Glu His Val His Ile Gly Leu Ser
25 30 35

ggc ggg ccg gat tca ttg gcg ctg gtg gct gct gtg ctc gcg gag aaa 259
Gly Gly Pro Asp Ser Leu Ala Leu Val Ala Ala Val Leu Ala Glu Lys
40 45 50

tcc cag gta acg gcg att tgt atc gat cat aat ctg cag acc ggt tct	307
Ser Gln Val Thr Ala Ile Cys Ile Asp His Asn Leu Gln Thr Gly Ser	
55 60 65	
gct gaa gtc acg cac aac gct gct gcg atg gcg cgc cac atg ggc gca	355
Ala Glu Val Thr His Asn Ala Ala Ala Met Ala Arg His Met Gly Ala	
70 75 80 85	
cag gcg atc gtg aag agc atc gag gtc gcg ccg ggg gag ggg atg gag	403
Gln Ala Ile Val Lys Ser Ile Glu Val Ala Pro Gly Glu Gly Met Glu	
90 95 100	
gcc gcc gcc agg gag gct cgg tac gcg gct ttt gcg cag ctc acc gat	451
Ala Ala Ala Arg Glu Ala Arg Tyr Ala Ala Phe Ala Gln Leu Thr Asp	
105 110 115	
gag att tgg gtg gcg cac acc atg gat gat caa gcc gag acc tat ctc	499
Glu Ile Trp Val Ala His Thr Met Asp Asp Gln Ala Glu Thr Tyr Leu	
120 125 130	
ctt ggc ggt ttg cgg ggg aat ccc gcg ggc atg aaa gat gct tct cga	547
Leu Gly Gly Leu Arg Gly Asn Pro Ala Gly Met Lys Asp Ala Ser Arg	
135 140 145	
cgc ccc gag cta tcc att att cga ccc ctt ctg ggg gct cgg cgt gcg	595
Arg Pro Glu Leu Ser Ile Ile Arg Pro Leu Leu Gly Ala Arg Arg Ala	
150 155 160 165	
cac acg cac ggg gcg tgc gtg gag ttg ggg ttg aaa ccg tgg cac gat	643
His Thr His Gly Ala Cys Val Glu Leu Gly Leu Lys Pro Trp His Asp	
170 175 180	
ccg caa aat ttt gac gat gcc ttt cgg cgg gta gcc atc cga aac cag	691
Pro Gln Asn Phe Asp Asp Ala Phe Arg Arg Val Ala Ile Arg Asn Gln	
185 190 195	
gtg att cct ctt ctt gcg cag gtg cac ggg gga gac cct gta cct ggt	739
Val Ile Pro Leu Leu Ala Gln Val His Gly Gly Asp Pro Val Pro Gly	
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Leu Ala Leu Ala Ala Arg Arg Ala Val Glu Asp Ala Glu Val Val Glu	
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Gly Asp Val Glu Lys Arg Arg Leu Glu Trp Gln Asp Gly Phe Pro Val	
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Thr Leu Ala Gly Glu Pro Thr Gly Leu Arg Arg Met Leu Ala Asp	
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Phe Leu Arg Gly Glu Gly Ile Ala Val Thr Ser Arg Lys Leu Asp Ala	
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Ile Asp Arg Leu Leu Thr Asp Trp Arg Gly Gln Gly Gly Val Ala Val	
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 Leu Lys Ile Thr Asp
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<213> Corynebacterium glutamicum

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His Ile Gly Leu Ser Gly Gly Pro Asp Ser Leu Ala Leu Val Ala Ala
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Val Leu Ala Glu Lys Ser Gln Val Thr Ala Ile Cys Ile Asp His Asn
 50 55 60

Leu Gln Thr Gly Ser Ala Glu Val Thr His Asn Ala Ala Ala Met Ala
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Arg His Met Gly Ala Gln Ala Ile Val Lys Ser Ile Glu Val Ala Pro
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Gly Glu Gly Met Glu Ala Ala Ala Arg Glu Ala Arg Tyr Ala Ala Phe
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Ala Gln Leu Thr Asp Glu Ile Trp Val Ala His Thr Met Asp Asp Gln
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Ala Glu Thr Tyr Leu Leu Gly Gly Leu Arg Gly Asn Pro Ala Gly Met
 130 135 140

Lys Asp Ala Ser Arg Arg Pro Glu Leu Ser Ile Ile Arg Pro Leu Leu
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Gly Ala Arg Arg Ala His Thr His Gly Ala Cys Val Glu Leu Gly Leu
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Lys Pro Trp His Asp Pro Gln Asn Phe Asp Asp Ala Phe Arg Arg Val
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Ala Ile Arg Asn Gln Val Ile Pro Leu Leu Ala Gln Val His Gly Gly
 195 200 205

Asp Pro Val Pro Gly Leu Ala Leu Ala Ala Arg Arg Ala Val Glu Asp
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Ala Glu Val Val Glu Gly Asp Val Glu Lys Arg Arg Leu Glu Trp Gln
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Asp Gly Phe Pro Val Thr Leu Ala Gly Glu Pro Thr Gly Leu Arg Arg

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Gln	Ile	Asp	Asp	Arg	Glu	Gln	Arg	Val	Arg	Leu	Thr	Leu	Arg	Glu	Pro	
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Pro	Ala	Arg	Thr	Ala	Pro	Ala	Ile	Phe	Glu	Lys	Val	Glu	Ala	Ser	Asn	
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Thr	Asp	Ser	Tyr	Thr	Thr	Asn	Val	Thr	Gln	Glu	Ser	Phe	Leu	Met	Ser	
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Phe	Phe	Leu	Thr	Arg	Met	Gln	Gly	Gly	Gly	Met	Phe	Gly	Ile	Gly	Gly		
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Gln	Ile	Leu	Glu	Val	His	Ala	Lys	Gly	Lys	Pro	Phe	Ala	Pro	Asp	Ala		
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Tyr	Asn	Arg	Asn	Glu	Leu	Phe	Ala	Arg	Leu	Val	Phe	Ala	Met	Gly	Gly		
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Ala	Asp	Ile	Glu	Met	Ala	Thr	Lys	Ile	Ala	Arg	Ser	Met	Val	Thr	Glu		
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Lys	Ala	His	Glu	Val	Ser	Tyr	Ser	Ile	Leu	Ala	Glu	Tyr	Arg	Asp	His		
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Leu	Asp	Arg	Leu	Ala	Glu	Lys	Leu	Leu	Glu	Lys	Glu	Thr	Leu	Arg	Arg		
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gaa aag gcg caa aaa gag tcg gtg ctg gat gct tct gaa acc aca gaa Glu Lys Ala Gln Lys Glu Ser Val Leu Asp Ala Ser Glu Thr Thr Glu 810 815 820	2563
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2682

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Phe Gln Glu Val Asp Thr Ser Val Ala Met Ala Gln Leu Asp Ala Gly
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Asn Val Ala Glu Ala Gln Ile Asp Asp Arg Glu Gln Arg Val Arg Leu
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Thr Leu Arg Glu Pro Ile Thr Val Asp Glu Arg Glu Gly Val Glu Glu
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Ile Leu Ala Gln Tyr Pro Ala Arg Thr Ala Pro Ala Ile Phe Glu Lys
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Val Glu Ala Ser Asn Thr Asp Ser Tyr Thr Thr Asn Val Thr Gln Glu
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Ser Phe Leu Met Ser Met Leu Ser Phe Ile Leu Pro Met Val Ile Ile
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Phe Gly Leu Leu Met Phe Phe Leu Thr Arg Met Gln Gly Gly Gly Met
 130 135 140

Phe Gly Ile Gly Gly Ser Lys Ala Lys Gln Leu Thr Lys Asp Met Pro
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Thr Asn Thr Phe Ala Asp Val Ala Gly Ala Glu Glu Ala Val Asp Glu
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Leu His Glu Ile Lys Asp Phe Leu Glu Asp Pro Thr Arg Tyr Glu Ala
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Leu Gly Ala Lys Ile Pro Arg Gly Val Leu Leu Tyr Gly Pro Pro Gly
 195 200 205

Thr Gly Lys Thr Leu Leu Ala Arg Ala Val Ala Gly Glu Ala Gly Val
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Pro Phe Tyr Ser Ile Ser Gly Ser Asp Phe Val Glu Met Phe Val Gly
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Val Gly Ala Ser Arg Val Arg Asp Leu Phe Lys Gln Ala Lys Glu Asn
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Ser Pro Cys Ile Ile Phe Val Asp Glu Ile Asp Ala Val Gly Arg Ala
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Gln	Phe	Leu	Leu	Asp	Lys	Ala	His	Glu	Val	Ser	Tyr	Ser	Ile	Leu	Ala
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Glu	Tyr	Arg	Asp	His	Leu	Asp	Arg	Leu	Ala	Glu	Lys	Leu	Leu	Glu	Lys
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 Arg Gln Glu Asn Arg Glu Pro Val Lys Thr Pro Val Glu Leu Ala Leu
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 Glu Arg Gly Glu Glu Pro Pro Lys Lys Phe Ser Ile Leu Glu Ala Ser
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 Arg Ala Thr Arg Glu Arg Arg Arg Lys Glu Leu Glu Ala Gln Gly Lys
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 675 680 685
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 Pro Gly Ser Ala Gly Lys His Arg Ser Arg Ala Glu Glu Gln Pro Ala
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 Glu Gln Gly Phe Pro Ala Gln Thr Pro Ala Gln Ala Pro Glu Gln Ser
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 Ser Gly Glu His Pro Gly Met Lys Ala Tyr Gly Phe Gly Asp Ser Glu
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 Leu Met Asp Gln Ser Thr Gly Ala Glu His Thr Pro Gly Asn Val Ser
 770 775 780
 Gln Glu Ser Pro Thr Glu Met Ile Gly Phe Arg Leu Pro Asp His Glu
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 Arg Ser Asp Tyr Pro Glu Lys Ala Gln Lys Glu Ser Val Leu Asp Ala
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 Ser Glu Thr Thr Glu Met Pro Val Val Pro Asp Gln Pro Ile Asp Gly
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 Gly Asp Asn Arg Gly
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tgg atc att gga cta gta gtc ctc gtg gtt ctc gcg atc atc att gta 163
Trp Ile Ile Gly Leu Val Val Leu Val Val Leu Ala Ile Ile Ile Val
      10                      15                      20

ttg atc gta gga aat cag cga ggt aaa tca aag acc gtt agt ttt gaa 211
Leu Ile Val Gly Asn Gln Arg Gly Lys Ser Lys Thr Val Ser Phe Glu
      25                      30                      35

aaa cct gaa gag aat aaa aaa gaa cta acc cag caa gag aag tct gga 259
Lys Pro Glu Glu Asn Lys Lys Glu Leu Thr Gln Gln Glu Lys Ser Gly
      40                      45                      50

aat tac caa gcc caa ggt gga ttc aac ttc gcc cca gct aaa caa aca 307
Asn Tyr Gln Ala Gln Gly Gly Phe Asn Phe Ala Pro Ala Lys Gln Thr
      55                      60                      65

gaa gag cca gtg ctg cgt gaa ggc caa gat ctt ggc gca cca aag gct 355
Glu Glu Pro Val Leu Arg Glu Gly Gln Asp Leu Gly Ala Pro Lys Ala
      70                      75                      80                      85

gaa aca aca ccg att gtt cca cca gta gtt att ccg ccg gca gct cct 403
Glu Thr Thr Pro Ile Val Pro Pro Val Val Ile Pro Pro Ala Ala Pro
      90                      95                      100

gaa gag gaa aag gcg ccg gag caa tcg act gaa act ttc gca gct caa 451
Glu Glu Glu Lys Ala Pro Glu Gln Ser Thr Glu Thr Phe Ala Ala Gln
      105                      110                      115

aag cct gct gaa gaa gca cct gca act cct gaa cca gaa acc tct gat 499
Lys Pro Ala Glu Glu Ala Pro Ala Thr Pro Glu Pro Glu Thr Ser Asp
      120                      125                      130

gat gtt gtc gag gaa cca gaa gtt aag gag cct gag gtt aaa gaa gtt 547
Asp Val Val Glu Glu Pro Glu Val Lys Glu Pro Glu Val Lys Glu Val
      135                      140                      145

gtc gct gtt gag cca gag gtc gaa act gaa gag cca gca gtt gtt gaa 595
Val Ala Val Glu Pro Glu Val Glu Thr Glu Glu Pro Ala Val Val Glu
      150                      155                      160                      165

gaa cct gca gta gca gag gaa cca gca att gtt gag gaa cct gca gta 643
Glu Pro Ala Val Ala Glu Glu Pro Ala Ile Val Glu Glu Pro Ala Val
      170                      175                      180

gca gag gaa cct gca gta gca gag gaa cct gca gta gca gag gaa cca 691
Ala Glu Glu Pro Ala Val Ala Glu Glu Pro Ala Val Ala Glu Glu Pro
      185                      190                      195

gca att gtt gag gaa cct gca gta gca gag gaa cct gca gtt gtt gag 739
Ala Ile Val Glu Glu Pro Ala Val Ala Glu Glu Pro Ala Val Val Glu
      200                      205                      210

gaa cct gca gta gcg gaa gtt ccc gaa aca atc gaa gaa cct gca gtt 787
Glu Pro Ala Val Ala Glu Val Pro Glu Thr Ile Glu Glu Pro Ala Val
      215                      220                      225

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gaa gaa ctt gcg gca gtt gct gag gtc acc gag gct gca gag gct gct	835
Glu Glu Leu Ala Ala Val Ala Glu Val Thr Glu Ala Ala Glu Ala Ala	
230 235 240 245	
cag gtt gct gtg gaa tct gcg gaa gct gcg ctg gag gaa act cca gtt	883
Gln Val Ala Val Glu Ser Ala Glu Ala Leu Glu Glu Thr Pro Val	
250 255 260	
cca gat gtg gag ccg gag cca gct gcg gag cct att gat gag atc gtg	931
Pro Asp Val Glu Pro Glu Pro Ala Ala Glu Pro Ile Asp Glu Ile Val	
265 270 275	
ccg gcg gcg ggt cgt atc ggt aag ctg cgt ggt cgt ctt tct cgg tca	979
Pro Ala Ala Gly Arg Ile Gly Lys Leu Arg Gly Arg Leu Ser Arg Ser	
280 285 290	
cag agt gtt ttc ggt aag tca gtg ttg ggc att ttg tct gcg ggt gac	1027
Gln Ser Val Phe Gly Lys Ser Val Leu Gly Ile Leu Ser Ala Gly Asp	
295 300 305	
ttg gat gaa gac gca tgg gaa gac atc gaa gcg atg ttg atc aag gcg	1075
Leu Asp Glu Asp Ala Trp Glu Asp Ile Glu Ala Met Leu Ile Lys Ala	
310 315 320 325	
gat ttg ggc gcc aag atc act gcg cgt gtg gtg gat gag ctg cgt gac	1123
Asp Leu Gly Ala Lys Ile Thr Ala Arg Val Val Asp Glu Leu Arg Asp	
330 335 340	
aag atc gca gag cat ggt gtt ggt agt gag gca gag gcg cgt gcg atg	1171
Lys Ile Ala Glu His Gly Val Gly Ser Glu Ala Glu Ala Arg Ala Met	
345 350 355	
ctg cgt gct tcg ctg att gat gct tgc cgt cct gac ctt gat cgc tcc	1219
Leu Arg Ala Ser Leu Ile Asp Ala Cys Arg Pro Asp Leu Asp Arg Ser	
360 365 370	
att aag gct atg ccg tat gag ggt aag cca ccg gtg gtg ttg gtt gtt	1267
Ile Lys Ala Met Pro Tyr Glu Gly Lys Pro Pro Val Val Leu Val Val	
375 380 385	
ggt gtg aac ggt acc ggt aag acg acg act act ggc aag ctt gct cgt	1315
Gly Val Asn Gly Thr Gly Lys Thr Thr Thr Gly Lys Leu Ala Arg	
390 395 400 405	
gtg ttg gtg tcc atg ggt cat aag gtg att ctt ggt gct gcg gat acg	1363
Val Leu Val Ser Met Gly His Lys Val Ile Leu Gly Ala Ala Asp Thr	
410 415 420	
ttc cgt gcg gcg gct gcg gat cag ttg gag acg tgg ggt cgc cgt gtg	1411
Phe Arg Ala Ala Ala Asp Gln Leu Glu Thr Trp Gly Arg Arg Val	
425 430 435	
ggt gcg gag act gtt cgt ggc gct gag ggc gcg gat cct gca tct att	1459
Gly Ala Glu Thr Val Arg Gly Ala Glu Gly Ala Asp Pro Ala Ser Ile	
440 445 450	
gcg ttt gat gct gtg gct aag ggt gtt gag cgt cag gcg gat gtc gtt	1507
Ala Phe Asp Ala Val Ala Lys Gly Val Glu Arg Gln Ala Asp Val Val	
455 460 465	

ttg gtt gac act gcg ggt cgt ttg cac acg tcg act ggt ttg atg gat 1555
 Leu Val Asp Thr Ala Gly Arg Leu His Thr Ser Thr Gly Leu Met Asp
 470 475 480 485

cag ttg ggc aag gtt aag cgc gtg gtg gag aag aag gca gtg gtg gat 1603
 Gln Leu Gly Lys Val Lys Arg Val Val Glu Lys Lys Ala Val Val Asp
 490 495 500

gaa gtg ctg ctg gtt ttg gat gcc acg gtt ggt cag aac ggt atg cag 1651
 Glu Val Leu Leu Val Leu Asp Ala Thr Val Gly Gln Asn Gly Met Gln
 505 510 515

cag gct cgt att ttc cgt gaa gtt gtg gat att acg ggt gtg gtg ttg 1699
 Gln Ala Arg Ile Phe Arg Glu Val Val Asp Ile Thr Gly Val Val Leu
 520 525 530

acc aag ctg gat ggt act gcg aag ggc gga atc gtg ttc cag gtg cag 1747
 Thr Lys Leu Asp Gly Thr Ala Lys Gly Gly Ile Val Phe Gln Val Gln
 535 540 545

gaa gag ttg ggt gtt cct gtg aag ctt gtt ggt ctt ggt gaa ggt gcg 1795
 Glu Glu Leu Gly Val Pro Val Lys Leu Val Gly Leu Gly Glu Gly Ala
 550 555 560 565

gat gat ttg gca ccg ttt gag gtt gag ggc ttc gtg gac gct ttg ctg 1843
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ggc tagaaacccg ataagcgaga acc 1869
 Gly

<210> 102

<211> 582

<212> PRT

<213> Corynebacterium glutamicum

<400> 102

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Thr Val Ser Phe Glu Lys Pro Glu Glu Asn Lys Lys Glu Leu Thr Gln
 35 40 45

Gln Glu Lys Ser Gly Asn Tyr Gln Ala Gln Gly Gly Phe Asn Phe Ala
 50 55 60

Pro Ala Lys Gln Thr Glu Glu Pro Val Leu Arg Glu Gly Gln Asp Leu
 65 70 75 80

Gly Ala Pro Lys Ala Glu Thr Thr Pro Ile Val Pro Pro Val Val Ile
 85 90 95

Pro Pro Ala Ala Pro Glu Glu Glu Lys Ala Pro Glu Gln Ser Thr Glu
 100 105 110

Thr Phe Ala Ala Gln Lys Pro Ala Glu Glu Ala Pro Ala Thr Pro Glu

115					120					125					
Pro	Glu	Thr	Ser	Asp	Asp	Val	Val	Glu	Glu	Pro	Glu	Val	Lys	Glu	Pro
130					135					140					
Glu	Val	Lys	Glu	Val	Val	Ala	Val	Glu	Pro	Glu	Val	Glu	Thr	Glu	Glu
145					150					155					160
Pro	Ala	Val	Val	Glu	Glu	Pro	Ala	Val	Ala	Glu	Glu	Pro	Ala	Ile	Val
				165					170					175	
Glu	Glu	Pro	Ala	Val	Ala	Glu	Glu	Pro	Ala	Val	Ala	Glu	Glu	Pro	Ala
			180					185					190		
Val	Ala	Glu	Glu	Pro	Ala	Ile	Val	Glu	Glu	Pro	Ala	Val	Ala	Glu	Glu
		195					200					205			
Pro	Ala	Val	Val	Glu	Glu	Pro	Ala	Val	Ala	Glu	Val	Pro	Glu	Thr	Ile
		210				215					220				
Glu	Glu	Pro	Ala	Val	Glu	Glu	Leu	Ala	Ala	Val	Ala	Glu	Val	Thr	Glu
225					230					235					240
Ala	Ala	Glu	Ala	Ala	Gln	Val	Ala	Val	Glu	Ser	Ala	Glu	Ala	Ala	Leu
				245					250					255	
Glu	Glu	Thr	Pro	Val	Pro	Asp	Val	Glu	Pro	Glu	Pro	Ala	Ala	Glu	Pro
			260					265					270		
Ile	Asp	Glu	Ile	Val	Pro	Ala	Ala	Gly	Arg	Ile	Gly	Lys	Leu	Arg	Gly
		275					280					285			
Arg	Leu	Ser	Arg	Ser	Gln	Ser	Val	Phe	Gly	Lys	Ser	Val	Leu	Gly	Ile
		290				295					300				
Leu	Ser	Ala	Gly	Asp	Leu	Asp	Glu	Asp	Ala	Trp	Glu	Asp	Ile	Glu	Ala
305					310					315					320
Met	Leu	Ile	Lys	Ala	Asp	Leu	Gly	Ala	Lys	Ile	Thr	Ala	Arg	Val	Val
			325						330					335	
Asp	Glu	Leu	Arg	Asp	Lys	Ile	Ala	Glu	His	Gly	Val	Gly	Ser	Glu	Ala
			340					345					350		
Glu	Ala	Arg	Ala	Met	Leu	Arg	Ala	Ser	Leu	Ile	Asp	Ala	Cys	Arg	Pro
		355					360					365			
Asp	Leu	Asp	Arg	Ser	Ile	Lys	Ala	Met	Pro	Tyr	Glu	Gly	Lys	Pro	Pro
		370				375					380				
Val	Val	Leu	Val	Val	Gly	Val	Asn	Gly	Thr	Gly	Lys	Thr	Thr	Thr	Thr
385					390					395					400
Gly	Lys	Leu	Ala	Arg	Val	Leu	Val	Ser	Met	Gly	His	Lys	Val	Ile	Leu
			405						410					415	
Gly	Ala	Ala	Asp	Thr	Phe	Arg	Ala	Ala	Ala	Ala	Asp	Gln	Leu	Glu	Thr
			420					425					430		
Trp	Gly	Arg	Arg	Val	Gly	Ala	Glu	Thr	Val	Arg	Gly	Ala	Glu	Gly	Ala
		435					440					445			

Asp Pro Ala Ser Ile Ala Phe Asp Ala Val Ala Lys Gly Val Glu Arg
 450 455 460
 Gln Ala Asp Val Val Leu Val Asp Thr Ala Gly Arg Leu His Thr Ser
 465 470 475 480
 Thr Gly Leu Met Asp Gln Leu Gly Lys Val Lys Arg Val Val Glu Lys
 485 490 495
 Lys Ala Val Val Asp Glu Val Leu Leu Val Leu Asp Ala Thr Val Gly
 500 505 510
 Gln Asn Gly Met Gln Gln Ala Arg Ile Phe Arg Glu Val Val Asp Ile
 515 520 525
 Thr Gly Val Val Leu Thr Lys Leu Asp Gly Thr Ala Lys Gly Gly Ile
 530 535 540
 Val Phe Gln Val Gln Glu Glu Leu Gly Val Pro Val Lys Leu Val Gly
 545 550 555 560
 Leu Gly Glu Gly Ala Asp Asp Leu Ala Pro Phe Glu Val Glu Gly Phe
 565 570 575
 Val Asp Ala Leu Leu Gly
 580

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1111)
 <223> RXA02713

<400> 103
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ttggacatct aggccggcag gaaaaggggg gaacacgcac atg gaa gat ttt tcc 115
 Met Glu Asp Phe Ser
 1 5

ttg gat ggc aac cac gga cac gtt ccc gta atg cgt gat cgt atg gcg 163
 Leu Asp Gly Asn His Gly His Val Pro Val Met Arg Asp Arg Met Ala
 10 15 20

gct ttg atc gcc gaa cac gtg gaa gca ttg gga gaa aac gct gtc att 211
 Ala Leu Ile Ala Glu His Val Glu Ala Leu Gly Glu Asn Ala Val Ile
 25 30 35

gtt gac gca acc ctt ggc gca ggc ggg cat gcg gag ttc ttc ctg aac 259
 Val Asp Ala Thr Leu Gly Ala Gly Gly His Ala Glu Phe Phe Leu Asn
 40 45 50

acg ttc ccc aaa gcg cgc ctg att ggc ctt gat cgt gac caa aat gcg 307
 Thr Phe Pro Lys Ala Arg Leu Ile Gly Leu Asp Arg Asp Gln Asn Ala
 55 60 65

ttg cgg gat gct cgc gcg cga ctt gct cct ttc ggg gag cgg ttc att	355
Leu Arg Asp Ala Arg Ala Arg Leu Ala Pro Phe Gly Glu Arg Phe Ile	
70 75 80 85	
ggc gtc cag acg cgt ttc gac gga ctc cgc gag gtg ttg gaa tct gtc	403
Gly Val Gln Thr Arg Phe Asp Gly Leu Arg Glu Val Leu Glu Ser Val	
90 95 100	
gag ggc gac atc att gat tta gct cgc gag cac ggt atc gct ggc gct	451
Glu Gly Asp Ile Ile Asp Leu Ala Arg Glu His Gly Ile Ala Gly Ala	
105 110 115	
ctg ttt gat ctg ggt gtc tcc tcg atg cag ctt gat cag gtg gag cgt	499
Leu Phe Asp Leu Gly Val Ser Ser Met Gln Leu Asp Gln Val Glu Arg	
120 125 130	
ggc ttt gcc tac cgc acg gac gcg cct ctg gac atg cgc atg gat gca	547
Gly Phe Ala Tyr Arg Thr Asp Ala Pro Leu Asp Met Arg Met Asp Ala	
135 140 145	
act cag ggt att acg gct gca gat atc ctc aac act tat tcg cat ggt	595
Thr Gln Gly Ile Thr Ala Ala Asp Ile Leu Asn Thr Tyr Ser His Gly	
150 155 160 165	
gac atc gct cga atc ttg aag act tac ggc gat gaa cgc ttc gcc ggc	643
Asp Ile Ala Arg Ile Leu Lys Thr Tyr Gly Asp Glu Arg Phe Ala Gly	
170 175 180	
aag att gct tct gcg gtg ctg aaa gaa cgt gaa aaa gag ccg ttc act	691
Lys Ile Ala Ser Ala Val Leu Lys Glu Arg Glu Lys Glu Pro Phe Thr	
185 190 195	
acc tct gct cgt ttg gtg gag ctt ctg tac gac gcc atc cct gca gcg	739
Thr Ser Ala Arg Leu Val Glu Leu Leu Tyr Asp Ala Ile Pro Ala Ala	
200 205 210	
acc cgc cga acc ggt gga cac ccc gcg aaa cgt act ttc cag gcg ttg	787
Thr Arg Arg Thr Gly Gly His Pro Ala Lys Arg Thr Phe Gln Ala Leu	
215 220 225	
cgc gtt gag gtg aac aac gag ctt gat tcc ctg aag aat gtg ctt cct	835
Arg Val Glu Val Asn Asn Glu Leu Asp Ser Leu Lys Asn Val Leu Pro	
230 235 240 245	
caa atc act gac gcc ctc aat gtt ggg gga cgt gca gtg ttt atg agc	883
Gln Ile Thr Asp Ala Leu Asn Val Gly Gly Arg Ala Val Phe Met Ser	
250 255 260	
tac cag tct cat gag gac aag ctg gtg aag aag ttc ttc acg gat ctg	931
Tyr Gln Ser His Glu Asp Lys Leu Val Lys Lys Phe Phe Thr Asp Leu	
265 270 275	
acc acc tct aag acc cct ccg ggc ttg cct gtt gat ctt cct gga act	979
Thr Thr Ser Lys Thr Pro Pro Gly Leu Pro Val Asp Leu Pro Gly Thr	
280 285 290	
gca cca cag ttt aag cag gtt act cgc ggt gct gaa acg gct tcg gaa	1027
Ala Pro Gln Phe Lys Gln Val Thr Arg Gly Ala Glu Thr Ala Ser Glu	
295 300 305	

gct gaa att gaa gaa aac cca cgt gcc gca cct gtg aag gtg cgc gca 1075
 Ala Glu Ile Glu Glu Asn Pro Arg Ala Ala Pro Val Lys Val Arg Ala
 310 315 320 325

atc gaa aga atc ggc aac aac tca gga gac ctc tca tgacctgac 1121
 Ile Glu Arg Ile Gly Asn Asn Ser Gly Asp Leu Ser
 330 335

aaatggctcc cgc 1134

<210> 104

<211> 337

<212> PRT

<213> Corynebacterium glutamicum

<400> 104

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Arg Asp Arg Met Ala Ala Leu Ile Ala Glu His Val Glu Ala Leu Gly
 20 25 30

Glu Asn Ala Val Ile Val Asp Ala Thr Leu Gly Ala Gly Gly His Ala
 35 40 45

Glu Phe Phe Leu Asn Thr Phe Pro Lys Ala Arg Leu Ile Gly Leu Asp
 50 55 60

Arg Asp Gln Asn Ala Leu Arg Asp Ala Arg Ala Arg Leu Ala Pro Phe
 65 70 75 80

Gly Glu Arg Phe Ile Gly Val Gln Thr Arg Phe Asp Gly Leu Arg Glu
 85 90 95

Val Leu Glu Ser Val Glu Gly Asp Ile Ile Asp Leu Ala Arg Glu His
 100 105 110

Gly Ile Ala Gly Ala Leu Phe Asp Leu Gly Val Ser Ser Met Gln Leu
 115 120 125

Asp Gln Val Glu Arg Gly Phe Ala Tyr Arg Thr Asp Ala Pro Leu Asp
 130 135 140

Met Arg Met Asp Ala Thr Gln Gly Ile Thr Ala Ala Asp Ile Leu Asn
 145 150 155 160

Thr Tyr Ser His Gly Asp Ile Ala Arg Ile Leu Lys Thr Tyr Gly Asp
 165 170 175

Glu Arg Phe Ala Gly Lys Ile Ala Ser Ala Val Leu Lys Glu Arg Glu
 180 185 190

Lys Glu Pro Phe Thr Thr Ser Ala Arg Leu Val Glu Leu Leu Tyr Asp
 195 200 205

Ala Ile Pro Ala Ala Thr Arg Arg Thr Gly Gly His Pro Ala Lys Arg
 210 215 220

Thr Phe Gln Ala Leu Arg Val Glu Val Asn Asn Glu Leu Asp Ser Leu
 225 230 235 240

Lys	Asn	Val	Leu	Pro	Gln	Ile	Thr	Asp	Ala	Leu	Asn	Val	Gly	Gly	Arg	
				245					250					255		
Ala	Val	Phe	Met	Ser	Tyr	Gln	Ser	His	Glu	Asp	Lys	Leu	Val	Lys	Lys	
				260					265					270		
Phe	Phe	Thr	Asp	Leu	Thr	Thr	Ser	Lys	Thr	Pro	Pro	Gly	Leu	Pro	Val	
				275					280					285		
Asp	Leu	Pro	Gly	Thr	Ala	Pro	Gln	Phe	Lys	Gln	Val	Thr	Arg	Gly	Ala	
				290					295					300		
Glu	Thr	Ala	Ser	Glu	Ala	Glu	Ile	Glu	Glu	Asn	Pro	Arg	Ala	Ala	Pro	
				305					310					315		
Val	Lys	Val	Arg	Ala	Ile	Glu	Arg	Ile	Gly	Asn	Asn	Ser	Gly	Asp	Leu	
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Ser

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<210> 105
<211> 789
<212> DNA
<213> Corynebacterium glutamicum
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<222> (101)..(766)  
<223> RXN02723
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											gtg	aac	aaa	aaa	gtc	115	
											Val	Asn	Lys	Lys	Val		
											1				5		
atc	gcc	att	gtt	gtg	ggc	gtg	gtt	gtt	gtc	ctc	gtg	gca	atc	ctg	ggc	163	
Ile	Ala	Ile	Val	Val	Gly	Val	Val	Val	Val	Leu	Val	Ala	Ile	Leu	Gly		
					10					15				20			
gtt	gtt	gcc	tgg	ttc	gtt	ccc	atc	ctc	aag	gtg	gga	aac	att	gaa	gta	211	
Val	Val	Ala	Trp	Phe	Val	Pro	Ile	Leu	Lys	Val	Gly	Asn	Ile	Glu	Val		
			25					30					35				
acc	ggc	gca	acg	cgc	aca	tat	ccg	gat	caa	gta	ctg	gaa	gtc	tcc	ggg	259	
Thr	Gly	Ala	Thr	Arg	Thr	Tyr	Pro	Asp	Gln	Val	Leu	Glu	Val	Ser	Gly		
		40					45					50					
att	gtt	gag	ggc	aaa	aac	ctc	ttc	cgc	gtc	gat	gcg	act	gca	gca	ggg	307	
Ile	Val	Glu	Gly	Lys	Asn	Leu	Phe	Arg	Val	Asp	Ala	Thr	Ala	Ala	Gly		
	55					60					65						
caa	aac	att	gtg	gaa	ttg	ccc	tgg	gtg	aaa	tcg	gtg	acc	gtt	aac	cgt	355	
Gln	Asn	Ile	Val	Glu	Leu	Pro	Trp	Val	Lys	Ser	Val	Thr	Val	Asn	Arg		
70					75					80					85		
gcc	ctg	cca	agc	acc	atc	acc	gtg	gag	ctg	aca	gag	cgt	gag	cct	gca	403	

Val Thr Val Asn Arg Ala Leu Pro Ser Thr Ile Thr Val Glu Leu Thr
85 90 95

Glu Arg Glu Pro Ala Val Phe Ile Lys Arg Ala Asp Gly Asp His Val

100								105				110				
Ile	Asp	Thr	Glu	Gly	Lys	Glu	Ile	Ile	Ile	Ile	Gly	Thr	Pro	Pro	Val	Gly
115							120				125					
Thr	Val	Glu	Val	Ser	Gly	Ala	Asp	Glu	Gly	Asn	Ser	Glu	Val	Leu	Pro	
130							135				140					
Ala	Val	Ile	Ala	Val	Ile	Asn	Ala	Ile	Lys	Ala	Gln	Asp	Ala	Gln	Met	
145							150				155					
Thr	Glu	Ser	Ile	Gln	Val	Val	Glu	Ala	Pro	Asp	Gln	Phe	Asp	Ile	Leu	
165							170				175					
Leu	Lys	Met	Asn	Asp	Gly	Arg	Glu	Ile	Tyr	Trp	Gly	Ser	Ser	Glu	Asn	
180							185				190					
Asn	His	Asp	Lys	Ala	Val	Ala	Met	Ser	Thr	Val	Leu	Lys	Arg	Glu	Gly	
195							200				205					
Gln	Arg	Trp	Asn	Ile	Ser	Ser	Pro	Ser	Met	Val	Thr	Val	Arg			
210							215				220					

<210> 107
 <211> 500
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(477)
 <223> FRXA02723

<400> 107																
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1				5					10					15		
tcg gtg acc gtt aac cgt gcc ctg cca agc acc atc acc gtg gag ctg																96
Ser	Val	Thr	Val	Asn	Arg	Ala	Leu	Pro	Ser	Thr	Ile	Thr	Val	Glu	Leu	
			20				25						30			
aca gag cgt gag cct gca gtg ttc atc aag cgt gct gat ggt gac cat																144
Thr	Glu	Arg	Glu	Pro	Ala	Val	Phe	Ile	Lys	Arg	Ala	Asp	Gly	Asp	His	
		35					40					45				
gtc att gac acc gag ggt aaa gaa att atc att gga aca ccc ccg gtg																192
Val	Ile	Asp	Thr	Glu	Gly	Lys	Glu	Ile	Ile	Ile	Gly	Thr	Pro	Pro	Val	
	50					55					60					
gga aca gta gaa gtt tct ggc gcg gat gaa gga aac tca gaa gtg ctt																240
Gly	Thr	Val	Glu	Val	Ser	Gly	Ala	Asp	Glu	Gly	Asn	Ser	Glu	Val	Leu	
65					70					75					80	
cct gcg gtt att gct gta atc aac gca att aaa gcg caa gat gcg cag																288
Pro	Ala	Val	Ile	Ala	Val	Ile	Asn	Ala	Ile	Lys	Ala	Gln	Asp	Ala	Gln	
				85					90					95		
atg aca gaa agt atc cag gta gtg gaa gct ccg gat caa ttt gat atc																336
Met	Thr	Glu	Ser	Ile	Gln	Val	Val	Glu	Ala	Pro	Asp	Gln	Phe	Asp	Ile	

100	105	110	
ttg ctg aaa atg aat gat ggc cgg gaa atc tac tgg gga tcc tcg gaa			384
Leu Leu Lys Met Asn Asp Gly Arg Glu Ile Tyr Trp Gly Ser Ser Glu			
115	120	125	
aac aac cac gat aaa gcg gtg gca atg tcg act gtt ttg aag cgg gaa			432
Asn Asn His Asp Lys Ala Val Ala Met Ser Thr Val Leu Lys Arg Glu			
130	135	140	
ggc caa cgt tgg aac att agc tca ccc tca atg gtg aca gtc cgc			477
Gly Gln Arg Trp Asn Ile Ser Ser Pro Ser Met Val Thr Val Arg			
145	150	155	
taaagtggct gggtagttcc ggt			500

<210> 108
 <211> 159
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 108
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 Ser Val Thr Val Asn Arg Ala Leu Pro Ser Thr Ile Thr Val Glu Leu
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 Thr Glu Arg Glu Pro Ala Val Phe Ile Lys Arg Ala Asp Gly Asp His
 35 40 45
 Val Ile Asp Thr Glu Gly Lys Glu Ile Ile Ile Gly Thr Pro Pro Val
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 Pro Ala Val Ile Ala Val Ile Asn Ala Ile Lys Ala Gln Asp Ala Gln
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 Met Thr Glu Ser Ile Gln Val Val Glu Ala Pro Asp Gln Phe Asp Ile
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 Leu Leu Lys Met Asn Asp Gly Arg Glu Ile Tyr Trp Gly Ser Ser Glu
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Asn Ile Thr Leu Ile Glu Pro Leu Leu Lys Arg Ser Val Tyr Leu Asn
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Ala Asp Ile Gly Ser Gly Ala Gly Leu Pro Gly Ile Pro Leu Ala Ile
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Ala Arg Pro Asp Leu Asn Ile Thr Leu Ile Glu Pro Leu Leu Lys Arg
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Ser Val Tyr Leu Asn Glu Val Lys Glu Ala Leu Asn Leu Asp Asn Val
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Thr Val Val Arg Gly Arg Ala Glu Glu Lys Val Val Arg Lys Gln Val
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Gly Leu Val Asp Ile Val Thr Ser Arg Ala Val Ala Pro Leu Gly Lys
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Leu Ala Thr Trp Ser Leu Pro Leu Val Lys Ile Gly Gly Arg Met Val
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Pro Arg His Glu Phe Asp Pro Gln Ala Leu Asp Glu Leu Val His Ser
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Asp Gly Tyr Glu Leu Ile Met Gly Glu Arg Arg Trp Arg Ala Ser Lys
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Arg Ala Gly Leu Glu Val Ile Pro Ala Ile Val Arg Glu Thr Glu Asp
185 190 195

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Ser Ala Met Leu Arg Asp Ala Leu Leu Glu Asn Ile His Arg Val Gln
200 205 210

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 Gln Thr Lys Val Ala Ala Gly Val Leu Ser Ala Gly His Ala Arg Ala
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Pro 130	Asn	Pro	Gln	Gln	Pro	Arg 135	His	Glu	Phe	Asp	Pro 140	Gln	Ala	Leu	Asp
Glu 145	Leu	Val	His	Ser	Ile 150	Ser	Glu	Phe	Gly	Leu 155	Met	Gln	Pro	Ile	Val 160
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Arg	Glu	Thr 195	Glu	Asp	Ser	Ala	Met 200	Leu	Arg	Asp	Ala	Leu 205	Leu	Glu	Asn
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Gln 225	Leu	Leu	Glu	Glu	Phe 230	Gly	Val	Thr	Gln	Ala 235	Glu	Leu	Ala	Asp	Lys 240
Leu	Gly	Arg	Ser	Arg 245	Pro	Val	Ile	Thr	Asn 250	Met	Ile	Arg	Leu	Leu 255	Gly
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Asp 290	Thr	Leu	Ala	Thr	Arg	Ile 295	Ile	Ala	Glu	Gly	Leu 300	Ser	Val	Arg	Ala
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Lys	Lys	Pro	Arg	Glu 325	Lys	Ala	Ala	Thr	Pro 330	Glu	Val	Phe	Thr	Arg 335	Ala
Ala	Glu	Ser	Leu 340	Ala	Asp	Asn	Leu	Asp 345	Thr	Lys	Val	Ser	Val 350	Met	Met
Gly	Lys	Lys 355	Lys	Gly	Lys	Leu	Val 360	Val	Glu	Phe	Gly	Asp 365	Lys	Asp	Asp
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Met Phe Ala Pro Pro															5
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His Glu Trp His Arg His Pro Asp Pro Ala Thr Leu Trp Ser Thr Leu															
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Gly Thr Arg Arg Met Trp Glu Arg Thr Gln Asp Asp Gln Asp Cys Leu															
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Val Ser Asp Ser Gly Ala Pro Glu Asp Leu Asp Pro Val Cys Ala Val															
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Val Ser Val Gln Leu Gln Ala Phe Arg Phe Ile Gly Leu Asn Gly Ala															
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Gly Ala His Asp Leu Ala Arg Ala Leu Val Val Gln Leu Leu Tyr His															
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His Gly Pro Glu Val Val Gly Ile Lys Ala Ile Gly Glu Ser Gly Trp															
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Glu Trp Leu Lys Trp Val Pro His Thr Arg Asp Pro Glu Lys Ala Ala															

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acc	agc	acc	gca	ttg	ggc	cag	ctg	gca	gag	gat	gaa	ggg	ctg	ctg	ttg	787		
Thr	Ser	Thr	Ala	Leu	Gly	Gln	Leu	Ala	Glu	Asp	Glu	Gly	Leu	Leu	Leu			
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His	Thr	Ser	Ala	Val	Ile	Thr	Asn	Leu	Glu	Glu	Glu	Pro	Val	Leu	Val			
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Tyr	Val	Ser	Gly	Pro	Ile	Met	Arg	Arg	His	His	Leu	Ala	Pro	Thr	Gln	
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Ser	Arg	Val	Arg	Leu	Phe	Thr	Ser	Trp	Glu	Glu	Pro	Lys	Glu	Glu	Val	
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Ile	Val	Glu	Gln	Ser	Thr	Glu	Thr	Leu	Ile	Asp	Ala	Val	Val	Ala	Arg	
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Ala	Ile	Ser	Ala	Ala	Lys	Leu	Arg	Gly	Leu	Ser	Ala	His	Arg	Ile	Trp	
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Gln	Arg	Gln	Asp	Pro	Leu	Leu	Ile	Asp	Phe	Ser	Leu	Thr	Gly	Gly	Ser	
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Leu Arg Ser Ile Val Ile Ser Met Ala Ala Thr His Ser Thr Glu Asn	
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Ser Arg Leu Pro His Val Ala Gly Val Ala Gly Arg Lys Asp Pro Glu	
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aaa gtc cgc cga gtt gtc gat gaa gta cga ggc ctg atc aac cac cct	2323
Lys Val Arg Arg Val Val Asp Glu Val Arg Gly Leu Ile Asn His Pro	
730 735 740	
gaa caa cgc cac acc ttc ctt att gtg gac ggc tgg cac acc atc acc	2371
Glu Gln Arg His Thr Phe Leu Ile Val Asp Gly Trp His Thr Ile Thr	
745 750 755	
caa gaa ttc gac gag ctt ttc gac gcc ttc gta gac atc gcc gcc aac	2419
Gln Glu Phe Asp Glu Leu Phe Asp Ala Phe Val Asp Ile Ala Ala Asn	
760 765 770	
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Gly Leu Ala Ser Arg Val His Leu Val Leu Ser Thr Gln Arg Trp Ser	
775 780 785	
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Ser Ile Arg Pro Ala Val Arg Asp Leu Val Thr Gly Arg Ile Glu Leu	
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Lys Leu Gly Glu Ala Met Asp Ser Val Ile Asp Arg Lys Ala Gln Leu	
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Arg Ile Pro Ser Lys Pro Gly Arg Gly Leu Asn Leu Asp Lys Glu His	
825 830 835	
atc ctt att gct cat gcg tct ggc caa gac atc gcc cag gta tgc gtc	2659
Ile Leu Ile Ala His Ala Ser Gly Gln Asp Ile Ala Gln Val Cys Val	
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Met Ala Asp Gly Gln Gly Trp Gln Gln Val Pro Gln Leu Ser Val Leu	
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Pro Ala His Ile Leu Leu His Glu Leu Glu Leu Ser Ala Thr Pro Gly	
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Ile Pro Ile Ala Arg Gly Gly Ala Glu Leu Ser Thr Leu Thr Trp Asp	
890 895 900	
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Pro Glu Ser Ser Arg His Leu Leu Ala Phe Gly Ser Gln Gly Cys Gly
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 Lys Ser Ser Leu Ile Arg Thr Ile Val Thr Gly Leu Thr Ile Val Gly
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 Gly Leu Val Pro Glu Asp Met Leu Ala Ala Tyr Cys Ala Thr Ser Thr
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 Trp Gln Gly Pro Asp Ile Tyr Leu Val Ile Asp Asp Tyr Asp Leu Leu
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Leu	Arg	Ala	Lys
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His	Ala		
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Ala	Met	Gln	Arg
35	Arg	His	Glu
40	Trp	His	Arg
45	Pro	Asp	Pro
Ala	Thr		
Leu	Trp	Ser	Thr
50	Leu	Gly	Thr
55	Arg	Arg	Met
60	Trp	Glu	Arg
65	Thr	Gln	Asp
Asp	Gln	Asp	Cys
70	Leu	Glu	Ile
75	Arg	Phe	Gly
80	Leu	Gly	Val
85	Thr	Arg	Leu
90	Asp	Leu	Asp
95	Pro	Ala	Ile
100	Val	Ser	Leu
105	Arg	His	Thr
110	Ile	Arg	Asp
115	Val	Gly	Ser
120	Val	Gln	Leu
125	Gln	Ala	Phe
130	Arg	Ala	Leu
135	Val	Val	Gly
140	Ile	Lys	Ala
145	Ile		
150	Gln	Leu	Leu
155	Tyr	His	His
160	Gly	Pro	Glu
165	Val	Val	Gly
170	Ile	Lys	Ala
175	Thr	Arg	Asp
180	Thr	Arg	Asp
185	Val	Leu	Thr
190	Val	Leu	Thr
195	Thr	Thr	Ile
200	Ile	Ile	
205	Asn	Gly	Thr
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215	Ile	Asp	Asp
220	Pro	Gln	Trp
225	Thr	Thr	Ile
230	Ile	Ile	
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245	Ser	Thr	Ala
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255	Leu	Ala	Glu
260	Asp	Lys	Arg
265	Leu	His	Val
270	Ala	Thr	Ala
275	Thr	Ala	Glu
280	Leu	Leu	Leu
285	Gly	Ile	Asp
290	Val	Glu	His
295	Leu	Thr	Pro
300	Glu	Thr	Leu
305	Trp	Met	Asn
310	Lys	Arg	Thr
315	Thr		
320	Gln	Pro	Lys
325	Thr	Arg	Leu
330	Ala	His	Gly
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	Gly		
	Arg	Pro	Met
	Val	Leu	Asp
	Leu	Lys	Glu
	Ser	Ala	His
	Gly	Gly	Met
	Gly		

Pro His Gly Leu Cys Ile Gly Ala Thr Gly Ser Gly Lys Ser Glu Leu
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Leu Asn Leu Val Leu Val Asp Phe Lys Gly Gly Ala Thr Phe Leu Gly
370 375 380

Phe Glu Gln Leu Pro His Thr Ser Ala Val Ile Thr Asn Leu Glu Glu
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Glu Pro Val Leu Val Glu Arg Met His Asp Ala Ile Ser Gly Glu Met
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Asn Arg Arg Gln Glu Ala Leu Arg Gln Ala Gly Gly Cys Ala Asn Val
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Asp Glu Tyr Asn Gln Arg Asp Gly Val Lys Pro Met Pro Ala Leu Leu
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Ala Asp Leu Phe Val Ala Val Gly Arg Leu Gly Arg Ser Leu His Ile
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Ser Gln Pro Gly Ala Gly Phe Leu Lys Ser Asp Val Asp Thr Val Thr
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Pro Lys Glu Glu Val Ile Val Glu Gln Ser Thr Glu Thr Leu Ile Asp
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Ala Leu Ala Asp Asp Val Gly Glu Leu Ser Ala Val Ile Gly Met Ile
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 Arg Lys Asp Pro Glu Lys Val Arg Arg Val Val Asp Glu Val Arg Gly
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 Trp His Thr Ile Thr Gln Glu Phe Asp Glu Leu Phe Asp Ala Phe Val
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 Thr Gln Arg Trp Ser Ser Ile Arg Pro Ala Val Arg Asp Leu Val Thr
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 Gly Arg Ile Glu Leu Lys Leu Gly Glu Ala Met Asp Ser Val Ile Asp
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 850 855 860
 Gln Leu Ser Val Leu Pro Ala His Ile Leu Leu His Glu Leu Glu Leu
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 Ser Ala Thr Pro Gly Ile Pro Ile Ala Arg Gly Gly Ala Glu Leu Ser
 885 890 895
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 Ser Gln Gly Cys Gly Lys Ser Ser Leu Ile Arg Thr Ile Val Thr Gly
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 Arg Arg Thr His Leu Gly Leu Val Pro Glu Asp Met Leu Ala Ala Tyr
 945 950 955 960
 Cys Ala Thr Ser Thr Ala Val His Asn Thr Ile Lys Asp Met Val Ala
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 Thr Leu Ser Ala Arg Leu Pro Gly Pro Asp Ile Thr Ala Gln Glu Leu

980 985 990
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 Met Asn Thr Leu Glu
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 Arg Leu Lys Leu Arg Arg Thr Glu Met Trp Leu Leu Ile Leu Ala Thr
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 Leu Val Val Ser Ile Met Phe Ile Ser Leu Glu Leu Ala Met Gly Asn
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 gag ttg ggt acc cat att ttg atg ctg atg ggc gga tat atc ggt atc 259
 Glu Leu Gly Thr His Ile Leu Met Leu Met Gly Gly Tyr Ile Gly Ile
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 ttc atc gtc gcg cac cta gcc atg gca tgg gtg gcg ccg ttt gct gat 307
 Phe Ile Val Ala His Leu Ala Met Ala Trp Val Ala Pro Phe Ala Asp
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 caa atc atg ctg cct gtg gtg gcg gtg ctc aat ggc att ggt ttg gtg 355

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Met	Ile	Tyr	Arg	Leu	Asp	Glu	Ala	Thr	Gly	Tyr	Ser	Thr	Val	Asn	Ser		
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Gln	Leu	Met	Trp	Thr	Val	Val	Gly	Val	Thr	Leu	Met	Val	Ala	Val	Leu		
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Gly	Val	Val	Gly	Ile	Val	Leu	Leu	Ala	Leu	Pro	Leu	Val	Trp	Pro	Gln		
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Pro	Gly	Gly	Val	Glu	Ala	Arg	Ile	Trp	Ile	Trp	Leu	Gly	Pro	Phe	Ser		
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Ile	Gln	Pro	Gly	Glu	Phe	Ser	Lys	Ile	Leu	Leu	Leu	Leu	Phe	Phe	Ala		
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Gln	Leu	Leu	Ala	Thr	Lys	Arg	Ala	Leu	Phe	Thr	Val	Ala	Gly	Tyr	Arg		
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Phe	Leu	Gly	Met	Asp	Phe	Pro	Arg	Leu	Arg	Asp	Leu	Ala	Pro	Ile	Leu		
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Val	Val	Trp	Ala	Leu	Ala	Ile	Leu	Ile	Met	Ala	Gly	Ala	Asn	Asp	Phe		
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Val	Gly	Ala	Phe	Thr	Val	Tyr	Gln	Val	Ser	Ser	Lys	Ile	Gln	Glu	Arg		
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Val	Gln	Asn	Phe	Val	Asp	Pro	Val	Ala	His	Tyr	Asp	Thr	Thr	Gly	Tyr		
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cag	ctg	tcc	cag	tcc	ttg	ttt	ggc	atg	agt	tgg	ggc	gga	atc	acc	ggc	1027	
Gln	Leu	Ser	Gln	Ser	Leu	Phe	Gly	Met	Ser	Trp	Gly	Gly	Ile	Thr	Gly		
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gcg gcc atc atc gtg ctg ttt ggt gtg ttt gtc acc cgc ggt atg cgc 1171
Ala Ala Ile Ile Val Leu Phe Gly Val Phe Val Thr Arg Gly Met Arg
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acc gct acc ctg gct cgt gac agc tac gga aag ctc gtg gca tct ggt 1219
Thr Ala Thr Leu Ala Arg Asp Ser Tyr Gly Lys Leu Val Ala Ser Gly
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ctg tcg atg acc atc atg atc cag att ttc gtc gtc gtg gca ggt att 1267
Leu Ser Met Thr Ile Met Ile Gln Ile Phe Val Val Val Ala Gly Ile
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tct tca ctg atg ccc atg aca ggt ttg acc act ccg ttt atg tcc cag 1315
Ser Ser Leu Met Pro Met Thr Gly Leu Thr Thr Pro Phe Met Ser Gln
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Gly Gly Ser Ser Leu Met Ala Asn Tyr Ile Leu Met Ala Ile Ile Leu
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cgt att tct gac agt gcc cgc cga cct gtc atg tcc aag caa gca tcg 1411
Arg Ile Ser Asp Ser Ala Arg Arg Pro Val Met Ser Lys Gln Ala Ser
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Leu Ala Met Gly Asn Glu Leu Gly Thr His Ile Leu Met Leu Met Gly
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Gly Tyr Ile Gly Ile Phe Ile Val Ala His Leu Ala Met Ala Trp Val
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Ala Pro Phe Ala Asp Gln Ile Met Leu Pro Val Val Ala Val Leu Asn
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Gly Ile Gly Leu Val Met Ile Tyr Arg Leu Asp Glu Ala Thr Gly Tyr
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Ser Thr Val Asn Ser Gln Leu Met Trp Thr Val Val Gly Val Thr Leu
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Pro	Val	Val	His	Ser	Asp	Phe	Ile	Leu	Ala	Ala	Ile	Gly	Glu	Glu	Leu		
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 Met Glu Asp Thr Thr
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 Trp Glu Asp Thr Pro Ile Ala Ala Ala Arg Arg Ala Ala Gln Val
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 Val Asn Leu Ala Ala Ser Leu Ala Ile His Gly Leu Lys Val Leu Val
 55 60 65
 gtg gat ttg gat ccg cag gga aat gcg tcg aca gcg ttg ggt gtc gag 355
 Val Asp Leu Asp Pro Gln Gly Asn Ala Ser Thr Ala Leu Gly Val Glu
 70 75 80 85
 cac cgc tct gga acc ttg tca tct tat gaa cta ctg atc ggt gaa tgc 403
 His Arg Ser Gly Thr Leu Ser Ser Tyr Glu Leu Leu Ile Gly Glu Cys
 90 95 100
 act gct gat gaa gca atg cag cca tcc aca gct aac gaa aac ctc ttc 451
 Thr Ala Asp Glu Ala Met Gln Pro Ser Thr Ala Asn Glu Asn Leu Phe
 105 110 115
 tgc att cca gca acc ctg gat ctt gct ggc gca gaa att gaa ttg gtc 499
 Cys Ile Pro Ala Thr Leu Asp Leu Ala Gly Ala Glu Ile Glu Leu Val
 120 125 130
 agc ttg gtc cgc cgc gaa tac cgt ttg gcg gat gcg ttg ggc cgt gag 547
 Ser Leu Val Arg Arg Glu Tyr Arg Leu Ala Asp Ala Leu Gly Arg Glu
 135 140 145
 ttc att gac aag cac gat ttt gat tac atg atc att gac tgc cca ccg 595
 Phe Ile Asp Lys His Asp Phe Asp Tyr Met Ile Ile Asp Cys Pro Pro
 150 155 160 165

tct ttg ggt ctg ctc acc att aac gcc atg acc gcg gtg aat gaa gtg 643
 Ser Leu Gly Leu Leu Thr Ile Asn Ala Met Thr Ala Val Asn Glu Val
 170 175 180

ctc att ccg atc cag tgt gag tac tac gct ctg gag ggc gtg ggc cag 691
 Leu Ile Pro Ile Gln Cys Glu Tyr Tyr Ala Leu Glu Gly Val Gly Gln
 185 190 195

cta ctg aac aac atc act atg ttg cgt cag cac ctg aac cgc cag ctg 739
 Leu Leu Asn Asn Ile Thr Met Leu Arg Gln His Leu Asn Arg Gln Leu
 200 205 210

cat att tcc gcg atc ttg ctg acc atg tat gac gcc cgc acc aac ctc 787
 His Ile Ser Ala Ile Leu Leu Thr Met Tyr Asp Ala Arg Thr Asn Leu
 215 220 225

gca gaa cag gtg gcc aca gag gtt aat gat cac ttc ggt gac gtg gtg 835
 Ala Glu Gln Val Ala Thr Glu Val Asn Asp His Phe Gly Asp Val Val
 230 235 240 245

ttg ggt aac aag att cca cgt tca gtg aag gtg tct gaa gct cct ggc 883
 Leu Gly Asn Lys Ile Pro Arg Ser Val Lys Val Ser Glu Ala Pro Gly
 250 255 260

tat ggg cag act gtc att gaa tat gat cca ggt tcc agg ggc gcc atg 931
 Tyr Gly Gln Thr Val Ile Glu Tyr Asp Pro Gly Ser Arg Gly Ala Met
 265 270 275

gcg tat ttg gat gct gct aaa gaa ttg gcc act cgt ggc gat tac ttg 979
 Ala Tyr Leu Asp Ala Ala Lys Glu Leu Ala Thr Arg Gly Asp Tyr Leu
 280 285 290

cct agc gat gaa tcc ggt ccg atc ggc cta aaa cct gcg aaa 1021
 Pro Ser Asp Glu Ser Gly Pro Ile Gly Leu Lys Pro Ala Lys
 295 300 305

tagcagtaaaa cttctttgaa tac 1044

<210> 118

<211> 307

<212> PRT

<213> Corynebacterium glutamicum

<400> 118

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Arg Ala Ala Gln Val Met Thr Pro Asn Ser Leu Thr Leu Pro Lys Pro
 20 25 30

Lys Glu Pro Arg Leu Ile Thr Ile Ala Asn Gln Lys Gly Gly Val Gly
 35 40 45

Lys Thr Thr Ser Thr Val Asn Leu Ala Ala Ser Leu Ala Ile His Gly
 50 55 60

Leu Lys Val Leu Val Val Asp Leu Asp Pro Gln Gly Asn Ala Ser Thr
 65 70 75 80

Ala Leu Gly Val Glu His Arg Ser Gly Thr Leu Ser Ser Tyr Glu Leu

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Val Ser Asp Ala Gly
1 5

aag aag gac tct tcc aag gtg gag atc gga ctg acc ggt cga ccc ctg	163
Lys Lys Asp Ser Ser Lys Val Glu Ile Gly Leu Thr Gly Arg Pro Leu	
10 15 20	
cgc gag ttg cct gag cca tct cct ttg gaa aaa cat ggc cca gca acg	211
Arg Glu Leu Pro Glu Pro Ser Pro Leu Glu Lys His Gly Pro Ala Thr	
25 30 35	
atc att gcc atg gcg aat caa aaa ggt ggc gtt ggt aaa acc acg tcc	259
Ile Ile Ala Met Ala Asn Gln Lys Gly Gly Val Gly Lys Thr Thr Ser	
40 45 50	
acc atc aac ctc gga gca tgc ctt gca gag gcg gga cgt aaa gtc ctg	307
Thr Ile Asn Leu Gly Ala Cys Leu Ala Glu Ala Gly Arg Lys Val Leu	
55 60 65	
ctc gtt gac ttg gat ccg caa ggt gcg ttg act gct ggt ttg gga atc	355
Leu Val Asp Leu Asp Pro Gln Gly Ala Leu Thr Ala Gly Leu Gly Ile	
70 75 80 85	
cac tac gac gac gtg gat atc acc gtg tat gac ctc atg gtg gac aac	403
His Tyr Asp Asp Val Asp Ile Thr Val Tyr Asp Leu Met Val Asp Asn	
90 95 100	
aat tcc acc att gat cag gcg atc cac cac act ggt ctt cct gat ctg	451
Asn Ser Thr Ile Asp Gln Ala Ile His His Thr Gly Leu Pro Asp Leu	
105 110 115	
gat gtc gtt cct gca aat att gac ttg tcc gct gca gaa att cag ctg	499
Asp Val Val Pro Ala Asn Ile Asp Leu Ser Ala Ala Glu Ile Gln Leu	
120 125 130	
gtc aat gaa gtt ggt cgt gaa caa aca ctt gcc agg gcg ctg cgt cct	547
Val Asn Glu Val Gly Arg Glu Gln Thr Leu Ala Arg Ala Leu Arg Pro	
135 140 145	
gtc atg aag gac tac gac ttc atc atc ctt gat tgt cag cca tca ctt	595
Val Met Lys Asp Tyr Asp Phe Ile Ile Leu Asp Cys Gln Pro Ser Leu	
150 155 160 165	
ggt ctt ttg acg gtg aac gct ttg gcg tgc gcg cac ggg gtt atc atc	643
Gly Leu Leu Thr Val Asn Ala Leu Ala Cys Ala His Gly Val Ile Ile	
170 175 180	
ccg atg gag tgc gag aac tta tca ctg cgc ggc ctc gca ttg ctc aca	691
Pro Met Glu Cys Glu Asn Leu Ser Leu Arg Gly Leu Ala Leu Leu Thr	
185 190 195	
gac acc gtg gaa aaa gtt gcc gat cgg ttg aac ttc gat ctg gaa atc	739
Asp Thr Val Glu Lys Val Ala Asp Arg Leu Asn Phe Asp Leu Glu Ile	
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ctc ggc atc ttg gtc	754
Leu Gly Ile Leu Val	
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<210> 120

<211> 218

<212> PRT

<213> Corynebacterium glutamicum

<400> 120

Val Ser Asp Ala Gly Lys Lys Asp Ser Ser Lys Val Glu Ile Gly Leu
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Thr Gly Arg Pro Leu Arg Glu Leu Pro Glu Pro Ser Pro Leu Glu Lys
20 25 30

His Gly Pro Ala Thr Ile Ile Ala Met Ala Asn Gln Lys Gly Gly Val
35 40 45

Gly Lys Thr Thr Ser Thr Ile Asn Leu Gly Ala Cys Leu Ala Glu Ala
50 55 60

Gly Arg Lys Val Leu Leu Val Asp Leu Asp Pro Gln Gly Ala Leu Thr
65 70 75 80

Ala Gly Leu Gly Ile His Tyr Asp Asp Val Asp Ile Thr Val Tyr Asp
85 90 95

Leu Met Val Asp Asn Asn Ser Thr Ile Asp Gln Ala Ile His His Thr
100 105 110

Gly Leu Pro Asp Leu Asp Val Val Pro Ala Asn Ile Asp Leu Ser Ala
115 120 125

Ala Glu Ile Gln Leu Val Asn Glu Val Gly Arg Glu Gln Thr Leu Ala
130 135 140

Arg Ala Leu Arg Pro Val Met Lys Asp Tyr Asp Phe Ile Ile Leu Asp
145 150 155 160

Cys Gln Pro Ser Leu Gly Leu Leu Thr Val Asn Ala Leu Ala Cys Ala
165 170 175

His Gly Val Ile Ile Pro Met Glu Cys Glu Asn Leu Ser Leu Arg Gly
180 185 190

Leu Ala Leu Leu Thr Asp Thr Val Glu Lys Val Ala Asp Arg Leu Asn
195 200 205

Phe Asp Leu Glu Ile Leu Gly Ile Leu Val
210 215

<210> 121

<211> 721

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(721)

<223> FRXA01603

<400> 121

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actataaaaag gcagtcctag tcaaggaaga aggttttgact gtg agt gat gca ggg 115
Val Ser Asp Ala Gly

	1	5	
aag aag gac tct tcc aag gtg gag atc gga ctg acc ggt cga ccc ctg			163
Lys Lys Asp Ser Ser Lys Val Glu Ile Gly Leu Thr Gly Arg Pro Leu	10	15 20	
cgc gag ttg cct gag cca tct cct ttg gaa aaa cat ggc cca gca acg			211
Arg Glu Leu Pro Glu Pro Ser Pro Leu Glu Lys His Gly Pro Ala Thr	25 30	35	
atc att gcc atg gcg aat caa aaa ggt ggc gtt ggt aaa acc acg tcc			259
Ile Ile Ala Met Ala Asn Gln Lys Gly Gly Val Gly Lys Thr Thr Ser	40 45	50	
acc atc aac ctc gga gca tgc ctt gca gag gcg gga cgt aaa gtc ctg			307
Thr Ile Asn Leu Gly Ala Cys Leu Ala Glu Ala Gly Arg Lys Val Leu	55 60	65	
ctc gtt gac ttg gat ccg caa ggt gcg ttg act gct ggt ttg gga atc			355
Leu Val Asp Leu Asp Pro Gln Gly Ala Leu Thr Ala Gly Leu Gly Ile	70 75	80 85	
cac tac gac gac gtg gat atc acc gtg tat gac ctc atg gtg gac aac			403
His Tyr Asp Asp Val Asp Ile Thr Val Tyr Asp Leu Met Val Asp Asn	90 95	100	
aat tcc acc att gat cag gcg atc cac cac act ggt ctt cct gat ctg			451
Asn Ser Thr Ile Asp Gln Ala Ile His His Thr Gly Leu Pro Asp Leu	105 110	115	
gat gtc gtt cct gca aat att gac ttg tcc gct gca gaa att cag ctg			499
Asp Val Val Pro Ala Asn Ile Asp Leu Ser Ala Ala Glu Ile Gln Leu	120 125	130	
gtc aat gaa gtt ggt cgt gaa caa aca ctt gcc agg gcg ctg cgt cct			547
Val Asn Glu Val Gly Arg Glu Gln Thr Leu Ala Arg Ala Leu Arg Pro	135 140	145	
gtc atg aag gac tac gac ttc atc atc ctt gat tgt cag cca tca ctt			595
Val Met Lys Asp Tyr Asp Phe Ile Ile Leu Asp Cys Gln Pro Ser Leu	150 155	160 165	
ggt ctt ttg acg gtg aac gct ttg gcg tgc gcg cac ggg gtt atc atc			643
Gly Leu Leu Thr Val Asn Ala Leu Ala Cys Ala His Gly Val Ile Ile	170 175	180	
ccg atg gag tgc gag tac ttc tca ctg cgt ggc ctc gca ttg ctc aca			691
Pro Met Glu Cys Glu Tyr Phe Ser Leu Arg Gly Leu Ala Leu Leu Thr	185 190	195	
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Asp Thr Val Glu Lys Val Ala Asp Arg Leu	200 205		

<210> 122

<211> 207

<212> PRT

<213> Corynebacterium glutamicum

<400> 122

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 His Gly Pro Ala Thr Ile Ile Ala Met Ala Asn Gln Lys Gly Gly Val
 35 40 45
 Gly Lys Thr Thr Ser Thr Ile Asn Leu Gly Ala Cys Leu Ala Glu Ala
 50 55 60
 Gly Arg Lys Val Leu Leu Val Asp Leu Asp Pro Gln Gly Ala Leu Thr
 65 70 75 80
 Ala Gly Leu Gly Ile His Tyr Asp Asp Val Asp Ile Thr Val Tyr Asp
 85 90 95
 Leu Met Val Asp Asn Asn Ser Thr Ile Asp Gln Ala Ile His His Thr
 100 105 110
 Gly Leu Pro Asp Leu Asp Val Val Pro Ala Asn Ile Asp Leu Ser Ala
 115 120 125
 Ala Glu Ile Gln Leu Val Asn Glu Val Gly Arg Glu Gln Thr Leu Ala
 130 135 140
 Arg Ala Leu Arg Pro Val Met Lys Asp Tyr Asp Phe Ile Ile Leu Asp
 145 150 155 160
 Cys Gln Pro Ser Leu Gly Leu Leu Thr Val Asn Ala Leu Ala Cys Ala
 165 170 175
 His Gly Val Ile Ile Pro Met Glu Cys Glu Tyr Phe Ser Leu Arg Gly
 180 185 190
 Leu Ala Leu Leu Thr Asp Thr Val Glu Lys Val Ala Asp Arg Leu
 195 200 205

<210> 123

<211> 963

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(940)

<223> RXN00818

<400> 123

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 Val Lys His Pro Asp
 1 5

ccc gcc caa aaa gta gag ggc acc act gcg acc acc ccc aca aag gtg 163
 Pro Ala Gln Lys Val Glu Gly Thr Thr Ala Thr Thr Pro Thr Lys Val
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gct gct ttt ttc gat ctg gac aag acc atc atc gcc atg agt tcc acc	211
Ala Ala Phe Phe Asp Leu Asp Lys Thr Ile Ile Ala Met Ser Ser Thr	
25 30 35	
tac gcc tac ggc cgt gag ttc atg aac agc ggg ctc atc tcc cct gtc	259
Tyr Ala Tyr Gly Arg Glu Phe Met Asn Ser Gly Leu Ile Ser Pro Val	
40 45 50	
gaa gcc ctg caa tta agc ctc gcg caa gca acg tac atg ttc gcc ggc	307
Glu Ala Leu Gln Leu Ser Leu Ala Gln Ala Thr Tyr Met Phe Ala Gly	
55 60 65	
cac acc agt gaa caa atg gac aac acc cgc gac caa ctc acc gcc atg	355
His Thr Ser Glu Gln Met Asp Asn Thr Arg Asp Gln Leu Thr Ala Met	
70 75 80 85	
atc cgc ggc tgg gaa gtc caa cag gtg cgc tcg atc gcg gag gaa acc	403
Ile Arg Gly Trp Glu Val Gln Gln Val Arg Ser Ile Ala Glu Glu Thr	
90 95 100	
atg cat tcg gtg gtc act ccc acc atc tac gca gag gcc cgc gaa ctg	451
Met His Ser Val Val Thr Pro Thr Ile Tyr Ala Glu Ala Arg Glu Leu	
105 110 115	
atc gag cac cac cag gag ctc ggc cac gat gtc atc atc att tcc gcc	499
Ile Glu His His Gln Glu Leu Gly His Asp Val Ile Ile Ile Ser Ala	
120 125 130	
tct gtg aaa gaa ctg gtg gaa ccc atc gcc cgc gaa ctg ggt gta cat	547
Ser Val Lys Glu Leu Val Glu Pro Ile Ala Arg Glu Leu Gly Val His	
135 140 145	
aaa act gtc acc acc gtg ctt gaa gcc cac gac ggt atg tac acc ggt	595
Lys Thr Val Thr Thr Val Leu Glu Ala His Asp Gly Met Tyr Thr Gly	
150 155 160 165	
gaa gtg ctg ttt tac tgc aaa ggc gac gct aaa gcg cag tcc atc ctg	643
Glu Val Leu Phe Tyr Cys Lys Gly Asp Ala Lys Ala Gln Ser Ile Leu	
170 175 180	
gat ctc gcc gag gcg aac aat tac gac ctt tcc tta agc ttc gcc tac	691
Asp Leu Ala Glu Ala Asn Asn Tyr Asp Leu Ser Leu Ser Phe Ala Tyr	
185 190 195	
tcc gat tcc ttc acg gac ctg ccc atg ttg gaa gct gtc ggc aac ccg	739
Ser Asp Ser Phe Thr Asp Leu Pro Met Leu Glu Ala Val Gly Asn Pro	
200 205 210	
gcc gcc gtc aac ccc gac cgc gcg ctg aag aaa atc gcc ctt gaa cag	787
Ala Ala Val Asn Pro Asp Arg Ala Leu Lys Lys Ile Ala Leu Glu Gln	
215 220 225	
ggg tgg aaa atc tta agc ttc aaa aac cct gaa ccg ctg ttc caa atg	835
Gly Trp Lys Ile Leu Ser Phe Lys Asn Pro Glu Pro Leu Phe Gln Met	
230 235 240 245	
ccc agc acc cgc gac gtc ggc atc gga acc gga gtt gtt gcc ggc atc	883
Pro Ser Thr Arg Asp Val Gly Ile Gly Thr Gly Val Val Ala Gly Ile	
250 255 260	
gca gct gtt aca gca ggt agt atc tgg tgg atg aaa cgc gca cgg cgc	931

Ala Ala Val Thr Ala Gly Ser Ile Trp Trp Met Lys Arg Ala Arg Arg
 265 270 275

gga tcg gcc tgagcctcac ctgacagcag tta
 Gly Ser Ala
 280

963

<210> 124
 <211> 280
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 124
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 20 25 30
 Ala Met Ser Ser Thr Tyr Ala Tyr Gly Arg Glu Phe Met Asn Ser Gly
 35 40 45
 Leu Ile Ser Pro Val Glu Ala Leu Gln Leu Ser Leu Ala Gln Ala Thr
 50 55 60
 Tyr Met Phe Ala Gly His Thr Ser Glu Gln Met Asp Asn Thr Arg Asp
 65 70 75 80
 Gln Leu Thr Ala Met Ile Arg Gly Trp Glu Val Gln Gln Val Arg Ser
 85 90 95
 Ile Ala Glu Glu Thr Met His Ser Val Val Thr Pro Thr Ile Tyr Ala
 100 105 110
 Glu Ala Arg Glu Leu Ile Glu His His Gln Glu Leu Gly His Asp Val
 115 120 125
 Ile Ile Ile Ser Ala Ser Val Lys Glu Leu Val Glu Pro Ile Ala Arg
 130 135 140
 Glu Leu Gly Val His Lys Thr Val Thr Thr Val Leu Glu Ala His Asp
 145 150 155 160
 Gly Met Tyr Thr Gly Glu Val Leu Phe Tyr Cys Lys Gly Asp Ala Lys
 165 170 175
 Ala Gln Ser Ile Leu Asp Leu Ala Glu Ala Asn Asn Tyr Asp Leu Ser
 180 185 190
 Leu Ser Phe Ala Tyr Ser Asp Ser Phe Thr Asp Leu Pro Met Leu Glu
 195 200 205
 Ala Val Gly Asn Pro Ala Ala Val Asn Pro Asp Arg Ala Leu Lys Lys
 210 215 220

Ile Ala Leu Glu Gln Gly Trp Lys Ile Leu Ser Phe Lys Asn Pro Glu
 225 230 235 240
 Pro Leu Phe Gln Met Pro Ser Thr Arg Asp Val Gly Ile Gly Thr Gly
 245 250 255

Val Val Ala Gly Ile Ala Ala Val Thr Ala Gly Ser Ile Trp Trp Met
 260 265 270

Lys Arg Ala Arg Arg Gly Ser Ala
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<210> 125

<211> 2898

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2875)

<223> RXN03028

<400> 125

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 Met Phe Glu Arg Phe
 1 5

acc gat cgt gca cgc cgc gtg att gtg ctc gcg cag gaa gag gcg cgc 163
 Thr Asp Arg Ala Arg Arg Val Ile Val Leu Ala Gln Glu Glu Ala Arg
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atg ctc aac cac aat tac atc ggc acg gag cac att ctc ctc ggc ctc 211
 Met Leu Asn His Asn Tyr Ile Gly Thr Glu His Ile Leu Leu Gly Leu
 25 30 35

att cac gag ggc gag ggc gtt gca gcc aag gct ttg gaa tcc atg gga 259
 Ile His Glu Gly Glu Gly Val Ala Ala Lys Ala Leu Glu Ser Met Gly
 40 45 50

att tcc ctg gac gcc gtc cgc cag gaa gtc gaa gag att atc ggc cag 307
 Ile Ser Leu Asp Ala Val Arg Gln Glu Val Glu Glu Ile Ile Gly Gln
 55 60 65

ggc tcc cag ccc acc acc ggc cac att cct ttt act cca cgt gcc aag 355
 Gly Ser Gln Pro Thr Thr Gly His Ile Pro Phe Thr Pro Arg Ala Lys
 70 75 80 85

aag gtc ctg gag ctc agc ctc cgc gaa ggc cta caa atg gga cac aag 403
 Lys Val Leu Glu Leu Ser Leu Arg Glu Gly Leu Gln Met Gly His Lys
 90 95 100

tac atc ggt act gag ttc ctg ctt ctc ggt ttg atc cgt gag ggc gag 451
 Tyr Ile Gly Thr Glu Phe Leu Leu Leu Gly Leu Ile Arg Glu Gly Glu
 105 110 115

ggc gtt gct gcc cag gtc ctg gtc aag ctt ggt gct gat ctg cca cgc 499
 Gly Val Ala Ala Gln Val Leu Val Lys Leu Gly Ala Asp Leu Pro Arg
 120 125 130

gtg cgt cag caa gtt att cag ctt ctc tcc ggc tac gaa ggt ggc cag 547
 Val Arg Gln Gln Val Ile Gln Leu Leu Ser Gly Tyr Glu Gly Gly Gln
 135 140 145

ggc gga tcc cca gag ggc ggc cag ggc gcc cct act ggc ggt gac gct Gly Gly Ser Pro Glu Gly Gly Gln Gly Ala Pro Thr Gly Gly Asp Ala 150 155 160 165	595
gtt ggt gca gga gct gct cct ggc ggt cgt cca tct tcg ggc agc cca Val Gly Ala Gly Ala Pro Gly Gly Arg Pro Ser Ser Gly Ser Pro 170 175 180	643
ggc gag cgt tct acc tct ttg gtc ctt gac cag ttc ggc cgc aac ctc Gly Glu Arg Ser Thr Ser Leu Val Leu Asp Gln Phe Gly Arg Asn Leu 185 190 195	691
acc cag gct gca aag gac ggc aag ctg gat cca gtt gtt ggt cgc gat Thr Gln Ala Ala Lys Asp Gly Lys Leu Asp Pro Val Val Gly Arg Asp 200 205 210	739
aag gaa atc gag cgc atc atg cag gtg ctc tcc cgt cgt acc aag aac Lys Glu Ile Glu Arg Ile Met Gln Val Leu Ser Arg Arg Thr Lys Asn 215 220 225	787
aac cca gtt ctt att ggt gag cca ggt gtt ggt aag acc gca gtt gtt Asn Pro Val Leu Ile Gly Glu Pro Gly Val Gly Lys Thr Ala Val Val 230 235 240 245	835
gaa ggt ctt gca cta gac att gtt aac ggc aag gtt cca gag acc ctc Glu Gly Leu Ala Leu Asp Ile Val Asn Gly Lys Val Pro Glu Thr Leu 250 255 260	883
aag gac aag cag gtt tac tcc ctt gac tta ggt tcc ctg gtt gca ggt Lys Asp Lys Gln Val Tyr Ser Leu Asp Leu Gly Ser Leu Val Ala Gly 265 270 275	931
tcc cgt tac cgc ggt gac ttc gaa gag cga ctg aag aag gtc ctc aag Ser Arg Tyr Arg Gly Asp Phe Glu Glu Arg Leu Lys Lys Val Leu Lys 280 285 290	979
gag att aac cag cgc ggc gac atc atc ctg ttt atc gat gag atc cac Glu Ile Asn Gln Arg Gly Asp Ile Ile Leu Phe Ile Asp Glu Ile His 295 300 305	1027
acc ctc gtg ggt gca ggt gca gca gaa ggc gca atc gac gct gcc tcc Thr Leu Val Gly Ala Gly Ala Ala Glu Gly Ala Ile Asp Ala Ala Ser 310 315 320 325	1075
ctg ctt aag cca aag ctt gcc cgc ggt gaa ctg cag acc att ggt gca Leu Leu Lys Pro Lys Leu Ala Arg Gly Glu Leu Gln Thr Ile Gly Ala 330 335 340	1123
acc acc ctg gat gag tac cgt aag cac att gaa aag gac gca gct ctt Thr Thr Leu Asp Glu Tyr Arg Lys His Ile Glu Lys Asp Ala Ala Leu 345 350 355	1171
gag cgt cgt ttc cag cca gtg cag gtt cca gag cct tcg gtt gat ctc Glu Arg Arg Phe Gln Pro Val Gln Val Pro Glu Pro Ser Val Asp Leu 360 365 370	1219
acc gtt gag atc ttg aag ggt ctg cgc gac cgc tac gaa gct cac cac Thr Val Glu Ile Leu Lys Gly Leu Arg Asp Arg Tyr Glu Ala His His 375 380 385	1267
cgc gta tcc atc acc gat ggt gct ctt act gca gca gct cag ctt gct	1315

Arg	Val	Ser	Ile	Thr	Asp	Gly	Ala	Leu	Thr	Ala	Ala	Ala	Gln	Leu	Ala		
390					395					400					405		
gat	cgc	tac	atc	aac	gac	cgc	ttc	ttg	cca	gat	aag	gcc	gtt	gac	ctc	1363	
Asp	Arg	Tyr	Ile	Asn	Asp	Arg	Phe	Leu	Pro	Asp	Lys	Ala	Val	Asp	Leu		
				410					415					420			
atc	gat	gag	gct	ggc	gcc	cgc	atg	cgc	atc	aag	cgc	atg	acc	gca	cct	1411	
Ile	Asp	Glu	Ala	Gly	Ala	Arg	Met	Arg	Ile	Lys	Arg	Met	Thr	Ala	Pro		
			425					430					435				
tcc	tcc	ctc	cgc	gag	gtt	gat	gag	cgt	atc	gct	gat	gtt	cgc	cgt	gag	1459	
Ser	Ser	Leu	Arg	Glu	Val	Asp	Glu	Arg	Ile	Ala	Asp	Val	Arg	Arg	Glu		
		440					445					450					
aag	gaa	gca	gcg	atc	gat	gct	cag	gac	ttt	gag	aag	gca	gca	ggg	ctt	1507	
Lys	Glu	Ala	Ala	Ile	Asp	Ala	Gln	Asp	Phe	Glu	Lys	Ala	Ala	Gly	Leu		
	455					460					465						
cgc	gat	aag	gag	cgc	aag	ctc	ggc	gaa	gag	cgt	tca	gag	aag	gaa	aag	1555	
Arg	Asp	Lys	Glu	Arg	Lys	Leu	Gly	Glu	Glu	Arg	Ser	Glu	Lys	Glu	Lys		
470					475					480					485		
cag	tgg	cgc	tcc	ggc	gac	ctc	gag	gac	atc	gct	gag	gtt	ggc	gaa	gag	1603	
Gln	Trp	Arg	Ser	Gly	Asp	Leu	Glu	Asp	Ile	Ala	Glu	Val	Gly	Glu	Glu		
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cag	atc	gca	gaa	gta	ctg	gcc	aac	tgg	act	ggg	att	cct	gtc	ttc	aag	1651	
Gln	Ile	Ala	Glu	Val	Leu	Ala	Asn	Trp	Thr	Gly	Ile	Pro	Val	Phe	Lys		
			505					510					515				
ctc	acc	gaa	gct	gaa	tct	tca	cgc	ctg	ctc	aac	atg	gaa	gaa	gag	ttg	1699	
Leu	Thr	Glu	Ala	Glu	Ser	Ser	Arg	Leu	Leu	Asn	Met	Glu	Glu	Glu	Leu		
		520					525					530					
cac	aag	cgc	atc	atc	gga	cag	gat	gaa	gct	gtc	aag	gct	gtc	tcc	cgt	1747	
His	Lys	Arg	Ile	Ile	Gly	Gln	Asp	Glu	Ala	Val	Lys	Ala	Val	Ser	Arg		
	535					540					545						
gcg	atc	cgt	cgt	acc	cgt	gca	ggg	ctg	aag	gat	cct	aag	cgt	cct	tcc	1795	
Ala	Ile	Arg	Arg	Thr	Arg	Ala	Gly	Leu	Lys	Asp	Pro	Lys	Arg	Pro	Ser		
550					555					560					565		
ggc	tcc	ttc	atc	ttc	gct	ggg	cca	tcc	ggc	gtt	ggg	aag	acc	gag	ctg	1843	
Gly	Ser	Phe	Ile	Phe	Ala	Gly	Pro	Ser	Gly	Val	Gly	Lys	Thr	Glu	Leu		
				570					575					580			
tcc	aag	gct	ctc	gca	gga	ttc	ctc	ttc	ggg	gac	gat	gat	tcc	ctc	atc	1891	
Ser	Lys	Ala	Leu	Ala	Gly	Phe	Leu	Phe	Gly	Asp	Asp	Asp	Ser	Leu	Ile		
			585					590					595				
caa	atc	gac	atg	ggg	gag	ttc	cac	gac	cgc	ttc	acc	gcg	tcc	cga	ctt	1939	
Gln	Ile	Asp	Met	Gly	Glu	Phe	His	Asp	Arg	Phe	Thr	Ala	Ser	Arg	Leu		
		600					605					610					
ttc	ggg	gcc	cct	ccg	gga	tac	gtt	ggc	tac	gaa	gaa	ggg	ggc	cag	ctg	1987	
Phe	Gly	Ala	Pro	Pro	Gly	Tyr	Val	Gly	Tyr	Glu	Glu	Gly	Gly	Gln	Leu		
	615					620				625							
acc	gag	aag	gtt	cgc	cgt	aag	cca	ttc	tcc	gtt	gtg	ctt	ttc	gac	gaa	2035	
Thr	Glu	Lys	Val	Arg	Arg	Lys	Pro	Phe	Ser	Val	Val	Leu	Phe	Asp	Glu		

630	635	640	645	
atc gag aag gcc cac aag gag atc tac aac acc ttg ctg cag gtg ttg				2083
Ile Glu Lys Ala His Lys Glu Ile Tyr Asn Thr Leu Leu Gln Val Leu	650	655	660	
gaa gat ggt cgc ctt acc gat ggt cag gga cgc atc gtg gac ttc aag				2131
Glu Asp Gly Arg Leu Thr Asp Gly Gln Gly Arg Ile Val Asp Phe Lys	665	670	675	
aac acc gtc ctg atc ttc acc tcc aac ctg ggc acc gct gac atc tcc				2179
Asn Thr Val Leu Ile Phe Thr Ser Asn Leu Gly Thr Ala Asp Ile Ser	680	685	690	
aag gct gtt ggc ctg ggc ttc tcc gga tcc tcc gag act gac agc gat				2227
Lys Ala Val Gly Leu Gly Phe Ser Gly Ser Ser Glu Thr Asp Ser Asp	695	700	705	
gct cag tac gac cgc atg aag aac aag gtc cac gac gag ctg aag aag				2275
Ala Gln Tyr Asp Arg Met Lys Asn Lys Val His Asp Glu Leu Lys Lys	710	715	720	725
cac ttc cgc cct gag ttc ctg aac cgt att gat gag atc gtg gtc ttc				2323
His Phe Arg Pro Glu Phe Leu Asn Arg Ile Asp Glu Ile Val Val Phe	730	735	740	
cac cag ctc acc aag gat cag atc gtt cag atg gtc gac ctt ctt atc				2371
His Gln Leu Thr Lys Asp Gln Ile Val Gln Met Val Asp Leu Leu Ile	745	750	755	
ggt cgc gtt tcc aac gca ctg gct gag aag gac atg agc atc gaa ctg				2419
Gly Arg Val Ser Asn Ala Leu Ala Glu Lys Asp Met Ser Ile Glu Leu	760	765	770	
act gag aag gcc aag gac ctc ctg gct aac cga ggc ttc gat cca gtt				2467
Thr Glu Lys Ala Lys Asp Leu Leu Ala Asn Arg Gly Phe Asp Pro Val	775	780	785	
ctg ggt gca cga cca ttg cgt cgc acc atc cag cgc gaa att gaa gac				2515
Leu Gly Ala Arg Pro Leu Arg Arg Thr Ile Gln Arg Glu Ile Glu Asp	790	795	800	805
cag atg tcc gag aag atc ctc ttc ggt gaa atc ggc gca ggc gag atc				2563
Gln Met Ser Glu Lys Ile Leu Phe Gly Glu Ile Gly Ala Gly Glu Ile	810	815	820	
gtc acc gtt gac gtc gaa ggc tgg gac ggc gag tcc aag gac acc gac				2611
Val Thr Val Asp Val Glu Gly Trp Asp Gly Glu Ser Lys Asp Thr Asp	825	830	835	
cgt gcg aag ttc acc ttc aca cca cgt cca aag cca atg cca gaa ggt				2659
Arg Ala Lys Phe Thr Phe Thr Pro Arg Pro Lys Pro Met Pro Glu Gly	840	845	850	
aag ttc tct gag atc tct gtc gag gct gcg gaa gca att caa gat gta				2707
Lys Phe Ser Glu Ile Ser Val Glu Ala Ala Glu Ala Ile Gln Asp Val	855	860	865	
gat tct gca gct gac ggc gat gtc cca gaa acc gat tca ctt tcc gac				2755
Asp Ser Ala Ala Asp Gly Asp Val Pro Glu Thr Asp Ser Leu Ser Asp	870	875	880	885

att gac ctt gaa acc ctt gaa aag ttt gag gaa gat gta gaa aac ggc 2803
 Ile Asp Leu Glu Thr Leu Glu Lys Phe Glu Glu Asp Val Glu Asn Gly
 890 895 900

acc gac att gat cag gtg tcc ggt gac tac tac ggc acc gat gat cag 2851
 Thr Asp Ile Asp Gln Val Ser Gly Asp Tyr Tyr Gly Thr Asp Asp Gln
 905 910 915

gga ggc act gct cca agc aag gag tagcaacctt ttgaaaaagg gcc 2898
 Gly Gly Thr Ala Pro Ser Lys Glu
 920 925

<210> 126

<211> 925

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 126

Met Phe Glu Arg Phe Thr Asp Arg Ala Arg Arg Val Ile Val Leu Ala
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Gln Glu Glu Ala Arg Met Leu Asn His Asn Tyr Ile Gly Thr Glu His
 20 25 30

Ile Leu Leu Gly Leu Ile His Glu Gly Glu Gly Val Ala Ala Lys Ala
 35 40 45

Leu Glu Ser Met Gly Ile Ser Leu Asp Ala Val Arg Gln Glu Val Glu
 50 55 60

Glu Ile Ile Gly Gln Gly Ser Gln Pro Thr Thr Gly His Ile Pro Phe
 65 70 75 80

Thr Pro Arg Ala Lys Lys Val Leu Glu Leu Ser Leu Arg Glu Gly Leu
 85 90 95

Gln Met Gly His Lys Tyr Ile Gly Thr Glu Phe Leu Leu Leu Gly Leu
 100 105 110

Ile Arg Glu Gly Glu Gly Val Ala Ala Gln Val Leu Val Lys Leu Gly
 115 120 125

Ala Asp Leu Pro Arg Val Arg Gln Gln Val Ile Gln Leu Leu Ser Gly
 130 135 140

Tyr Glu Gly Gly Gln Gly Gly Ser Pro Glu Gly Gly Gln Gly Ala Pro
 145 150 155 160

Thr Gly Gly Asp Ala Val Gly Ala Gly Ala Ala Pro Gly Gly Arg Pro
 165 170 175

Ser Ser Gly Ser Pro Gly Glu Arg Ser Thr Ser Leu Val Leu Asp Gln
 180 185 190

Phe Gly Arg Asn Leu Thr Gln Ala Ala Lys Asp Gly Lys Leu Asp Pro
 195 200 205

Val Val Gly Arg Asp Lys Glu Ile Glu Arg Ile Met Gln Val Leu Ser
 210 215 220

Arg Arg Thr Lys Asn Asn Pro Val Leu Ile Gly Glu Pro Gly Val Gly
 225 230 235 240
 Lys Thr Ala Val Val Glu Gly Leu Ala Leu Asp Ile Val Asn Gly Lys
 245 250 255
 Val Pro Glu Thr Leu Lys Asp Lys Gln Val Tyr Ser Leu Asp Leu Gly
 260 265 270
 Ser Leu Val Ala Gly Ser Arg Tyr Arg Gly Asp Phe Glu Glu Arg Leu
 275 280 285
 Lys Lys Val Leu Lys Glu Ile Asn Gln Arg Gly Asp Ile Ile Leu Phe
 290 295 300
 Ile Asp Glu Ile His Thr Leu Val Gly Ala Gly Ala Ala Glu Gly Ala
 305 310 315 320
 Ile Asp Ala Ala Ser Leu Leu Lys Pro Lys Leu Ala Arg Gly Glu Leu
 325 330 335
 Gln Thr Ile Gly Ala Thr Thr Leu Asp Glu Tyr Arg Lys His Ile Glu
 340 345 350
 Lys Asp Ala Ala Leu Glu Arg Arg Phe Gln Pro Val Gln Val Pro Glu
 355 360 365
 Pro Ser Val Asp Leu Thr Val Glu Ile Leu Lys Gly Leu Arg Asp Arg
 370 375 380
 Tyr Glu Ala His His Arg Val Ser Ile Thr Asp Gly Ala Leu Thr Ala
 385 390 395 400
 Ala Ala Gln Leu Ala Asp Arg Tyr Ile Asn Asp Arg Phe Leu Pro Asp
 405 410 415
 Lys Ala Val Asp Leu Ile Asp Glu Ala Gly Ala Arg Met Arg Ile Lys
 420 425 430
 Arg Met Thr Ala Pro Ser Ser Leu Arg Glu Val Asp Glu Arg Ile Ala
 435 440 445
 Asp Val Arg Arg Glu Lys Glu Ala Ala Ile Asp Ala Gln Asp Phe Glu
 450 455 460
 Lys Ala Ala Gly Leu Arg Asp Lys Glu Arg Lys Leu Gly Glu Glu Arg
 465 470 475 480
 Ser Glu Lys Glu Lys Gln Trp Arg Ser Gly Asp Leu Glu Asp Ile Ala
 485 490 495
 Glu Val Gly Glu Glu Gln Ile Ala Glu Val Leu Ala Asn Trp Thr Gly
 500 505 510

~~Ile Pro Val Phe Lys Leu Thr Glu Ala Glu Ser Ser Arg Leu Leu Asn~~
~~515 520 525~~
 Met Glu Glu Glu Leu His Lys Arg Ile Ile Gly Gln Asp Glu Ala Val
 530 535 540

Lys Ala Val Ser Arg Ala Ile Arg Arg Thr Arg Ala Gly Leu Lys Asp
 545 550 555 560
 Pro Lys Arg Pro Ser Gly Ser Phe Ile Phe Ala Gly Pro Ser Gly Val
 565 570 575
 Gly Lys Thr Glu Leu Ser Lys Ala Leu Ala Gly Phe Leu Phe Gly Asp
 580 585 590
 Asp Asp Ser Leu Ile Gln Ile Asp Met Gly Glu Phe His Asp Arg Phe
 595 600 605
 Thr Ala Ser Arg Leu Phe Gly Ala Pro Pro Gly Tyr Val Gly Tyr Glu
 610 615 620
 Glu Gly Gly Gln Leu Thr Glu Lys Val Arg Arg Lys Pro Phe Ser Val
 625 630 635 640
 Val Leu Phe Asp Glu Ile Glu Lys Ala His Lys Glu Ile Tyr Asn Thr
 645 650 655
 Leu Leu Gln Val Leu Glu Asp Gly Arg Leu Thr Asp Gly Gln Gly Arg
 660 665 670
 Ile Val Asp Phe Lys Asn Thr Val Leu Ile Phe Thr Ser Asn Leu Gly
 675 680 685
 Thr Ala Asp Ile Ser Lys Ala Val Gly Leu Gly Phe Ser Gly Ser Ser
 690 695 700
 Glu Thr Asp Ser Asp Ala Gln Tyr Asp Arg Met Lys Asn Lys Val His
 705 710 715 720
 Asp Glu Leu Lys Lys His Phe Arg Pro Glu Phe Leu Asn Arg Ile Asp
 725 730 735
 Glu Ile Val Val Phe His Gln Leu Thr Lys Asp Gln Ile Val Gln Met
 740 745 750
 Val Asp Leu Leu Ile Gly Arg Val Ser Asn Ala Leu Ala Glu Lys Asp
 755 760 765
 Met Ser Ile Glu Leu Thr Glu Lys Ala Lys Asp Leu Leu Ala Asn Arg
 770 775 780
 Gly Phe Asp Pro Val Leu Gly Ala Arg Pro Leu Arg Arg Thr Ile Gln
 785 790 795 800
 Arg Glu Ile Glu Asp Gln Met Ser Glu Lys Ile Leu Phe Gly Glu Ile
 805 810 815
 Gly Ala Gly Glu Ile Val Thr Val Asp Val Glu Gly Trp Asp Gly Glu
 820 825 830
 Ser Lys Asp Thr Asp Arg Ala Lys Phe Thr Phe Thr Pro Arg Pro Lys
 835 840 845
 Pro Met Pro Glu Gly Lys Phe Ser Glu Ile Ser Val Glu Ala Ala Glu
 850 855 860
 Ala Ile Gln Asp Val Asp Ser Ala Ala Asp Gly Asp Val Pro Glu Thr

865		870		875		880
Asp Ser Leu Ser	Asp Ile Asp Leu Glu Thr Leu Glu Lys Phe Glu Glu					
	885		890			895
Asp Val Glu Asn Gly Thr Asp Ile Asp Gln Val Ser Gly Asp Tyr Tyr						
	900		905			910
Gly Thr Asp Asp Gln Gly Gly Thr Ala Pro Ser Lys Glu						
	915		920			925

<210> 127
 <211> 1104
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1081)
 <223> FRXA02470

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gtgaaagcga atttagaaat aaagaattaa ggggagagac	atg ttc gag agg ttt	115
	Met Phe Glu Arg Phe	
	1 5	

acc gat cgt gca cgc cgc gtg att gtg ctc gcg cag gaa gag gcg cgc	163
Thr Asp Arg Ala Arg Val Ile Val Leu Ala Gln Glu Glu Ala Arg	
10 15 20	

atg ctc aac cac aat tac atc ggc acg gag cac att ctc ctc ggc ctc	211
Met Leu Asn His Asn Tyr Ile Gly Thr Glu His Ile Leu Leu Gly Leu	
25 30 35	

att cac gag ggc gag ggc gtt gca gcc aag gct ttg gaa tcc atg gga	259
Ile His Glu Gly Glu Gly Val Ala Ala Lys Ala Leu Glu Ser Met Gly	
40 45 50	

att tcc ctg gac gcc gtc cgc cag gaa gtc gaa gag att atc ggc cag	307
Ile Ser Leu Asp Ala Val Arg Gln Glu Val Glu Glu Ile Ile Gly Gln	
55 60 65	

ggc tcc cag ccc acc acc ggc cac att cct ttt act cca cgt gcc aag	355
Gly Ser Gln Pro Thr Thr Gly His Ile Pro Phe Thr Pro Arg Ala Lys	
70 75 80 85	

aag gtc ctg gag ctc agc ctc cgc gaa ggc cta caa atg gga cac aag	403
Lys Val Leu Glu Leu Ser Leu Arg Glu Gly Leu Gln Met Gly His Lys	
90 95 100	

tac atc ggt act gag ttc ctg ctt ctc ggt ttg atc cgt gag ggc gag	451
Tyr Ile Gly Thr Glu Phe Leu Leu Leu Gly Leu Ile Arg Glu Gly Glu	
105 110 115	

ggc gtt gct gcc cag gtc ctg gtc aag ctt ggt gct gat ctg cca cgc	499
Gly Val Ala Ala Gln Val Leu Val Lys Leu Gly Ala Asp Leu Pro Arg	
120 125 130	

gtg cgt cag caa gtt att cag ctt ctc tcc ggc tac gaa ggt ggc cag 547
Val Arg Gln Gln Val Ile Gln Leu Leu Ser Gly Tyr Glu Gly Gly Gln
135 140 145

ggc gga tcc cca gag ggc ggc cag ggc gcc cct act ggc ggt gac gct 595
Gly Gly Ser Pro Glu Gly Gly Gln Gly Ala Pro Thr Gly Gly Asp Ala
150 155 160 165

gtt ggt gca gga gct gct cct ggc ggt cgt cca tct tcg ggc agc cca 643
Val Gly Ala Gly Ala Ala Pro Gly Gly Arg Pro Ser Ser Gly Ser Pro
170 175 180

ggc gag cgt tct acc tct ttg gtc ctt gac cag ttc ggc cgc aac ctc 691
Gly Glu Arg Ser Thr Ser Leu Val Leu Asp Gln Phe Gly Arg Asn Leu
185 190 195

acc cag gct gca aag gac ggc aag ctg gat cca gtt gtt ggt cgc gat 739
Thr Gln Ala Ala Lys Asp Gly Lys Leu Asp Pro Val Val Gly Arg Asp
200 205 210

aag gaa atc gag cgc atc atg cag gtg ctc tcc cgt cgt acc aag aac 787
Lys Glu Ile Glu Arg Ile Met Gln Val Leu Ser Arg Arg Thr Lys Asn
215 220 225

aac cca gtt ctt att ggt gag cca ggt gtt ggt aag acc gca gtt gtt 835
Asn Pro Val Leu Ile Gly Glu Pro Gly Val Gly Lys Thr Ala Val Val
230 235 240 245

gaa ggt ctt gca cta gac att gtt aac ggc aag gtt cca gag acc ctc 883
Glu Gly Leu Ala Leu Asp Ile Val Asn Gly Lys Val Pro Glu Thr Leu
250 255 260

aag gac aag cag gtt tac tcc ctt gac tta ggt tcc ctg gtt gca ggt 931
Lys Asp Lys Gln Val Tyr Ser Leu Asp Leu Gly Ser Leu Val Ala Gly
265 270 275

tcc cgt tac cgc ggt gac ttc gaa gag cga ctg aag aag gtc ctc aag 979
Ser Arg Tyr Arg Gly Asp Phe Glu Glu Arg Leu Lys Lys Val Leu Lys
280 285 290

gag att aac cag cgc ggc gac atc atc ctg ttt atc gat gag atc cac 1027
Glu Ile Asn Gln Arg Gly Asp Ile Ile Leu Phe Ile Asp Glu Ile His
295 300 305

acc ctc gtg ggt gca ggt gca gca cga agg cgc aat cga cgc tgc ctc 1075
Thr Leu Val Gly Ala Gly Ala Ala Arg Arg Arg Asn Arg Arg Cys Leu
310 315 320 325

cct gct taagccaaag cttgcccgcg gtg 1104
Pro Ala

<210> 128

<211> 327

<212> PRT

<213> Corynebacterium glutamicum

<400> 128

Met Phe Glu Arg Phe Thr Asp Arg Ala Arg Arg Val Ile Val Leu Ala
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Gln Glu Glu Ala Arg Met Leu Asn His Asn Tyr Ile Gly Thr Glu His
 20 25 30
 Ile Leu Leu Gly Leu Ile His Glu Gly Glu Gly Val Ala Ala Lys Ala
 35 40 45
 Leu Glu Ser Met Gly Ile Ser Leu Asp Ala Val Arg Gln Glu Val Glu
 50 55 60
 Glu Ile Ile Gly Gln Gly Ser Gln Pro Thr Thr Gly His Ile Pro Phe
 65 70 75 80
 Thr Pro Arg Ala Lys Lys Val Leu Glu Leu Ser Leu Arg Glu Gly Leu
 85 90 95
 Gln Met Gly His Lys Tyr Ile Gly Thr Glu Phe Leu Leu Leu Gly Leu
 100 105 110
 Ile Arg Glu Gly Glu Gly Val Ala Ala Gln Val Leu Val Lys Leu Gly
 115 120 125
 Ala Asp Leu Pro Arg Val Arg Gln Gln Val Ile Gln Leu Leu Ser Gly
 130 135 140
 Tyr Glu Gly Gly Gln Gly Gly Ser Pro Glu Gly Gly Gln Gly Ala Pro
 145 150 155 160
 Thr Gly Gly Asp Ala Val Gly Ala Gly Ala Ala Pro Gly Gly Arg Pro
 165 170 175
 Ser Ser Gly Ser Pro Gly Glu Arg Ser Thr Ser Leu Val Leu Asp Gln
 180 185 190
 Phe Gly Arg Asn Leu Thr Gln Ala Ala Lys Asp Gly Lys Leu Asp Pro
 195 200 205
 Val Val Gly Arg Asp Lys Glu Ile Glu Arg Ile Met Gln Val Leu Ser
 210 215 220
 Arg Arg Thr Lys Asn Asn Pro Val Leu Ile Gly Glu Pro Gly Val Gly
 225 230 235 240
 Lys Thr Ala Val Val Glu Gly Leu Ala Leu Asp Ile Val Asn Gly Lys
 245 250 255
 Val Pro Glu Thr Leu Lys Asp Lys Gln Val Tyr Ser Leu Asp Leu Gly
 260 265 270
 Ser Leu Val Ala Gly Ser Arg Tyr Arg Gly Asp Phe Glu Glu Arg Leu
 275 280 285
 Lys Lys Val Leu Lys Glu Ile Asn Gln Arg Gly Asp Ile Ile Leu Phe
 290 295 300
~~Ile Asp Glu Ile His Thr Leu Val Gly Ala Gly Ala Ala Arg Arg Arg~~
~~305 310 315 320~~
 Asn Arg Arg Cys Leu Pro Ala
 325

<400> 129															
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atcctgttta tcgatgagat ccacaccctc gtgggtgcag															115
Val Gln His Glu Gly															5
1															
gca atc gac gct gcc tcc ctg ctt aag cca aag ctt gcc cgc ggt gaa															163
Ala Ile Asp Ala Ala Ser Leu Leu Lys Pro Lys Leu Ala Arg Gly Glu															20
10 15															
ctg cag acc att ggt gca acc acc ctg gat gag tac cgt aag cac att															211
Leu Gln Thr Ile Gly Ala Thr Thr Leu Asp Glu Tyr Arg Lys His Ile															35
25 30															
gaa aag gac gca gct ctt gag cgt cgt ttc cag cca gtg cag gtt cca															259
Glu Lys Asp Ala Ala Leu Glu Arg Arg Phe Gln Pro Val Gln Val Pro															50
40 45															
gag cct tcg gtt gat ctc acc gtt gag atc ttg aag ggt ctg cgc gac															307
Glu Pro Ser Val Asp Leu Thr Val Glu Ile Leu Lys Gly Leu Arg Asp															65
55 60															
cgc tac gaa gct cac cac cgc gta tcc atc acc gat ggt gct ctt act															355
Arg Tyr Glu Ala His His Arg Val Ser Ile Thr Asp Gly Ala Leu Thr															85
70 75															
gca gca gct cag ctt gct gat cgc tac atc aac gac cgc ttc ttg cca															403
Ala Ala Ala Gln Leu Ala Asp Arg Tyr Ile Asn Asp Arg Phe Leu Pro															100
90 95															
gat aag gcc gtt gac ctc atc gat gag gct ggc gcc cgc atg cgc atc															451
Asp Lys Ala Val Asp Leu Ile Asp Glu Ala Gly Ala Arg Met Arg Ile															115
105 110															
aag cgc atg acc gca cct tcc tcc ctc cgc gag gtt gat gag cgt atc															499
Lys Arg Met Thr Ala Pro Ser Ser Leu Arg Glu Val Asp Glu Arg Ile															130
120 125															
gct gat gtt cgc cgt gag aag gaa gca gcg atc gat gct cag gac ttt															547
Ala Asp Val Arg Arg Glu Lys Gaa Glu Ala Ala Ile Asp Ala Gln Asp Phe															145
135 140															
gag aag gca gca ggt ctt cgc gat aag gag cgc aag ctc ggc gaa gag															595
Glu Lys Ala Ala Gly Leu Arg Asp Lys Glu Arg Lys Leu Gly Glu Glu															165
150 155 160															
cgt tca gag aag gaa aag cag tgg cgc tcc ggc gac ctc gag gac atc															643
Arg Ser Glu Lys Glu Lys Gln Trp Arg Ser Gly Asp Leu Glu Asp Ile															180
170 175 180															

gct	gag	gtt	ggc	gaa	gag	cag	atc	gca	gaa	gta	ctg	gcc	aac	tgg	act	691
Ala	Glu	Val	Gly	Glu	Glu	Gln	Ile	Ala	Glu	Val	Leu	Ala	Asn	Trp	Thr	
			185					190					195			
ggt	att	cct	gtc	ttc	aag	ctc	acc	gaa	gct	gaa	tct	tca	cgc	ctg	ctc	739
Gly	Ile	Pro	Val	Phe	Lys	Leu	Thr	Glu	Ala	Glu	Ser	Ser	Arg	Leu	Leu	
		200					205					210				
aac	atg	gaa	gaa	gag	ttg	cac	aag	cgc	atc	atc	gga	cag	gat	gaa	gct	787
Asn	Met	Glu	Glu	Glu	Leu	His	Lys	Arg	Ile	Ile	Gly	Gln	Asp	Glu	Ala	
	215					220					225					
gtc	aag	gct	gtc	tcc	cgt	gcg	atc	cgt	cgt	acc	cgt	gca	ggg	ctg	aag	835
Val	Lys	Ala	Val	Ser	Arg	Ala	Ile	Arg	Arg	Thr	Arg	Ala	Gly	Leu	Lys	
230					235					240					245	
gat	cct	aag	cgt	cct	tcc	ggc	tcc	ttc	atc	ttc	gct	ggg	cca	tcc	ggc	883
Asp	Pro	Lys	Arg	Pro	Ser	Gly	Ser	Phe	Ile	Phe	Ala	Gly	Pro	Ser	Gly	
				250					255					260		
gtt	ggg	aag	acc	gag	ctg	tcc	aag	gct	ctc	gca	gga	ttc	ctc	ttc	ggg	931
Val	Gly	Lys	Thr	Glu	Leu	Ser	Lys	Ala	Leu	Ala	Gly	Phe	Leu	Phe	Gly	
			265					270					275			
gac	gat	gat	tcc	ctc	atc	caa	atc	gac	atg	ggg	gag	ttc	cac	gac	cgc	979
Asp	Asp	Asp	Ser	Leu	Ile	Gln	Ile	Asp	Met	Gly	Glu	Phe	His	Asp	Arg	
		280					285					290				
ttc	acc	gcg	tcc	cga	ctt	ttc	ggg	gcc	cct	ccg	gga	tac	gtt	ggc	tac	1027
Phe	Thr	Ala	Ser	Arg	Leu	Phe	Gly	Ala	Pro	Pro	Gly	Tyr	Val	Gly	Tyr	
	295					300					305					
gaa	gaa	ggg	ggc	cag	ctg	acc	gag	aag	gtt	cgc	cgt	aag	cca	ttc	tcc	1075
Glu	Glu	Gly	Gly	Gln	Leu	Thr	Glu	Lys	Val	Arg	Arg	Lys	Pro	Phe	Ser	
310					315					320					325	
gtt	gtg	ctt	ttc	gac	gaa	atc	gag	aag	gcc	cac	aag	gag	atc	tac	aac	1123
Val	Val	Leu	Phe	Asp	Glu	Ile	Glu	Lys	Ala	His	Lys	Glu	Ile	Tyr	Asn	
				330					335					340		
acc	ttg	ctg	cag	gtg	ttg	gaa	gat	ggg	cgc	ctt	acc	gat	ggg	cag	gga	1171
Thr	Leu	Leu	Gln	Val	Leu	Glu	Asp	Gly	Arg	Leu	Thr	Asp	Gly	Gln	Gly	
			345					350					355			
cgc	atc	gtg	gac	ttc	aag	aac	acc	gtc	ctg	atc	ttc	acc	tcc	aac	ctg	1219
Arg	Ile	Val	Asp	Phe	Lys	Asn	Thr	Val	Leu	Ile	Phe	Thr	Ser	Asn	Leu	
		360					365					370				
ggc	acc	gct	gac	atc	tcc	aag	gct	gtt	ggc	ctg	ggc	ttc	tcc	gga	tcc	1267
Gly	Thr	Ala	Asp	Ile	Ser	Lys	Ala	Val	Gly	Leu	Gly	Phe	Ser	Gly	Ser	
	375					380					385					
tcc	gag	act	gac	agc	gat	gct	cag	tac	gac	cgc	atg	aag	aac	aag	gtc	1315
Ser	Glu	Thr	Asp	Ser	Asp	Ala	Gln	Tyr	Asp	Arg	Met	Lys	Asn	Lys	Val	
390					395					400					405	
cac	gac	gag	ctg	aag	aag	cac	ttc	cgc	cct	gag	ttc	ctg	aac	cgt	att	1363
His	Asp	Glu	Leu	Lys	Lys	His	Phe	Arg	Pro	Glu	Phe	Leu	Asn	Arg	Ile	
				410					415					420		

gat gag atc gtg gtc ttc cac cag ctc acc aag gat cag atc gtt cag 1411
Asp Glu Ile Val Val Phe His Gln Leu Thr Lys Asp Gln Ile Val Gln
425 430 435

atg gtc gac ctt ctt atc ggt cgc gtt tcc aac gca ctg gct gag aag 1459
Met Val Asp Leu Leu Ile Gly Arg Val Ser Asn Ala Leu Ala Glu Lys
440 445 450

gac atg agc atc gaa ctg act gag aag gcc aag gac ctc ctg gct aac 1507
Asp Met Ser Ile Glu Leu Thr Glu Lys Ala Lys Asp Leu Leu Ala Asn
455 460 465

cga ggc ttc gat cca gtt ctg ggt gca cga cca ttg cgt cgc acc atc 1555
Arg Gly Phe Asp Pro Val Leu Gly Ala Arg Pro Leu Arg Arg Thr Ile
470 475 480 485

cag cgc gaa att gaa gac cag atg tcc gag aag atc ctc ttc ggt gaa 1603
Gln Arg Glu Ile Glu Asp Gln Met Ser Glu Lys Ile Leu Phe Gly Glu
490 495 500

atc ggc gca ggc gag atc gtc acc gtt gac gtc gaa ggc tgg gac ggc 1651
Ile Gly Ala Gly Glu Ile Val Thr Val Asp Val Glu Gly Trp Asp Gly
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gag tcc aag gac acc gac cgt gcg aag ttc acc ttc aca cca cgt cca 1699
Glu Ser Lys Asp Thr Asp Arg Ala Lys Phe Thr Phe Thr Pro Arg Pro
520 525 530

aag cca atg cca gaa ggt aag ttc tct gag atc tct gtc gag gct gcg 1747
Lys Pro Met Pro Glu Gly Lys Phe Ser Glu Ile Ser Val Glu Ala Ala
535 540 545

gaa gca att caa gat gta gat tct gca gct gac ggc gat gtc cca gaa 1795
Glu Ala Ile Gln Asp Val Asp Ser Ala Ala Asp Gly Asp Val Pro Glu
550 555 560 565

acc gat tca ctt tcc gac att gac ctt gaa acc ctt gaa aag ttt gag 1843
Thr Asp Ser Leu Ser Asp Ile Asp Leu Glu Thr Leu Glu Lys Phe Glu
570 575 580

gaa gat gta gaa aac ggc acc gac att gat cag gtg tcc ggt gac tac 1891
Glu Asp Val Glu Asn Gly Thr Asp Ile Asp Gln Val Ser Gly Asp Tyr
585 590 595

tac ggc acc gat gat cag gga ggc act gct cca agc aag gag 1933
Tyr Gly Thr Asp Asp Gln Gly Gly Thr Ala Pro Ser Lys Glu
600 605 610

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<210> 130

<211> 611

<212> PRT

<213> Corynebacterium glutamicum

<400> 130

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Tyr	Arg	Lys	His	Ile	Glu	Lys	Asp	Ala	Ala	Leu	Glu	Arg	Arg	Phe	Gln	
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Pro	Val	Gln	Val	Pro	Glu	Pro	Ser	Val	Asp	Leu	Thr	Val	Glu	Ile	Leu	
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Lys	Gly	Leu	Arg	Asp	Arg	Tyr	Glu	Ala	His	His	Arg	Val	Ser	Ile	Thr	
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Asp	Gly	Ala	Leu	Thr	Ala	Ala	Ala	Gln	Leu	Ala	Asp	Arg	Tyr	Ile	Asn	
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Asp	Arg	Phe	Leu	Pro	Asp	Lys	Ala	Val	Asp	Leu	Ile	Asp	Glu	Ala	Gly	
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Leu	Ala	Asn	Trp	Thr	Gly	Ile	Pro	Val	Phe	Lys	Leu	Thr	Glu	Ala	Glu	
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Ser	Ser	Arg	Leu	Leu	Asn	Met	Glu	Glu	Glu	Leu	His	Lys	Arg	Ile	Ile	
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Arg	Ala	Gly	Leu	Lys	Asp	Pro	Lys	Arg	Pro	Ser	Gly	Ser	Phe	Ile	Phe	
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Gly	Phe	Leu	Phe	Gly	Asp	Asp	Asp	Ser	Leu	Ile	Gln	Ile	Asp	Met	Gly	
275					280					285						
Glu	Phe	His	Asp	Arg	Phe	Thr	Ala	Ser	Arg	Leu	Phe	Gly	Ala	Pro	Pro	
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Gly	Tyr	Val	Gly	Tyr	Glu	Glu	Gly	Gly	Gln	Leu	Thr	Glu	Lys	Val	Arg	
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Thr Asp Gly Gln Gly Arg Ile Val Asp Phe Lys Asn Thr Val Leu Ile
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 Phe Thr Ser Asn Leu Gly Thr Ala Asp Ile Ser Lys Ala Val Gly Leu
 370 375 380
 Gly Phe Ser Gly Ser Ser Glu Thr Asp Ser Asp Ala Gln Tyr Asp Arg
 385 390 395 400
 Met Lys Asn Lys Val His Asp Glu Leu Lys Lys His Phe Arg Pro Glu
 405 410 415
 Phe Leu Asn Arg Ile Asp Glu Ile Val Val Phe His Gln Leu Thr Lys
 420 425 430
 Asp Gln Ile Val Gln Met Val Asp Leu Leu Ile Gly Arg Val Ser Asn
 435 440 445
 Ala Leu Ala Glu Lys Asp Met Ser Ile Glu Leu Thr Glu Lys Ala Lys
 450 455 460
 Asp Leu Leu Ala Asn Arg Gly Phe Asp Pro Val Leu Gly Ala Arg Pro
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 Leu Arg Arg Thr Ile Gln Arg Glu Ile Glu Asp Gln Met Ser Glu Lys
 485 490 495
 Ile Leu Phe Gly Glu Ile Gly Ala Gly Glu Ile Val Thr Val Asp Val
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 Glu Gly Trp Asp Gly Glu Ser Lys Asp Thr Asp Arg Ala Lys Phe Thr
 515 520 525
 Phe Thr Pro Arg Pro Lys Pro Met Pro Glu Gly Lys Phe Ser Glu Ile
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 Ser Val Glu Ala Ala Glu Ala Ile Gln Asp Val Asp Ser Ala Ala Asp
 545 550 555 560
 Gly Asp Val Pro Glu Thr Asp Ser Leu Ser Asp Ile Asp Leu Glu Thr
 565 570 575
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 Ser Lys Glu
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<210> 131

<211> 1875

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1852)

<400> 131

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cca act acc aaa acc aat gaa gcc atg cag gct gct ctt cag cag gca 163
Pro Thr Thr Lys Thr Asn Glu Ala Met Gln Ala Ala Leu Gln Gln Ala
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tcc tcg gct ggc aac cct gat att cgt cca gct cac ctg ttg gct gcc 211
Ser Ser Ala Gly Asn Pro Asp Ile Arg Pro Ala His Leu Leu Ala Ala
25 30 35

atc ttg gag caa act gat ggc gta gca gcg cca gtc ctc atg gct act 259
Ile Leu Glu Gln Thr Asp Gly Val Ala Ala Pro Val Leu Met Ala Thr
40 45 50

ggt gtg gat cct aag gag atc ctc gca gag gcc aag aag ttg gtt gct 307
Gly Val Asp Pro Lys Glu Ile Leu Ala Glu Ala Lys Lys Leu Val Ala
55 60 65

tct tac ccc aag gct tct .ggc .gcc aat atg gct aat cca aac ttc aac 355
Ser Tyr Pro Lys Ala Ser Gly Ala Asn Met Ala Asn Pro Asn Phe Asn
70 75 80 85

cgg gat gcc ctc aat gcg ttc act gca gct cag gag ctt gcc ggt gag 403
Arg Asp Ala Leu Asn Ala Phe Thr Ala Ala Gln Glu Leu Ala Gly Glu
90 95 100

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Leu Gly Asp Glu Tyr Val Ser Thr Glu Val Leu Leu Ala Gly Ile Ala
          105                      110                      115

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cgc gga aag tct gat gct gcg gat ctg ttg acc aac aag ggt gca acc 499
Arg Gly Lys Ser Asp Ala Ala Asp Leu Leu Thr Asn Lys Gly Ala Thr
120 125 130

tat gac gcc atc aaa gag gct ttc cct tcg gtt cgt gga tct cag cgt 547
Tyr Asp Ala Ile Lys Glu Ala Phe Pro Ser Val Arg Gly Ser Gln Arg
135 140 145

gtc acc act cag gat cca gag gga cag ttc cag gct ttg gaa aag tac 595
Val Thr Thr Gln Asp Pro Glu Gly Gln Phe Gln Ala Leu Glu Lys Tyr
150 155 160 165

tcc	act	gac	ctg	acc	aag	ctt	gct	cgt	gaa	ggc	aag	att	gat	cct	gtt	643
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Ile Gly Arg Asp Gln Glu Ile Arg Arg Val Val Gln Val Leu Ser Arg
185 190 195

cgt acc aag aac aac cct gtt ctg atc ggt gag cca ggt gtc ggt aaa 739
Arg Thr Lys Asn Asn Pro Val Leu Ile Gly Glu Pro Gly Val Gly Lys
200 205 210

acc gcc atc gtg gaa ggc ctt gca cgc cgc atc gtt gct ggt gac gtt	787
Thr Ala Ile Val Glu Gly Leu Ala Arg Arg Ile Val Ala Gly Asp Val	
215 220 225	
cca gaa tcc ctc aag ggc aaa act ctg atc agt ctt gat ctt ggt tcc	835
Pro Glu Ser Leu Lys Gly Lys Thr Leu Ile Ser Leu Asp Leu Gly Ser	
230 235 240 245	
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Met Val Ala Gly Ala Lys Tyr Arg Gly Glu Phe Glu Glu Arg Leu Lys	
250 255 260	
gct gtt ctg gat gag atc aag gga gct aac ggc gaa gtc gtt acc ttc	931
Ala Val Leu Asp Glu Ile Lys Gly Ala Asn Gly Glu Val Val Thr Phe	
265 270 275	
atc gat gag ctg cac acc atc gtc ggc gct ggt gct tcg ggt gaa tcc	979
Ile Asp Glu Leu His Thr Ile Val Gly Ala Gly Ala Ser Gly Glu Ser	
280 285 290	
gcc atg gat gcc gga aac atg att aag cca ctg ctt gcc cgc ggt gag	1027
Ala Met Asp Ala Gly Asn Met Ile Lys Pro Leu Leu Ala Arg Gly Glu	
295 300 305	
ctg cgc ttg gtt ggt gcc acc acg ctg aat gag tac cgc aag tac atc	1075
Leu Arg Leu Val Gly Ala Thr Thr Leu Asn Glu Tyr Arg Lys Tyr Ile	
310 315 320 325	
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Glu Lys Asp Ala Ala Leu Glu Arg Arg Phe Gln Gln Val Tyr Val Gly	
330 335 340	
gag cca acg gta gaa gat gcc atc ggt att ctt cgt gga ttg aag gaa	1171
Glu Pro Thr Val Glu Asp Ala Ile Gly Ile Leu Arg Gly Leu Lys Glu	
345 350 355	
cgc tac gag gtc cat cac ggt gtc cgc atc cag gac tcc gca ctg gtc	1219
Arg Tyr Glu Val His His Gly Val Arg Ile Gln Asp Ser Ala Leu Val	
360 365 370	
gcc gca gct gaa ctc tca aac cgc tat atc acc agc cgt ttc ctt cct	1267
Ala Ala Ala Glu Leu Ser Asn Arg Tyr Ile Thr Ser Arg Phe Leu Pro	
375 380 385	
gat aag gct att gac tta gtt gat gag gca gca tca cgc ctg cgc atg	1315
Asp Lys Ala Ile Asp Leu Val Asp Glu Ala Ala Ser Arg Leu Arg Met	
390 395 400 405	
gag att gat tct tca cct cag gaa atc gat gag ctg gag cgt atc gtc	1363
Glu Ile Asp Ser Ser Pro Gln Glu Ile Asp Glu Leu Glu Arg Ile Val	
410 415 420	
cgc cgc ctc gag atc gaa gag atg gcg ctg tcc aag gaa tcc gat gca	1411
Arg Arg Leu Glu Ile Glu Glu Met Ala Leu Ser Lys Glu Ser Asp Ala	
425 430 435	
gct tcc aag gaa cgt cta gaa aag ctg cgc tcg gaa ctt gct gat gaa	1459
Ala Ser Lys Glu Arg Leu Glu Lys Leu Arg Ser Glu Leu Ala Asp Glu	
440 445 450	
cgc gaa aag ctc tct gag ttg aag gct cgt tgg cag aat gag aaa act	1507

Arg Glu Lys Leu Ser Glu Leu Lys Ala Arg Trp Gln Asn Glu Lys Thr
 455 460 465
 gct att gac gat gtc cgg gag atg aaa gaa gag ctg gaa gcg ctg cgt 1555
 Ala Ile Asp Asp Val Arg Glu Met Lys Glu Glu Leu Glu Ala Leu Arg
 470 475 480 485
 tct gag tcg gat att gca aaa cgt gac ggc aat tat tgt cgt gtc gca 1603
 Ser Glu Ser Asp Ile Ala Lys Arg Asp Gly Asn Tyr Cys Arg Val Ala
 490 495 500
 aag ctt cgc tac ggc cga atc cct gag ctg gaa aag cag atc gag gat 1651
 Lys Leu Arg Tyr Gly Arg Ile Pro Glu Leu Glu Lys Gln Ile Glu Asp
 505 510 515
 gca gaa tcc aag gtc gag gtc aat gaa aat gcc atg ctc act gag gag 1699
 Ala Glu Ser Lys Val Glu Val Asn Glu Asn Ala Met Leu Thr Glu Glu
 520 525 530
 gtc acg cca gac acg atc gcc gat gtg gtt tcc gca tgg acg ggc att 1747
 Val Thr Pro Asp Thr Ile Ala Asp Val Val Ser Ala Trp Thr Gly Ile
 535 540 545
 cct gca ggc aag atg atg cag ggt gag acc gag aag ctg ctc aac atg 1795
 Pro Ala Gly Lys Met Met Gln Gly Glu Thr Glu Lys Leu Leu Asn Met
 550 555 560 565
 gag cgc gtc ttg ggc aac cgt gtg gtc ggt cag cta gaa agc ggt aac 1843
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 Cys Ser Val

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<211> 584

<212> PRT

<213> Corynebacterium glutamicum

<400> 132

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 His Leu Leu Ala Ala Ile Leu Glu Gln Thr Asp Gly Val Ala Ala Pro
 35 40 45
 Val Leu Met Ala Thr Gly Val Asp Pro Lys Glu Ile Leu Ala Glu Ala
 50 55 60
 Lys Lys Leu Val Ala Ser Tyr Pro Lys Ala Ser Gly Ala Asn Met Ala
 65 70 75 80
 Asn Pro Asn Phe Asn Arg Asp Ala Leu Asn Ala Phe Thr Ala Ala Gln
 85 90 95
 Glu Leu Ala Gly Glu Leu Gly Asp Glu Tyr Val Ser Thr Glu Val Leu

100					105					110					
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Arg	Gly	Ser	Gln	Arg	Val	Thr	Thr	Gln	Asp	Pro	Glu	Gly	Gln	Phe	Gln
145					150					155					160
Ala	Leu	Glu	Lys	Tyr	Ser	Thr	Asp	Leu	Thr	Lys	Leu	Ala	Arg	Glu	Gly
				165					170					175	
Lys	Ile	Asp	Pro	Val	Ile	Gly	Arg	Asp	Gln	Glu	Ile	Arg	Arg	Val	Val
		180						185					190		
Gln	Val	Leu	Ser	Arg	Arg	Thr	Lys	Asn	Asn	Pro	Val	Leu	Ile	Gly	Glu
		195					200					205			
Pro	Gly	Val	Gly	Lys	Thr	Ala	Ile	Val	Glu	Gly	Leu	Ala	Arg	Arg	Ile
	210					215					220				
Val	Ala	Gly	Asp	Val	Pro	Glu	Ser	Leu	Lys	Gly	Lys	Thr	Leu	Ile	Ser
225					230					235					240
Leu	Asp	Leu	Gly	Ser	Met	Val	Ala	Gly	Ala	Lys	Tyr	Arg	Gly	Glu	Phe
				245					250					255	
Glu	Glu	Arg	Leu	Lys	Ala	Val	Leu	Asp	Glu	Ile	Lys	Gly	Ala	Asn	Gly
			260					265					270		
Glu	Val	Val	Thr	Phe	Ile	Asp	Glu	Leu	His	Thr	Ile	Val	Gly	Ala	Gly
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Ala	Ser	Gly	Glu	Ser	Ala	Met	Asp	Ala	Gly	Asn	Met	Ile	Lys	Pro	Leu
	290					295					300				
Leu	Ala	Arg	Gly	Glu	Leu	Arg	Leu	Val	Gly	Ala	Thr	Thr	Leu	Asn	Glu
305					310					315					320
Tyr	Arg	Lys	Tyr	Ile	Glu	Lys	Asp	Ala	Ala	Leu	Glu	Arg	Arg	Phe	Gln
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Gln	Val	Tyr	Val	Gly	Glu	Pro	Thr	Val	Glu	Asp	Ala	Ile	Gly	Ile	Leu
			340					345					350		
Arg	Gly	Leu	Lys	Glu	Arg	Tyr	Glu	Val	His	His	Gly	Val	Arg	Ile	Gln
	355						360					365			
Asp	Ser	Ala	Leu	Val	Ala	Ala	Ala	Glu	Leu	Ser	Asn	Arg	Tyr	Ile	Thr
	370					375					380				
Ser	Arg	Phe	Leu	Pro	Asp	Lys	Ala	Ile	Asp	Leu	Val	Asp	Glu	Ala	Ala
385					390					395					400
Ser	Arg	Leu	Arg	Met	Glu	Ile	Asp	Ser	Ser	Pro	Gln	Glu	Ile	Asp	Glu
				405					410					415	
Leu	Glu	Arg	Ile	Val	Arg	Arg	Leu	Glu	Ile	Glu	Glu	Met	Ala	Leu	Ser
			420					425					430		

Lys Glu Ser Asp Ala Ala Ser Lys Glu Arg Leu Glu Lys Leu Arg Ser
435 440 445

Glu Leu Ala Asp Glu Arg Glu Lys Leu Ser Glu Leu Lys Ala Arg Trp
450 455 460

Gln Asn Glu Lys Thr Ala Ile Asp Asp Val Arg Glu Met Lys Glu Glu
465 470 475 480

Leu Glu Ala Leu Arg Ser Glu Ser Asp Ile Ala Lys Arg Asp Gly Asn
485 490 495

Tyr Cys Arg Val Ala Lys Leu Arg Tyr Gly Arg Ile Pro Glu Leu Glu
500 505 510

Lys Gln Ile Glu Asp Ala Glu Ser Lys Val Glu Val Asn Glu Asn Ala
515 520 525

Met Leu Thr Glu Glu Val Thr Pro Asp Thr Ile Ala Asp Val Val Ser
530 535 540

Ala Trp Thr Gly Ile Pro Ala Gly Lys Met Met Gln Gly Glu Thr Glu
545 550 555 560

Lys Leu Leu Asn Met Glu Arg Val Leu Gly Asn Arg Val Val Gly Gln
565 570 575

Leu Glu Ser Gly Asn Cys Ser Val
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<210> 133

<211> 1816

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1816)

<223> FRXA01668

<400> 133

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Met Ser Ser Phe Asn
1 5

cca act acc aaa acc aat gaa gcc atg cag gct gct ctt cag cag gca 163
Pro Thr Thr Lys Thr Asn Glu Ala Met Gln Ala Ala Leu Gln Gln Ala
10 15 20

tcc tcg gct ggc aac cct gat att cgt cca gct cac ctg ttg gct gcc 211
Ser Ser Ala Gly Asn Pro Asp Ile Arg Pro Ala His Leu Leu Ala Ala
25 30 35

atc ttg gag caa act gat ggc gta gca gcg cca gtc ctc atg gct act 259
Ile Leu Glu Gln Thr Asp Gly Val Ala Ala Pro Val Leu Met Ala Thr
40 45 50

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Gly	Val	Asp	Pro	Lys	Glu	Ile	Leu	Ala	Glu	Ala	Lys	Lys	Leu	Val	Ala	
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tct	tac	ccc	aag	gct	tct	ggc	gcc	aat	atg	gct	aat	cca	aac	ttc	aac	355
Ser	Tyr	Pro	Lys	Ala	Ser	Gly	Ala	Asn	Met	Ala	Asn	Pro	Asn	Phe	Asn	
70					75					80					85	
cgg	gat	gcc	ctc	aat	gcg	ttc	act	gca	gct	cag	gag	ctt	gcc	ggg	gag	403
Arg	Asp	Ala	Leu	Asn	Ala	Phe	Thr	Ala	Ala	Gln	Glu	Leu	Ala	Gly	Glu	
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ttg	ggc	gat	gag	tac	gtc	tca	acc	gaa	gta	ctt	ctt	gcc	ggg	atc	gct	451
Leu	Gly	Asp	Glu	Tyr	Val	Ser	Thr	Glu	Val	Leu	Leu	Ala	Gly	Ile	Ala	
			105					110					115			
cgc	gga	aag	tct	gat	gct	gcg	gat	ctg	ttg	acc	aac	aag	ggg	gca	acc	499
Arg	Gly	Lys	Ser	Asp	Ala	Ala	Asp	Leu	Leu	Thr	Asn	Lys	Gly	Ala	Thr	
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Tyr	Asp	Ala	Ile	Lys	Glu	Ala	Phe	Pro	Ser	Val	Arg	Gly	Ser	Gln	Arg	
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gtc	acc	act	cag	gat	cca	gag	gga	cag	ttc	cag	gct	ttg	gaa	aag	tac	595
Val	Thr	Thr	Gln	Asp	Pro	Glu	Gly	Gln	Phe	Gln	Ala	Leu	Glu	Lys	Tyr	
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Ser	Thr	Asp	Leu	Thr	Lys	Leu	Ala	Arg	Glu	Gly	Lys	Ile	Asp	Pro	Val	
				170					175					180		
att	ggc	cgt	gac	cag	gaa	att	cgt	cgc	gtc	gtt	cag	gtg	ctt	agc	cgt	691
Ile	Gly	Arg	Asp	Gln	Glu	Ile	Arg	Arg	Val	Val	Gln	Val	Leu	Ser	Arg	
			185					190					195			
cgt	acc	aag	aac	aac	cct	gtt	ctg	atc	ggg	gag	cca	ggg	gtc	ggg	aaa	739
Arg	Thr	Lys	Asn	Asn	Pro	Val	Leu	Ile	Gly	Glu	Pro	Gly	Val	Gly	Lys	
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acc	gcc	atc	gtg	gaa	ggc	ctt	gca	cgc	cgc	atc	gtt	gct	ggg	gac	gtt	787
Thr	Ala	Ile	Val	Glu	Gly	Leu	Ala	Arg	Arg	Ile	Val	Ala	Gly	Asp	Val	
	215					220					225					
cca	gaa	tcc	ctc	aag	ggc	aaa	act	ctg	atc	agt	ctt	gat	ctt	ggg	tcc	835
Pro	Glu	Ser	Leu	Lys	Gly	Lys	Thr	Leu	Ile	Ser	Leu	Asp	Leu	Gly	Ser	
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atg	gtt	gcc	ggc	gct	aag	tat	cgc	ggg	gaa	ttc	gag	gag	cga	ctg	aag	883
Met	Val	Ala	Gly	Ala	Lys	Tyr	Arg	Gly	Glu	Phe	Glu	Glu	Arg	Leu	Lys	
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gct	gtt	ctg	gat	gag	atc	aag	gga	gct	aac	ggc	gaa	gtc	gtt	acc	ttc	931
Ala	Val	Leu	Asp	Glu	Ile	Lys	Gly	Ala	Asn	Gly	Glu	Val	Val	Thr	Phe	
			265					270					275			
atc	gat	gag	ctg	cac	acc	atc	gtc	ggc	gct	ggg	gct	tcg	ggg	gaa	tcc	979
Ile	Asp	Glu	Leu	His	Thr	Ile	Val	Gly	Ala	Gly	Ala	Ser	Gly	Glu	Ser	
		280					285					290				
gcc	atg	gat	gcc	gga	aac	atg	att	aag	cca	ctg	ctt	gcc	cgc	ggg	gag	1027

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Leu	Arg	Leu	Val	Gly	Ala	Thr	Thr	Leu	Asn	Glu	Tyr	Arg	Lys	Tyr	Ile		
310					315					320					325		
gaa	aag	gac	gct	gcc	ctg	gag	cgt	agg	ttc	cag	cag	gtt	tat	gtc	ggc	1123	
Glu	Lys	Asp	Ala	Ala	Leu	Glu	Arg	Arg	Phe	Gln	Gln	Val	Tyr	Val	Gly		
				330					335					340			
gag	cca	acg	gta	gaa	gat	gcc	atc	ggc	att	ctt	cgt	gga	ttg	aag	gaa	1171	
Glu	Pro	Thr	Val	Glu	Asp	Ala	Ile	Gly	Ile	Leu	Arg	Gly	Leu	Lys	Glu		
			345					350					355				
cgc	tac	gag	gtc	cat	cac	ggc	gtc	cgc	atc	cag	gac	tcc	gca	ctg	gtc	1219	
Arg	Tyr	Glu	Val	His	His	Gly	Val	Arg	Ile	Gln	Asp	Ser	Ala	Leu	Val		
		360					365					370					
gcc	gca	gct	gaa	ctc	tca	aac	cgc	tat	atc	acc	agc	cgt	ttc	ctt	cct	1267	
Ala	Ala	Ala	Glu	Leu	Ser	Asn	Arg	Tyr	Ile	Thr	Ser	Arg	Phe	Leu	Pro		
			375			380					385						
gat	aag	gct	att	gac	tta	gtt	gat	gag	gca	gca	tca	cgc	ctg	cgc	atg	1315	
Asp	Lys	Ala	Ile	Asp	Leu	Val	Asp	Glu	Ala	Ala	Ser	Arg	Leu	Arg	Met		
390					395				400						405		
gag	att	gat	tct	tca	cct	cag	gaa	atc	gat	gag	ctg	gag	cgt	atc	gtc	1363	
Glu	Ile	Asp	Ser	Ser	Pro	Gln	Glu	Ile	Asp	Glu	Leu	Glu	Arg	Ile	Val		
				410				415						420			
cgc	cgc	ctc	gag	atc	gaa	gag	atg	gcg	ctg	tcc	aag	gaa	tcc	gat	gca	1411	
Arg	Arg	Leu	Glu	Ile	Glu	Glu	Met	Ala	Leu	Ser	Lys	Glu	Ser	Asp	Ala		
			425					430					435				
gct	tcc	aag	gaa	cgt	cta	gaa	aag	ctg	cgc	tcg	gaa	ctt	gct	gat	gaa	1459	
Ala	Ser	Lys	Glu	Arg	Leu	Glu	Lys	Leu	Arg	Ser	Glu	Leu	Ala	Asp	Glu		
		440					445					450					
cgc	gaa	aag	ctc	tct	gag	ttg	aag	gct	cgt	tgg	cag	aat	gag	aaa	act	1507	
Arg	Glu	Lys	Leu	Ser	Glu	Leu	Lys	Ala	Arg	Trp	Gln	Asn	Glu	Lys	Thr		
	455					460					465						
gct	att	gac	gat	gtc	cgg	gag	atg	aaa	gaa	gag	ctg	gaa	gcg	ctg	cgt	1555	
Ala	Ile	Asp	Asp	Val	Arg	Glu	Met	Lys	Glu	Glu	Leu	Glu	Ala	Leu	Arg		
470					475					480					485		
tct	gag	tcg	gat	att	gca	aaa	cgt	gac	ggc	aat	tat	tgt	cgt	gtc	gca	1603	
Ser	Glu	Ser	Asp	Ile	Ala	Lys	Arg	Asp	Gly	Asn	Tyr	Cys	Arg	Val	Ala		
				490					495					500			
aag	ctt	cgc	tac	ggc	cga	atc	cct	gag	ctg	gaa	aag	cag	atc	gag	gat	1651	
Lys	Leu	Arg	Tyr	Gly	Arg	Ile	Pro	Glu	Leu	Glu	Lys	Gln	Ile	Glu	Asp		
			505					510					515				
gca	gaa	tcc	aag	gtc	gag	gtc	aat	gaa	aat	gcc	atg	ctc	act	gag	gag	1699	
Ala	Glu	Ser	Lys	Val	Glu	Val	Asn	Glu	Asn	Ala	Met	Leu	Thr	Glu	Glu		
			520				525					530					
gtc	acg	cca	gac	acg	atc	gcc	gat	gtg	gtt	tcc	gca	tgg	acg	ggc	att	1747	
Val	Thr	Pro	Asp	Thr	Ile	Ala	Asp	Val	Val	Ser	Ala	Trp	Thr	Gly	Ile		

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Pro Ala Gly Lys Met Met Gln Gly Glu Thr Glu Lys Leu Leu Asn Met			
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Glu Arg Val Leu Gly Asn Pro		
570		

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 <213> Corynebacterium glutamicum

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His Leu Leu Ala Ala Ile Leu Glu Gln Thr Asp Gly Val Ala Ala Pro	
35 40 45	
Val Leu Met Ala Thr Gly Val Asp Pro Lys Glu Ile Leu Ala Glu Ala	
50 55 60	
Lys Lys Leu Val Ala Ser Tyr Pro Lys Ala Ser Gly Ala Asn Met Ala	
65 70 75 80	
Asn Pro Asn Phe Asn Arg Asp Ala Leu Asn Ala Phe Thr Ala Ala Gln	
85 90 95	
Glu Leu Ala Gly Glu Leu Gly Asp Glu Tyr Val Ser Thr Glu Val Leu	
100 105 110	
Leu Ala Gly Ile Ala Arg Gly Lys Ser Asp Ala Ala Asp Leu Leu Thr	
115 120 125	
Asn Lys Gly Ala Thr Tyr Asp Ala Ile Lys Glu Ala Phe Pro Ser Val	
130 135 140	
Arg Gly Ser Gln Arg Val Thr Thr Gln Asp Pro Glu Gly Gln Phe Gln	
145 150 155 160	
Ala Leu Glu Lys Tyr Ser Thr Asp Leu Thr Lys Leu Ala Arg Glu Gly	
165 170 175	
Lys Ile Asp Pro Val Ile Gly Arg Asp Gln Glu Ile Arg Arg Val Val	
180 185 190	
Gln Val Leu Ser Arg Arg Thr Lys Asn Asn Pro Val Leu Ile Gly Glu	
195 200 205	
Pro Gly Val Gly Lys Thr Ala Ile Val Glu Gly Leu Ala Arg Arg Ile	
210 215 220	
Val Ala Gly Asp Val Pro Glu Ser Leu Lys Gly Lys Thr Leu Ile Ser	
225 230 235 240	

Leu	Asp	Leu	Gly	Ser	Met	Val	Ala	Gly	Ala	Lys	Tyr	Arg	Gly	Glu	Phe
				245				250						255	
Glu	Glu	Arg	Leu	Lys	Ala	Val	Leu	Asp	Glu	Ile	Lys	Gly	Ala	Asn	Gly
			260					265					270		
Glu	Val	Val	Thr	Phe	Ile	Asp	Glu	Leu	His	Thr	Ile	Val	Gly	Ala	Gly
			275				280					285			
Ala	Ser	Gly	Glu	Ser	Ala	Met	Asp	Ala	Gly	Asn	Met	Ile	Lys	Pro	Leu
						295					300				
Leu	Ala	Arg	Gly	Glu	Leu	Arg	Leu	Val	Gly	Ala	Thr	Thr	Leu	Asn	Glu
305					310					315					320
Tyr	Arg	Lys	Tyr	Ile	Glu	Lys	Asp	Ala	Ala	Leu	Glu	Arg	Arg	Phe	Gln
				325					330					335	
Gln	Val	Tyr	Val	Gly	Glu	Pro	Thr	Val	Glu	Asp	Ala	Ile	Gly	Ile	Leu
			340					345					350		
Arg	Gly	Leu	Lys	Glu	Arg	Tyr	Glu	Val	His	His	Gly	Val	Arg	Ile	Gln
			355				360					365			
Asp	Ser	Ala	Leu	Val	Ala	Ala	Ala	Glu	Leu	Ser	Asn	Arg	Tyr	Ile	Thr
						375					380				
Ser	Arg	Phe	Leu	Pro	Asp	Lys	Ala	Ile	Asp	Leu	Val	Asp	Glu	Ala	Ala
385					390					395					400
Ser	Arg	Leu	Arg	Met	Glu	Ile	Asp	Ser	Ser	Pro	Gln	Glu	Ile	Asp	Glu
				405					410					415	
Leu	Glu	Arg	Ile	Val	Arg	Arg	Leu	Glu	Ile	Glu	Glu	Met	Ala	Leu	Ser
			420					425					430		
Lys	Glu	Ser	Asp	Ala	Ala	Ser	Lys	Glu	Arg	Leu	Glu	Lys	Leu	Arg	Ser
			435				440					445			
Glu	Leu	Ala	Asp	Glu	Arg	Glu	Lys	Leu	Ser	Glu	Leu	Lys	Ala	Arg	Trp
						455					460				
Gln	Asn	Glu	Lys	Thr	Ala	Ile	Asp	Asp	Val	Arg	Glu	Met	Lys	Glu	Glu
465					470					475					480
Leu	Glu	Ala	Leu	Arg	Ser	Glu	Ser	Asp	Ile	Ala	Lys	Arg	Asp	Gly	Asn
				485					490					495	
Tyr	Cys	Arg	Val	Ala	Lys	Leu	Arg	Tyr	Gly	Arg	Ile	Pro	Glu	Leu	Glu
			500					505					510		
Lys	Gln	Ile	Glu	Asp	Ala	Glu	Ser	Lys	Val	Glu	Val	Asn	Glu	Asn	Ala
			515				520					525			
Met	Leu	Thr	Glu	Glu	Val	Thr	Pro	Asp	Thr	Ile	Ala	Asp	Val	Val	Ser
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Val Ile Ser Asn Gly															115
1 5															
gaa ggt ccg gtt gtt gcg ctt cgt ggc gac att gat gcg ttg ccc atg															163
Glu Gly Pro Val Val Ala Leu Arg Gly Asp Ile Asp Ala Leu Pro Met															
10 15 20															
gcg gag cga tcc ggc aaa gaa tac gca gca acc gga gtg aca cag gtg															211
Ala Glu Arg Ser Gly Lys Glu Tyr Ala Ala Thr Gly Val Thr Gln Val															
25 30 35															
gat aac acc acc ggt caa gaa act ccg gtg gcg cat acc tgt ggc cac															259
Asp Asn Thr Thr Gly Gln Glu Thr Pro Val Ala His Thr Cys Gly His															
40 45 50															
gat gtg cat att tca tca ctg ttg ggt gcg gtg cag gcg ttc aat tct															307
Asp Val His Ile Ser Ser Leu Leu Gly Ala Val Gln Ala Phe Asn Ser															
55 60 65															
cat cgg gaa ttg tgg aac gga acg ttg atg gcc gtt ttc cag cca gcg															355
His Arg Glu Leu Trp Asn Gly Thr Leu Met Ala Val Phe Gln Pro Ala															
70 75 80 85															
gaa gag acg gca gct ggt gcg agg atg atg gcg gat cag gac aac gcg															403
Glu Glu Thr Ala Ala Gly Ala Arg Met Met Ala Asp Gln Asp Asn Ala															
90 95 100															
ccg gga aat cac tct cca gcg ttc gcg cca gat atg cag cca act ctt															451
Pro Gly Asn His Ser Pro Ala Phe Ala Pro Asp Met Gln Pro Thr Leu															
105 110 115															
gat cgt ggt gtg gaa gcg ctg gtt gta gct gct tct gcg tgg cta gta															499
Asp Arg Gly Val Glu Ala Leu Val Val Ala Ala Ser Ala Trp Leu Val															
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Lys															

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<213> Corynebacterium glutamicum

<400> 136

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Asp Ala Leu Pro Met Ala Glu Arg Ser Gly Lys Glu Tyr Ala Ala Thr
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Gly Val Thr Gln Val Asp Asn Thr Thr Gly Gln Glu Thr Pro Val Ala
 35 40 45

His Thr Cys Gly His Asp Val His Ile Ser Ser Leu Leu Gly Ala Val
 50 55 60

Gln Ala Phe Asn Ser His Arg Glu Leu Trp Asn Gly Thr Leu Met Ala
 65 70 75 80

Val Phe Gln Pro Ala Glu Glu Thr Ala Ala Gly Ala Arg Met Met Ala
 85 90 95

Asp Gln Asp Asn Ala Pro Gly Asn His Ser Pro Ala Phe Ala Pro Asp
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Met Gln Pro Thr Leu Asp Arg Gly Val Glu Ala Leu Val Val Ala Ala
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Ser Ala Trp Leu Val Lys
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<210> 137

<211> 1308

<212> DNA

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<220>

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<222> (101)..(1285)

<223> RXN03077

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 Val Met Glu Ile Gly
 1 5

gtg cag gtt gcc tca tgg atg gac cgc cac cat gac gag gtc ata aag 163
 Val Gln Val Ala Ser Trp Met Asp Arg His His Asp Glu Val Ile Lys
 10 15 20

tgg cgc agg cat ttg cac agc cat cct gag ctc tcc cac atg gaa tac 211
 Trp Arg Arg His Leu His Ser His Pro Glu Leu Ser His Met Glu Tyr
 25 30 35

cgc acg act gag tat ttg gcc tcg gtt ctg aaa gat cac ggc atg gaa 259
 Arg Thr Thr Glu Tyr Leu Ala Ser Val Leu Lys Asp His Gly Met Glu
 40 45 50

cca cac ctg ttc cca gga acc ggt ttg atg gtg gat atc gga cca gaa 307

Pro	His	Leu	Phe	Pro	Gly	Thr	Gly	Leu	Met	Val	Asp	Ile	Gly	Pro	Glu		
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ggg	gac	tcc	cgc	ctg	gcg	ttt	cgc	gct	gat	atc	gat	gcc	ctt	ccg	ctg	355	
Gly	Asp	Ser	Arg	Leu	Ala	Phe	Arg	Ala	Asp	Ile	Asp	Ala	Leu	Pro	Leu		
70					75				80						85		
ctt	gaa	tca	acc	ggc	tta	gag	ttc	tct	tcc	aca	gcc	act	ggc	gtt	gcg	403	
Leu	Glu	Ser	Thr	Gly	Leu	Glu	Phe	Ser	Ser	Thr	Ala	Thr	Gly	Val	Ala		
				90				95						100			
cat	gcc	tgc	gga	cat	gac	gtg	cac	acg	gtg	atc	gct	ttg	gca	ctt	gcc	451	
His	Ala	Cys	Gly	His	Asp	Val	His	Thr	Val	Ile	Ala	Leu	Ala	Leu	Ala		
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tgt	gca	ctg	aac	acc	atc	gaa	ctg	ccc	atc	ggc	att	cgg	gtg	att	ttc	499	
Cys	Ala	Leu	Asn	Thr	Ile	Glu	Leu	Pro	Ile	Gly	Ile	Arg	Val	Ile	Phe		
		120					125					130					
cag	ccg	gca	gaa	gaa	gtc	atg	act	ggt	ggc	gca	acg	gac	gtc	att	gcc	547	
Gln	Pro	Ala	Glu	Glu	Val	Met	Thr	Gly	Gly	Ala	Thr	Asp	Val	Ile	Ala		
	135					140					145						
cac	ggt	ggc	ctt	gat	ggt	gtg	gat	gcg	att	tac	gcc	atc	cac	gtt	gaa	595	
His	Gly	Gly	Leu	Asp	Gly	Val	Asp	Ala	Ile	Tyr	Ala	Ile	His	Val	Glu		
150					155				160						165		
ccc	aaa	ttg	aag	gtc	ggt	cgc	gtc	ggt	gta	cgc	gct	ggc	gcg	att	act	643	
Pro	Lys	Leu	Lys	Val	Gly	Arg	Val	Gly	Val	Arg	Ala	Gly	Ala	Ile	Thr		
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tct	gcc	tca	gat	gtg	atc	gaa	atc	aga	gtc	aag	ggt	gaa	gga	gga	cat	691	
Ser	Ala	Ser	Asp	Val	Ile	Glu	Ile	Arg	Val	Lys	Gly	Glu	Gly	Gly	His		
			185					190					195				
agc	gca	cgt	cca	cac	ctc	tcc	gct	gat	gtt	gtt	tac	gcc	ttg	agc	aaa	739	
Ser	Ala	Arg	Pro	His	Leu	Ser	Ala	Asp	Val	Val	Tyr	Ala	Leu	Ser	Lys		
		200					205					210					
ttg	gtc	gtt	gat	ctt	ccc	ggt	ttg	ctg	tcc	agg	cgc	gtc	gat	cca	cgc	787	
Leu	Val	Val	Asp	Leu	Pro	Gly	Leu	Leu	Ser	Arg	Arg	Val	Asp	Pro	Arg		
	215					220					225						
acc	ggc	acc	gtg	ctt	gtt	ttc	ggc	acc	atc	aac	gcc	ggc	tat	gcg	ccc	835	
Thr	Gly	Thr	Val	Leu	Val	Phe	Gly	Thr	Ile	Asn	Ala	Gly	Tyr	Ala	Pro		
230					235				240						245		
aac	gcg	atc	cca	gat	tcc	ggc	atc	gtg	tca	ggc	acc	ttg	cgt	aca	gcc	883	
Asn	Ala	Ile	Pro	Asp	Ser	Gly	Ile	Val	Ser	Gly	Thr	Leu	Arg	Thr	Ala		
				250				255						260			
gac	atc	tct	acc	tgg	cgt	gac	atg	cgt	ccg	ctt	atc	tct	gag	ctg	gtg	931	
Asp	Ile	Ser	Thr	Trp	Arg	Asp	Met	Arg	Pro	Leu	Ile	Ser	Glu	Leu	Val		
			265				270						275				
gaa	cag	gtg	ctc	gca	ccc	acc	gga	gtc	acc	cat	gaa	ctg	atc	tac	aat	979	
Glu	Gln	Val	Leu	Ala	Pro	Thr	Gly	Val	Thr	His	Glu	Leu	Ile	Tyr	Asn		
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ccg	ggt	gtt	cca	cca	gtg	ctt	aac	gac	gat	gtc	gcc	acc	gct	ttg	ttg	1027	
Pro	Gly	Val	Pro	Pro	Val	Leu	Asn	Asp	Asp	Val	Ala	Thr	Ala	Leu	Leu		

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Ala Ser Ala Ala Arg Asp Met Asp Thr Gln Ser Val Val Gln Ala Pro			
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cag tca tcc ggt gga gaa gac ttc tcg tgg tac ctt gaa cac gtc cca			1123
Gln Ser Ser Gly Gly Glu Asp Phe Ser Trp Tyr Leu Glu His Val Pro			
	330	335	340
gga tca atg gcc cgg ttg ggt tgc tgg ccg ggg cac gga ccc aag caa			1171
Gly Ser Met Ala Arg Leu Gly Cys Trp Pro Gly His Gly Pro Lys Gln			
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gac ctc cat caa agt gac ctg gtt gtg gat gag cga gcc atc gga gtt			1219
Asp Leu His Gln Ser Asp Leu Val Val Asp Glu Arg Ala Ile Gly Val			
	360	365	370
ggc gtc agg ctc ttt ggc tcc ctt gtg cag cag tac agt agc cga tct			1267
Gly Val Arg Leu Phe Gly Ser Leu Val Gln Gln Tyr Ser Ser Arg Ser			
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Glu Ala Phe Leu Asn Ser			
390	395		

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<211> 395

<212> PRT

<213> Corynebacterium glutamicum

<400> 138

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Asp Glu Val Ile Lys Trp Arg Arg His Leu His Ser His Pro Glu Leu			
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Ser His Met Glu Tyr Arg Thr Thr Glu Tyr Leu Ala Ser Val Leu Lys			
	35	40	45
Asp His Gly Met Glu Pro His Leu Phe Pro Gly Thr Gly Leu Met Val			
	50	55	60
Asp Ile Gly Pro Glu Gly Asp Ser Arg Leu Ala Phe Arg Ala Asp Ile			
	65	70	75
Asp Ala Leu Pro Leu Leu Glu Ser Thr Gly Leu Glu Phe Ser Ser Thr			
	85	90	95
Ala Thr Gly Val Ala His Ala Cys Gly His Asp Val His Thr Val Ile			
	100	105	110
Ala Leu Ala Leu Ala Cys Ala Leu Asn Thr Ile Glu Leu Pro Ile Gly			
	115	120	125

Ile Arg Val Ile Phe Gln Pro Ala Glu Glu Val Met Thr Gly Gly Ala		
130	135	140

Thr Asp Val Ile Ala His Gly Gly Leu Asp Gly Val Asp Ala Ile Tyr	
---	--

145		150		155		160
Ala Ile His Val Glu Pro Lys Leu Lys Val Gly Arg Val Gly Val Arg	165		170		175	
Ala Gly Ala Ile Thr Ser Ala Ser Asp Val Ile Glu Ile Arg Val Lys	180		185		190	
Gly Glu Gly Gly His Ser Ala Arg Pro His Leu Ser Ala Asp Val Val	195		200		205	
Tyr Ala Leu Ser Lys Leu Val Val Asp Leu Pro Gly Leu Leu Ser Arg	210		215		220	
Arg Val Asp Pro Arg Thr Gly Thr Val Leu Val Phe Gly Thr Ile Asn	225		230		235	240
Ala Gly Tyr Ala Pro Asn Ala Ile Pro Asp Ser Gly Ile Val Ser Gly	245		250		255	
Thr Leu Arg Thr Ala Asp Ile Ser Thr Trp Arg Asp Met Arg Pro Leu	260		265		270	
Ile Ser Glu Leu Val Glu Gln Val Leu Ala Pro Thr Gly Val Thr His	275		280		285	
Glu Leu Ile Tyr Asn Pro Gly Val Pro Pro Val Leu Asn Asp Asp Val	290		295		300	
Ala Thr Ala Leu Leu Ala Ser Ala Ala Arg Asp Met Asp Thr Gln Ser	305		310		315	320
Val Val Gln Ala Pro Gln Ser Ser Gly Gly Glu Asp Phe Ser Trp Tyr	325		330		335	
Leu Glu His Val Pro Gly Ser Met Ala Arg Leu Gly Cys Trp Pro Gly	340		345		350	
His Gly Pro Lys Gln Asp Leu His Gln Ser Asp Leu Val Val Asp Glu	355		360		365	
Arg Ala Ile Gly Val Gly Val Arg Leu Phe Gly Ser Leu Val Gln Gln	370		375		380	
Tyr Ser Ser Arg Ser Glu Ala Phe Leu Asn Ser	385		390		395	

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<211> 1308

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1285)

<223> FRXA02855

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 Asn Ala Ile Pro Asp Ser Gly Ile Val Ser Gly Thr Leu Arg Thr Ala
 250 255 260
 gac atc tct acc tgg cgt gac atg cgt ccg ctt atc tct gag ctg gtg 931
 Asp Ile Ser Thr Trp Arg Asp Met Arg Pro Leu Ile Ser Glu Leu Val
 265 270 275
 gaa cag gtg ctc gca ccc acc gga gtc acc cat gaa ctg atc tac aat 979
 Glu Gln Val Leu Ala Pro Thr Gly Val Thr His Glu Leu Ile Tyr Asn
 280 285 290
 ccg ggt gtt cca cca gtg ctt aac gac gat gtc gcc acc gct ttg ttg 1027
 Pro Gly Val Pro Pro Val Leu Asn Asp Asp Val Ala Thr Ala Leu Leu
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 gca agc gca gca cgc gac atg gac aca caa tct gtt gtc caa gcg ccg 1075
 Ala Ser Ala Ala Arg Asp Met Asp Thr Gln Ser Val Val Gln Ala Pro
 310 315 320 325
 cag tca tcc ggt gga gaa gac ttc tcg tgg tac ctt gaa cac gtc cca 1123
 Gln Ser Ser Gly Gly Glu Asp Phe Ser Trp Tyr Leu Glu His Val Pro
 330 335 340
 gga tca atg gcc cgg ttg ggt tgc tgg ccg ggg cac gga ccc aag caa 1171
 Gly Ser Met Ala Arg Leu Gly Cys Trp Pro Gly His Gly Pro Lys Gln
 345 350 355
 gac ctc cat caa agt gac ctg gtt gtg gat gag cga gcc atc gga gtt 1219
 Asp Leu His Gln Ser Asp Leu Val Asp Glu Arg Ala Ile Gly Val
 360 365 370
 ggc gtc agg ctc ttt ggc tcc ctt gtg cag cag tac agt agc cga tct 1267
 Gly Val Arg Leu Phe Gly Ser Leu Val Gln Gln Tyr Ser Ser Arg Ser
 375 380 385
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 Glu Ala Phe Leu Asn Ser
 390 395

<210> 140

<211> 395

<212> PRT

<213> Corynebacterium glutamicum

<400> 140

Val Met Glu Ile Gly Val Gln Val Ala Ser Trp Met Asp Arg His His
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Asp Glu Val Ile Lys Trp Arg Arg His Leu His Ser His Pro Glu Leu
 20 25 30

Ser His Met Glu Tyr Arg Thr Thr Glu Tyr Leu Ala Ser Val Leu Lys
 35 40 45

Asp His Gly Met Glu Pro His Leu Phe Pro Gly Thr Gly Leu Met Val
 50 55 60

Asp	Ile	Gly	Pro	Glu	Gly	Asp	Ser	Arg	Leu	Ala	Phe	Arg	Ala	Asp	Ile		65	70	75	80
Asp	Ala	Leu	Pro	Leu	Leu	Glu	Ser	Thr	Gly	Leu	Glu	Phe	Ser	Ser	Thr			85	90	95
Ala	Thr	Gly	Val	Ala	His	Ala	Cys	Gly	His	Asp	Val	His	Thr	Val	Ile		100	105	110	
Ala	Leu	Ala	Leu	Ala	Cys	Ala	Leu	Asn	Thr	Ile	Glu	Leu	Pro	Ile	Gly		115	120	125	
Ile	Arg	Val	Ile	Phe	Gln	Pro	Ala	Glu	Glu	Val	Met	Thr	Gly	Gly	Ala		130	135	140	
Thr	Asp	Val	Ile	Ala	His	Gly	Gly	Leu	Asp	Gly	Val	Asp	Ala	Ile	Tyr		145	150	155	160
Ala	Ile	His	Val	Glu	Pro	Lys	Leu	Lys	Val	Gly	Arg	Val	Gly	Val	Arg		165	170	175	
Ala	Gly	Ala	Ile	Thr	Ser	Ala	Ser	Asp	Val	Ile	Glu	Ile	Arg	Val	Lys		180	185	190	
Gly	Glu	Gly	Gly	His	Ser	Ala	Arg	Pro	His	Leu	Ser	Ala	Asp	Val	Val		195	200	205	
Tyr	Ala	Leu	Ser	Lys	Leu	Val	Val	Asp	Leu	Pro	Gly	Leu	Leu	Ser	Arg		210	215	220	
Arg	Val	Asp	Pro	Arg	Thr	Gly	Thr	Val	Leu	Val	Phe	Gly	Thr	Ile	Asn		225	230	235	240
Ala	Gly	Tyr	Ala	Pro	Asn	Ala	Ile	Pro	Asp	Ser	Gly	Ile	Val	Ser	Gly		245	250	255	
Thr	Leu	Arg	Thr	Ala	Asp	Ile	Ser	Thr	Trp	Arg	Asp	Met	Arg	Pro	Leu		260	265	270	
Ile	Ser	Glu	Leu	Val	Glu	Gln	Val	Leu	Ala	Pro	Thr	Gly	Val	Thr	His		275	280	285	
Glu	Leu	Ile	Tyr	Asn	Pro	Gly	Val	Pro	Pro	Val	Leu	Asn	Asp	Asp	Val		290	295	300	
Ala	Thr	Ala	Leu	Leu	Ala	Ser	Ala	Ala	Arg	Asp	Met	Asp	Thr	Gln	Ser		305	310	315	320
Val	Val	Gln	Ala	Pro	Gln	Ser	Ser	Gly	Gly	Glu	Asp	Phe	Ser	Trp	Tyr		325	330	335	
Leu	Glu	His	Val	Pro	Gly	Ser	Met	Ala	Arg	Leu	Gly	Cys	Trp	Pro	Gly		340	345	350	
His	Gly	Pro	Lys	Gln	Asp	Leu	His	Gln	Ser	Asp	Leu	Val	Val	Asp	Glu		355	360	365	
Arg	Ala	Ile	Gly	Val	Gly	Val	Arg	Leu	Phe	Gly	Ser	Leu	Val	Gln	Gln		370	375	380	

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<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(1606)

<223> RXN00982

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gcg caa gaa aac atc cgc tgg gaa gaa tgc cca cct cag gta gat att 163
Ala Gln Glu Asn Ile Arg Trp Glu Glu Cys Pro Pro Gln Val Asp Ile
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gcc tcc gct caa tgt ggc agc atc gac gtg ccc atg cac tat tct gat 211
Ala Ser Ala Gln Cys Gly Ser Ile Asp Val Pro Met His Tyr Ser Asp
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ccc tca ctt ggc gat atc agc gtg ggc ttt gtc aag gtc cct gcc caa 259
Pro Ser Leu Gly Asp Ile Ser Val Gly Phe Val Lys Val Pro Ala Gln
40 45 50

ggc gaa aag cac ggc acc atc ttc ggt aac tcc ggt ggc cct ggt ggc 307
Gly Glu Lys His Gly Thr Ile Phe Gly Asn Ser Gly Gly Pro Gly Gly
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gat gcc tat agc ttc ttc ggc agc caa tcc atg aac tgg cca gaa gcc 355
Asp Ala Tyr Ser Phe Phe Gly Ser Gln Ser Met Asn Trp Pro Glu Ala
70 75 80 85

atg tac caa aac tac gac ctc gtt gca gtg cag cct cgc gga atg gtc 403
Met Tyr Gln Asn Tyr Asp Leu Val Ala Val Gln Pro Arg Gly Met Val
90 95 100

ggc tcc aca ccg gtt aac tgc gac aac atc gca cca gga tac gat ttc 451
Gly Ser Thr Pro Val Asn Cys Asp Asn Ile Ala Pro Gly Tyr Asp Phe
105 110 115

ctc tcg ctg ctc acc cgc gaa ggc gct ttc gtt aaa gaa tcc tgc gag 499
Leu Ser Leu Leu Thr Arg Glu Gly Ala Phe Val Lys Glu Ser Cys Glu
120 125 130

atc ggc acc ccc ggc tac acc tcc agc ctg acc acc gac aac acc gcc 547
Ile Gly Thr Pro Gly Tyr Thr Ser Ser Leu Thr Thr Asp Asn Thr Ala
135 140 145

aac gac tgg gag cgc gtc cgc caa gca ctt ggc gat gac aag atc tcc 595
Asn Asp Trp Glu Arg Val Arg Gln Ala Leu Gly Asp Asp Lys Ile Ser
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gta act gac acc ggc gac gac cca tac gtc atc gaa agc atc aac gcc Val Thr Asp Thr Gly Asp Asp Pro Tyr Val Ile Glu Ser Ile Asn Ala 345 350 355	1171
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cca gac cca gta gca atg gca cgc atg gcc tgg aca agc atg gtc acc Pro Asp Pro Val Ala Met Ala Arg Met Ala Trp Thr Ser Met Val Thr 375 380 385	1267
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Pro	Gln	Pro	Ser	Thr	Trp	Pro	Met	Leu	Ala	Gly	Ala	Ile	Ser	Gly	Gln	
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 Ile Phe Gly Leu Ser Tyr Gly Thr Tyr Leu Gly Ser Val Tyr Ala Thr
 170 175 180

 cgc tac cca cag cac acc gac aag gtt gtc ctc gat tcc gca atg gcg 691
 Arg Tyr Pro Gln His Thr Asp Lys Val Val Leu Asp Ser Ala Met Ala
 185 190 195

 ccc agc ctg gca tgg aac ggc atc atg gcc tcc caa gaa cag ggc tac 739
 Pro Ser Leu Ala Trp Asn Gly Ile Met Ala Ser Gln Glu Gln Gly Tyr
 200 205 210

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 Lys Asn Ser Leu Asn Asp Phe Phe Thr Trp Val Ala Glu Asn Asn Asp
 215 220 225

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 Thr Tyr Gly Leu Gly Thr Thr Pro Leu Ala Val Tyr Gln Asn Trp Ser
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 Asn Lys Ile Val Ala Glu Thr Gly Thr Asn Pro Thr Val Ala Pro Pro
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 Pro Ala Gln Val Gly Asp Val Pro Pro Ala Phe Ala Trp Ala Gly Gln
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 Ala Gly Ala Asp Met Met Thr Ala Thr Asn Pro Thr Ser Val Gln Leu
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 Gln Gly Leu Ala Thr Gln Leu Leu Asn Pro Gly Ser Asn Gln Ser Leu
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 Ser Pro Leu Leu Asn Val Thr Arg Ala Tyr Ile Pro Gln Pro Ser Thr
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 caa acc cca tac tgg acc cac aac gag ctt gcc gac gcc atg aac gcc 96
 Gln Thr Pro Tyr Trp Thr His Asn Glu Leu Ala Asp Ala Met Asn Ala
 20 25 30
 cac gtg gtc acc gtc aac gga cca gga cac ggc caa tcc atc ggc ggc 144
 His Val Val Thr Val Asn Gly Pro Gly His Gly Gln Ser Ile Gly Gly
 35 40 45
 acc aac caa gca atc aac gac att gtt gtg gac tac ctc cgc acc gga 192
 Thr Asn Gln Ala Ile Asn Asp Ile Val Val Asp Tyr Leu Arg Thr Gly
 50 55 60
 cac acc gac gcc acc tgg gtc gaa ggc aac aca ccc acc cca att acg 240
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 Ala Gly

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<400> 146
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 35 40 45
 Thr Asn Gln Ala Ile Asn Asp Ile Val Val Asp Tyr Leu Arg Thr Gly
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Tyr Pro Glu Ser Tyr Ser Val Ile Ala Ser Asn Glu Ala Ser Lys His	
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ggc ttg cag acc acc atc ctg gat gag aag cag ctt gct gat caa ggt	144
Gly Leu Gln Thr Thr Ile Leu Asp Glu Lys Gln Leu Ala Asp Gln Gly	
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Phe Gly Gly Ile Leu Ala Val Gly Asn Gly Ser Ser Arg Lys Pro Arg	
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Leu Leu Arg Ile Asp Trp Lys Pro Arg Lys Ala Lys Lys Ser Ile Ala	
65 70 75 80	
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Leu Val Gly Lys Gly Ile Thr Phe Asp Thr Gly Gly Ile Ser Ile Lys	
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cct ggc gca agc atg gag aac atg atc tcc gac atg ggt gga tcc gca	336
Pro Gly Ala Ser Met Glu Asn Met Ile Ser Asp Met Gly Gly Ser Ala	
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tcc gta ttg gcc acc att atc gct gca gct cgt ttg aac ctg tcg atc	384
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115 120 125	
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Asn Val Phe Ala Phe Leu Pro Met Ala Glu Asn Met Pro Ser Gly Asp	
130 135 140	
gct ttc cgc ccc ggc gat gtc atc act cat ttc ggt ggt atc acc tcc	480
Ala Phe Arg Pro Gly Asp Val Ile Thr His Phe Gly Gly Ile Thr Ser	
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Glu Ile Leu Asn Thr Asp Ala Glu Gly Arg Leu Ile Leu Ala Asp Ala	
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180 185 190	
acc ctg act ggt gct caa tta gtc gct tta ggc ctg cgg act tca ggt	624

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Val	Met	Gly	Thr	Asp	Glu	Phe	Arg	Asp	Ser	Val	Ala	Lys	Thr	Gly	Arg		
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cgt	ttc	gca	gga	atg	tct	gct	gcg	ggg	cgt	tac	ttg	cag	gaa	ttc	gtt	816	
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Asn	Thr	Ala	Gly	Glu	Phe	Gly	Tyr	Thr	Pro	Lys	Arg	Ala	Thr	Gly	Gln		
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Pro	Val	Arg	Thr	Phe	Val	Gln	Val	Leu	Lys	Asp	Leu	Ser	Glu	Ser			
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Gly	Leu	Gln	Thr	Thr	Ile	Leu	Asp	Glu	Lys	Gln	Leu	Ala	Asp	Gln	Gly
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Phe	Gly	Gly	Ile	Leu	Ala	Val	Gly	Asn	Gly	Ser	Ser	Arg	Lys	Pro	Arg
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Leu	Leu	Arg	Ile	Asp	Trp	Lys	Pro	Arg	Lys	Ala	Lys	Lys	Ser	Ile	Ala
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Leu	Val	Gly	Lys	Gly	Ile	Thr	Phe	Asp	Thr	Gly	Gly	Ile	Ser	Ile	Lys
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Pro	Gly	Ala	Ser	Met	Glu	Asn	Met	Ile	Ser	Asp	Met	Gly	Gly	Ser	Ala
			100					105					110		

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 115 120 125
 Asn Val Phe Ala Phe Leu Pro Met Ala Glu Asn Met Pro Ser Gly Asp
 130 135 140
 Ala Phe Arg Pro Gly Asp Val Ile Thr His Phe Gly Gly Ile Thr Ser
 145 150 155 160
 Glu Ile Leu Asn Thr Asp Ala Glu Gly Arg Leu Ile Leu Ala Asp Ala
 165 170 175
 Ile Ala Tyr Ala Ser Glu Asp Lys Pro Asp Tyr Leu Ile Asp Ala Ala
 180 185 190
 Thr Leu Thr Gly Ala Gln Leu Val Ala Leu Gly Leu Arg Thr Ser Gly
 195 200 205
 Val Met Gly Thr Asp Glu Phe Arg Asp Ser Val Ala Lys Thr Gly Arg
 210 215 220
 Glu Val Gly Glu Gln Ala Trp Ala Met Pro Leu Pro Glu Glu Leu Asp
 225 230 235 240
 Glu Gln Val Lys Ser Pro Val Ala Asp Leu Arg Asn Val Thr Asn Ser
 245 250 255
 Arg Phe Ala Gly Met Ser Ala Ala Gly Arg Tyr Leu Gln Glu Phe Val
 260 265 270
 Gly Ala Asp Ile Glu Trp Ala His Val Asp Ile Ala Gly Pro Ala Tyr
 275 280 285
 Asn Thr Ala Gly Glu Phe Gly Tyr Thr Pro Lys Arg Ala Thr Gly Gln
 290 295 300
 Pro Val Arg Thr Phe Val Gln Val Leu Lys Asp Leu Ser Glu Ser
 305 310 315

<210> 149

<211> 980

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(957)

<223> FRXA01181

<400> 149

tct gta ctg ctc gct cgc gac ttg gtg aac acc cct tca tca cac ctg 48

Ser Val Leu Leu Ala Arg Asp Leu Val Asn Thr Pro Ser Ser His Leu

1

5

10

15

tac cca gag tcc tac tca gta att gca tcc aac gaa gcg tcc aag cac 96

Tyr Pro Glu Ser Tyr Ser Val Ile Ala Ser Asn Glu Ala Ser Lys His

20

25

30

ggc ttg cag acc acc atc ctg gat gag aag cag ctt gct gat caa ggt 144

Gly Leu Gln Thr Thr Ile Leu Asp Glu Lys Gln Leu Ala Asp Gln Gly

35	40	45	
ttc ggc ggc atc ctc gca gtc ggt aac ggc tcc tcc cgc aag cct cgt Phe Gly Gly Ile Leu Ala Val Gly Asn Gly Ser Ser Arg Lys Pro Arg 50 55 60			192
ctg ctg cgc atc gat tgg aag cca cgc aag gct aag aag tcg atc gct Leu Leu Arg Ile Asp Trp Lys Pro Arg Lys Ala Lys Lys Ser Ile Ala 65 70 75 80			240
ttg gtt ggc aag ggc atc acc ttt gac acc ggc gga att tcc atc aag Leu Val Gly Lys Gly Ile Thr Phe Asp Thr Gly Gly Ile Ser Ile Lys 85 90 95			288
cct ggc gca agc atg gag aac atg atc tcc gac atg ggt gga tcc gca Pro Gly Ala Ser Met Glu Asn Met Ile Ser Asp Met Gly Gly Ser Ala 100 105 110			336
tcc gta ttg gcc acc att atc gct gca gct cgt ttg aac ctg tcg atc Ser Val Leu Ala Thr Ile Ile Ala Ala Ala Arg Leu Asn Leu Ser Ile 115 120 125			384
aac gtc ttc gcg ttc cta cca atg gct gag aac atg cca tcc ggt gac Asn Val Phe Ala Phe Leu Pro Met Ala Glu Asn Met Pro Ser Gly Asp 130 135 140			432
gct ttc cgc ccc ggc gat gtc atc act cat ttc ggt ggt atc acc tcc Ala Phe Arg Pro Gly Asp Val Ile Thr His Phe Gly Gly Ile Thr Ser 145 150 155 160			480
gaa atc ttg aac acc gac gct gaa ggc cgc ctc att ctg gca gat gcc Glu Ile Leu Asn Thr Asp Ala Glu Gly Arg Leu Ile Leu Ala Asp Ala 165 170 175			528
att gct tac gct tct gaa gat aag cct gac tac ctc att gat gcg gca Ile Ala Tyr Ala Ser Glu Asp Lys Pro Asp Tyr Leu Ile Asp Ala Ala 180 185 190			576
acc ctg act ggt gct caa tta gtc gct tta ggc ctg cgg act tca ggt Thr Leu Thr Gly Ala Gln Leu Val Ala Leu Gly Leu Arg Thr Ser Gly 195 200 205			624
gtc atg ggt acc gat gag ttc cgc gac agc gtt gcc aag act ggc cgc Val Met Gly Thr Asp Glu Phe Arg Asp Ser Val Ala Lys Thr Gly Arg 210 215 220			672
gag gtt ggc gag caa gca tgg gca atg cct ctt cct gaa gag ctc gat Glu Val Gly Glu Gln Ala Trp Ala Met Pro Leu Pro Glu Glu Leu Asp 225 230 235 240			720
gag cag gtt aag tcc cct gtc gct gac ctg cgc aat gtc acc aat tcc Glu Gln Val Lys Ser Pro Val Ala Asp Leu Arg Asn Val Thr Asn Ser 245 250 255			768
cgt ttc gca gga atg tct gct gcg ggt cgt tac ttg cag gaa ttc gtt Arg Phe Ala Gly Met Ser Ala Ala Gly Arg Tyr Leu Gln Glu Phe Val 260 265 270			816
ggt gcc gac atc gag tgg gct cac gtc gat atc gct ggc cct gca tac Gly Ala Asp Ile Glu Trp Ala His Val Asp Ile Ala Gly Pro Ala Tyr 275 280 285			864

aac act gct ggt gaa ttc ggt tac acg cca aag cgc gca acc gga caa 912
 Asn Thr Ala Gly Glu Phe Gly Tyr Thr Pro Lys Arg Ala Thr Gly Gln
 290 295 300

cca gtg cgc acc ttc gtt cag gtt ctg aag gat ctg tcg gaa agc 957
 Pro Val Arg Thr Phe Val Gln Val Leu Lys Asp Leu Ser Glu Ser
 305 310 315

taaacgctag ttaaagatca gga 980

<210> 150

<211> 319

<212> PRT

<213> Corynebacterium glutamicum

<400> 150

Ser Val Leu Leu Ala Arg Asp Leu Val Asn Thr Pro Ser Ser His Leu
 1 5 10 15

Tyr Pro Glu Ser Tyr Ser Val Ile Ala Ser Asn Glu Ala Ser Lys His
 20 25 30

Gly Leu Gln Thr Thr Ile Leu Asp Glu Lys Gln Leu Ala Asp Gln Gly
 35 40 45

Phe Gly Gly Ile Leu Ala Val Gly Asn Gly Ser Ser Arg Lys Pro Arg
 50 55 60

Leu Leu Arg Ile Asp Trp Lys Pro Arg Lys Ala Lys Lys Ser Ile Ala
 65 70 75 80

Leu Val Gly Lys Gly Ile Thr Phe Asp Thr Gly Gly Ile Ser Ile Lys
 85 90 95

Pro Gly Ala Ser Met Glu Asn Met Ile Ser Asp Met Gly Gly Ser Ala
 100 105 110

Ser Val Leu Ala Thr Ile Ile Ala Ala Ala Arg Leu Asn Leu Ser Ile
 115 120 125

Asn Val Phe Ala Phe Leu Pro Met Ala Glu Asn Met Pro Ser Gly Asp
 130 135 140

Ala Phe Arg Pro Gly Asp Val Ile Thr His Phe Gly Gly Ile Thr Ser
 145 150 155 160

Glu Ile Leu Asn Thr Asp Ala Glu Gly Arg Leu Ile Leu Ala Asp Ala
 165 170 175

Ile Ala Tyr Ala Ser Glu Asp Lys Pro Asp Tyr Leu Ile Asp Ala Ala
 180 185 190

Thr Leu Thr Gly Ala Gln Leu Val Ala Leu Gly Leu Arg Thr Ser Gly
 195 200 205

Val Met Gly Thr Asp Glu Phe Arg Asp Ser Val Ala Lys Thr Gly Arg
 210 215 220

Glu Val Gly Glu Gln Ala Trp Ala Met Pro Leu Pro Glu Glu Leu Asp

225		230		235		240
Glu Gln Val Lys Ser Pro Val Ala Asp Leu Arg Asn Val Thr Asn Ser						
	245			250		255
Arg Phe Ala Gly Met Ser Ala Ala Gly Arg Tyr Leu Gln Glu Phe Val						
	260			265		270
Gly Ala Asp Ile Glu Trp Ala His Val Asp Ile Ala Gly Pro Ala Tyr						
	275			280		285
Asn Thr Ala Gly Glu Phe Gly Tyr Thr Pro Lys Arg Ala Thr Gly Gln						
	290			295		300
Pro Val Arg Thr Phe Val Gln Val Leu Lys Asp Leu Ser Glu Ser						
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 <222> (101)..(2701)
 <223> RXN01014

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tctaagggtta gcgccccctc aaatttcaag gagcattaaa ttg acg tcc act aat 115
 Leu Thr Ser Thr Asn
 1 5

ctc acc cga cag gaa gct tcg gat cgt tcg agg tta ctg agt gta gaa 163
 Leu Thr Arg Gln Glu Ala Ser Asp Arg Ser Arg Leu Leu Ser Val Glu
 10 15 20

aac tat gac att gca ctt gat ctc aac aac ggt gat gag ttt ttt agt 211
 Asn Tyr Asp Ile Ala Leu Asp Leu Asn Asn Gly Asp Glu Phe Phe Ser
 25 30 35

tcc tcc acc gtt gtc agc ttc act gtc agg aag gct ggc gat acc ttt 259
 Ser Ser Thr Val Val Ser Phe Thr Val Arg Lys Ala Gly Asp Thr Phe
 40 45 50

att gat ctc cgc gca gca agc gtt gag gag gtt cgc ctg gac aat gtg 307
 Ile Asp Leu Arg Ala Ala Ser Val Glu Glu Val Arg Leu Asp Asn Val
 55 60 65

tcc atc aaa gat gag gct cta acc ctt ggc aag aac ggc tac gac gag 355
 Ser Ile Lys Asp Glu Ala Leu Thr Leu Gly Lys Asn Gly Tyr Asp Glu
 70 75 80 85

acg ttc ggc atc gcc ctg aag ggt ctt act ccc ggc gcg cac acc ttg 403
 Thr Phe Gly Ile Ala Leu Lys Gly Leu Thr Pro Gly Ala His Thr Leu
 90 95 100

cgg gta acg gcg tct atc ccc tat tcc cgc acc ggt gaa ggc ctg cac 451
 Arg Val Thr Ala Ser Ile Pro Tyr Ser Arg Thr Gly Glu Gly Leu His

105								110				115					
cgc	atg	gtg	gat	cca	gca	gac	aat	gag	gtg	tat	ttg	tac	acc	cag	ttt	499	
Arg	Met	Val	Asp	Pro	Ala	Asp	Asn	Glu	Val	Tyr	Leu	Tyr	Thr	Gln	Phe		
		120					125					130					
gag	acc	gcc	gat	gcc	aag	cgt	atg	ttc	gcg	tgt	ttc	gat	cag	cca	gac	547	
Glu	Thr	Ala	Asp	Ala	Lys	Arg	Met	Phe	Ala	Cys	Phe	Asp	Gln	Pro	Asp		
		135				140					145						
ctc	aag	gct	acc	tat	gat	ctg	aac	atc	aaa	act	cct	aag	ggt	tgg	aag	595	
Leu	Lys	Ala	Thr	Tyr	Asp	Leu	Asn	Ile	Lys	Thr	Pro	Lys	Gly	Trp	Lys		
					155					160					165		
atc	att	tcc	aac	tct	gag	cag	cag	gtt	tcc	act	cag	cac	act	gat	tac	643	
Ile	Ile	Ser	Asn	Ser	Glu	Gln	Gln	Val	Ser	Thr	Gln	His	Thr	Asp	Tyr		
				170					175					180			
gat	acc	cac	att	tcc	cga	gtg	gac	tat	ccc	ctc	tcc	acc	tac	ctg	att	691	
Asp	Thr	His	Ile	Ser	Arg	Val	Asp	Tyr	Pro	Leu	Ser	Thr	Tyr	Leu	Ile		
			185					190					195				
gcg	gtg	tgc	gcg	ggt	cgt	tac	cac	gag	gtg	tgc	gat	gtc	tgg	aag	ggt	739	
Ala	Val	Cys	Ala	Gly	Arg	Tyr	His	Glu	Val	Cys	Asp	Val	Trp	Lys	Gly		
		200					205					210					
acg	ctc	acc	cac	cat	gca	gaa	aca	cct	gcc	gat	cag	cca	act	gag	ctg	787	
Thr	Leu	Thr	His	His	Ala	Glu	Thr	Pro	Ala	Asp	Gln	Pro	Thr	Glu	Leu		
		215				220					225						
act	gtt	ccg	ctt	gct	ctc	tac	tgc	cgc	agt	tct	ttg	gct	aaa	gat	ctt	835	
Thr	Val	Pro	Leu	Ala	Leu	Tyr	Cys	Arg	Ser	Ser	Leu	Ala	Lys	Asp	Leu		
					235					240					245		
gat	gcg	gtg	cgt	ctg	ttt	acc	gaa	acg	aag	cag	ggc	ttt	gat	tgg	tac	883	
Asp	Ala	Val	Arg	Leu	Phe	Thr	Glu	Thr	Lys	Gln	Gly	Phe	Asp	Trp	Tyr		
				250					255					260			
cac	cgc	aac	ttc	ggt	gtg	gcg	tac	cca	ttc	ggc	aag	tac	gat	cag	atc	931	
His	Arg	Asn	Phe	Gly	Val	Ala	Tyr	Pro	Phe	Gly	Lys	Tyr	Asp	Gln	Ile		
			265					270					275				
ttc	gtc	cct	gaa	ttt	aat	gct	ggc	gcg	atg	gag	aac	gcc	ggc	gct	gtc	979	
Phe	Val	Pro	Glu	Phe	Asn	Ala	Gly	Ala	Met	Glu	Asn	Ala	Gly	Ala	Val		
		280					285					290					
acc	atc	cgc	gat	gag	tac	gtt	ttt	gca	tcc	aag	gca	acc	cgt	tac	cgc	1027	
Thr	Ile	Arg	Asp	Glu	Tyr	Val	Phe	Ala	Ser	Lys	Ala	Thr	Arg	Tyr	Arg		
		295				300					305						
tac	gag	cgc	cgc	gct	gaa	acc	atc	ctt	cac	gag	ctc	gct	cac	atg	tgg	1075	
Tyr	Glu	Arg	Arg	Ala	Glu	Thr	Ile	Leu	His	Glu	Leu	Ala	His	Met	Trp		
					315					320					325		
ttc	ggt	gtg	ctg	gtg	acc	atg	cag	tgg	tgg	gat	gat	ctg	tgg	ctc	aac	1123	
Phe	Gly	Val	Leu	Val	Thr	Met	Gln	Trp	Trp	Asp	Asp	Leu	Trp	Leu	Asn		
				330				335					340				
gag	tcc	ttc	gcc	act	tgg	tcc	gcg	gca	att	tct	cag	gct	gag	gaa	act	1171	
Glu	Ser	Phe	Ala	Thr	Trp	Ser	Ala	Ala	Ile	Ser	Gln	Ala	Glu	Glu	Thr		
			345					350					355				

gaa tac aac act gca tgg gtg act ttc gcc aat gtg gag aag tcg tgg	1219
Glu Tyr Asn Thr Ala Trp Val Thr Phe Ala Asn Val Glu Lys Ser Trp	
360 365 370	
gcg tac cag cag gat cag ctg cct tcc acc cac ccg gtg ttc tct gac	1267
Ala Tyr Gln Gln Asp Gln Leu Pro Ser Thr His Pro Val Phe Ser Asp	
375 380 385	
gga tac gac att gag act gtc gac cag aac ttc gac ggc atc acc tac	1315
Gly Tyr Asp Ile Glu Thr Val Asp Gln Asn Phe Asp Gly Ile Thr Tyr	
390 395 400 405	
gca aag ggc gcc tcg gtg ctc aag cag ctg cag gca tac gtt ggc cgt	1363
Ala Lys Gly Ala Ser Val Leu Lys Gln Leu Gln Ala Tyr Val Gly Arg	
410 415 420	
gag gaa ttc ctg gca ggc gta cgc agg cac ttt gcc aac cac gca tgg	1411
Glu Glu Phe Leu Ala Gly Val Arg Arg His Phe Ala Asn His Ala Trp	
425 430 435	
ggc aac gcc agc ttt gat gat ctg ctc ggc gcc ctc gag cag tcc tcc	1459
Gly Asn Ala Ser Phe Asp Asp Leu Leu Gly Ala Leu Glu Gln Ser Ser	
440 445 450	
ggc cgc gac ctc tcc gac tgg gca aac cag tgg ctc aag acc acc ggc	1507
Gly Arg Asp Leu Ser Asp Trp Ala Asn Gln Trp Leu Lys Thr Thr Gly	
455 460 465	
atc aac acc ctc ggc gca aag ttc acc acc gac aac ggc aaa tac acc	1555
Ile Asn Thr Leu Gly Ala Lys Phe Thr Thr Asp Asn Gly Lys Tyr Thr	
470 475 480 485	
tcc ttc tcc gtc acc cag acc ggc gcc gcg ccg ggt gcc ggt gag ctg	1603
Ser Phe Ser Val Thr Gln Thr Gly Ala Ala Pro Gly Ala Gly Glu Leu	
490 495 500	
cgg act cac cgc atc gcg gtg ggt ctt tat aag ctt gtc gac gga tcc	1651
Arg Thr His Arg Ile Ala Val Gly Leu Tyr Lys Leu Val Asp Gly Ser	
505 510 515	
ctc aac cgc tac gca cga gta gaa ctt gac tgc agt ggc gcg tcg aca	1699
Leu Asn Arg Tyr Ala Arg Val Glu Leu Asp Cys Ser Gly Ala Ser Thr	
520 525 530	
agc gtt gaa gag atc gtt gga ctt gag cag gct gac ttc gtg ctg gtc	1747
Ser Val Glu Glu Ile Val Gly Leu Glu Gln Ala Asp Phe Val Leu Val	
535 540 545	
aac gat gat gat ctg acg tat gcg ctg ctg gat ctg gat gat gat tca	1795
Asn Asp Asp Asp Leu Thr Tyr Ala Leu Leu Asp Leu Asp Asp Asp Ser	
550 555 560 565	
cgc aat ttt gtc atc gac aat att gat aag ttc agc gac cct atg cct	1843
Arg Asn Phe Val Ile Asp Asn Ile Asp Lys Phe Ser Asp Pro Met Pro	
570 575 580	
cgc acg ctg gtg tgg tcc gct gcg tgg gag atg act cgc gct ggt cag	1891
Arg Thr Leu Val Trp Ser Ala Ala Trp Glu Met Thr Arg Ala Gly Gln	
585 590 595	

atg aag gct cgt gat ttc atc gcg ctg gtt gct cgt ggc gct gct gcg	1939
Met Lys Ala Arg Asp Phe Ile Ala Leu Val Ala Arg Gly Ala Ala Ala	
600 605 610	
gaa act gaa att gct gtg ctg gag cgc att ctc gcg cag gct acc tct	1987
Glu Thr Glu Ile Ala Val Leu Glu Arg Ile Leu Ala Gln Ala Thr Ser	
615 620 625	
gcg ctg aag agc tac gcc gac cca gcg tgg gca gaa gca act gga aat	2035
Ala Leu Lys Ser Tyr Ala Asp Pro Ala Trp Ala Glu Ala Thr Gly Asn	
630 635 640 645	
gac ctg ctg gcc gat gct ttc ctt gag ggt gct cgc tcc gca gaa cca	2083
Asp Leu Leu Ala Asp Ala Phe Leu Glu Gly Ala Arg Ser Ala Glu Pro	
650 655 660	
gac tcc gac act cag ttg gcg ttc att cag gct ctg gca aaa gca acg	2131
Asp Ser Asp Thr Gln Leu Ala Phe Ile Gln Ala Leu Ala Lys Ala Thr	
665 670 675	
ctc aat gat gct gct gcc gat tac ttc cgc gac att ctt gcc ggc aac	2179
Leu Asn Asp Ala Ala Ala Asp Tyr Phe Arg Asp Ile Leu Ala Gly Asn	
680 685 690	
gtc gaa ggc ctg acc gtg gat cct gac ctg cgt tgg tgg gca ctg act	2227
Val Glu Gly Leu Thr Val Asp Pro Asp Leu Arg Trp Trp Ala Leu Thr	
695 700 705	
gcg ctt atc gcc cgt ggt gac atc gag gct gtc gaa gat gca atc gcc	2275
Ala Leu Ile Ala Arg Gly Asp Ile Glu Ala Val Glu Asp Ala Ile Ala	
710 715 720 725	
gct gaa ctt tcc cgc gac aac tcc agt gcc tcc ttc ctc gca tca ctt	2323
Ala Glu Leu Ser Arg Asp Asn Ser Ser Ala Ser Phe Leu Ala Ser Leu	
730 735 740	
cga gcc ggt gcc gct gtg aac act gaa gaa gtg aag gct gct gca tac	2371
Arg Ala Gly Ala Ala Val Asn Thr Glu Glu Val Lys Ala Ala Ala Tyr	
745 750 755	
aag cat gtc acg gca gtt gat agt ggc cta tcc aac ctg gag ctg cgc	2419
Lys His Val Thr Ala Val Asp Ser Gly Leu Ser Asn Leu Glu Leu Arg	
760 765 770	
cac aag att gaa ggc ctc aca ttc act ggc tct tct gaa ctg ctg caa	2467
His Lys Ile Glu Gly Leu Thr Phe Thr Gly Ser Ser Glu Leu Leu Gln	
775 780 785	
gcc tac aac gag cag tac ttc gaa atc ctt gat gat gtg tgg gcg aac	2515
Ala Tyr Asn Glu Gln Tyr Phe Glu Ile Leu Asp Asp Val Trp Ala Asn	
790 795 800 805	
ttc tcc ggc gaa atg gca cag cag atc gtc ctc gga ctg ttc cct tca	2563
Phe Ser Gly Glu Met Ala Gln Gln Ile Val Leu Gly Leu Phe Pro Ser	
810 815 820	
tggt aac gtt tcc gaa gag ggt ctc aag cgt acc gac gag ttt ctt gat	2611
Trp Asn Val Ser Glu Glu Gly Leu Lys Arg Thr Asp Glu Phe Leu Asp	
825 830 835	
ggc gaa cat gtc gca ggc atc aag cga att gtt tcc gaa tcc ctc gac	2659

Gly Glu His Val Ala Gly Ile Lys Arg Ile Val Ser Glu Ser Leu Asp
 840 845 850

cgc act gcc cgt gct ctg cgc aac cgt gcg gca gat gct gcg 2701
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<210> 152

<211> 867

<212> PRT

<213> Corynebacterium glutamicum

<400> 152

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Leu Leu Ser Val Glu Asn Tyr Asp Ile Ala Leu Asp Leu Asn Asn Gly
 20 25 30

Asp Glu Phe Phe Ser Ser Ser Thr Val Val Ser Phe Thr Val Arg Lys
 35 40 45

Ala Gly Asp Thr Phe Ile Asp Leu Arg Ala Ala Ser Val Glu Glu Val
 50 55 60

Arg Leu Asp Asn Val Ser Ile Lys Asp Glu Ala Leu Thr Leu Gly Lys
 65 70 75 80

Asn Gly Tyr Asp Glu Thr Phe Gly Ile Ala Leu Lys Gly Leu Thr Pro
 85 90 95

Gly Ala His Thr Leu Arg Val Thr Ala Ser Ile Pro Tyr Ser Arg Thr
 100 105 110

Gly Glu Gly Leu His Arg Met Val Asp Pro Ala Asp Asn Glu Val Tyr
 115 120 125

Leu Tyr Thr Gln Phe Glu Thr Ala Asp Ala Lys Arg Met Phe Ala Cys
 130 135 140

Phe Asp Gln Pro Asp Leu Lys Ala Thr Tyr Asp Leu Asn Ile Lys Thr
 145 150 155 160

Pro Lys Gly Trp Lys Ile Ile Ser Asn Ser Glu Gln Gln Val Ser Thr
 165 170 175

Gln His Thr Asp Tyr Asp Thr His Ile Ser Arg Val Asp Tyr Pro Leu
 180 185 190

Ser Thr Tyr Leu Ile Ala Val Cys Ala Gly Arg Tyr His Glu Val Cys
 195 200 205

Asp Val Trp Lys Gly Thr Leu Thr His His Ala Glu Thr Pro Ala Asp
 210 215 220

Gln Pro Thr Glu Leu Thr Val Pro Leu Ala Leu Tyr Cys Arg Ser Ser
 225 230 235 240

Leu Ala Lys Asp Leu Asp Ala Val Arg Leu Phe Thr Glu Thr Lys Gln
 245 250 255
 Gly Phe Asp Trp Tyr His Arg Asn Phe Gly Val Ala Tyr Pro Phe Gly
 260 265 270
 Lys Tyr Asp Gln Ile Phe Val Pro Glu Phe Asn Ala Gly Ala Met Glu
 275 280 285
 Asn Ala Gly Ala Val Thr Ile Arg Asp Glu Tyr Val Phe Ala Ser Lys
 290 295 300
 Ala Thr Arg Tyr Arg Tyr Glu Arg Arg Ala Glu Thr Ile Leu His Glu
 305 310 315 320
 Leu Ala His Met Trp Phe Gly Val Leu Val Thr Met Gln Trp Trp Asp
 325 330 335
 Asp Leu Trp Leu Asn Glu Ser Phe Ala Thr Trp Ser Ala Ala Ile Ser
 340 345 350
 Gln Ala Glu Glu Thr Glu Tyr Asn Thr Ala Trp Val Thr Phe Ala Asn
 355 360 365
 Val Glu Lys Ser Trp Ala Tyr Gln Gln Asp Gln Leu Pro Ser Thr His
 370 375 380
 Pro Val Phe Ser Asp Gly Tyr Asp Ile Glu Thr Val Asp Gln Asn Phe
 385 390 395 400
 Asp Gly Ile Thr Tyr Ala Lys Gly Ala Ser Val Leu Lys Gln Leu Gln
 405 410 415
 Ala Tyr Val Gly Arg Glu Glu Phe Leu Ala Gly Val Arg Arg His Phe
 420 425 430
 Ala Asn His Ala Trp Gly Asn Ala Ser Phe Asp Asp Leu Leu Gly Ala
 435 440 445
 Leu Glu Gln Ser Ser Gly Arg Asp Leu Ser Asp Trp Ala Asn Gln Trp
 450 455 460
 Leu Lys Thr Thr Gly Ile Asn Thr Leu Gly Ala Lys Phe Thr Thr Asp
 465 470 475 480
 Asn Gly Lys Tyr Thr Ser Phe Ser Val Thr Gln Thr Gly Ala Ala Pro
 485 490 495
 Gly Ala Gly Glu Leu Arg Thr His Arg Ile Ala Val Gly Leu Tyr Lys
 500 505 510
 Leu Val Asp Gly Ser Leu Asn Arg Tyr Ala Arg Val Glu Leu Asp Cys
 515 520 525
 Ser Gly Ala Ser Thr Ser Val Glu Glu Ile Val Gly Leu Glu Gln Ala
 530 535 540

Asp Phe Val Leu Val Asn Asp Asp Asp Leu Thr Tyr Ala Leu Leu Asp
 545 550 555 560
 Leu Asp Asp Asp Ser Arg Asn Phe Val Ile Asp Asn Ile Asp Lys Phe

565					570					575					
Ser	Asp	Pro	Met	Pro	Arg	Thr	Leu	Val	Trp	Ser	Ala	Ala	Trp	Glu	Met
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Thr	Arg	Ala	Gly	Gln	Met	Lys	Ala	Arg	Asp	Phe	Ile	Ala	Leu	Val	Ala
		595					600					605			
Arg	Gly	Ala	Ala	Ala	Glu	Thr	Glu	Ile	Ala	Val	Leu	Glu	Arg	Ile	Leu
	610					615					620				
Ala	Gln	Ala	Thr	Ser	Ala	Leu	Lys	Ser	Tyr	Ala	Asp	Pro	Ala	Trp	Ala
625					630					635					640
Glu	Ala	Thr	Gly	Asn	Asp	Leu	Leu	Ala	Asp	Ala	Phe	Leu	Glu	Gly	Ala
				645					650					655	
Arg	Ser	Ala	Glu	Pro	Asp	Ser	Asp	Thr	Gln	Leu	Ala	Phe	Ile	Gln	Ala
			660					665						670	
Leu	Ala	Lys	Ala	Thr	Leu	Asn	Asp	Ala	Ala	Ala	Asp	Tyr	Phe	Arg	Asp
		675					680					685			
Ile	Leu	Ala	Gly	Asn	Val	Glu	Gly	Leu	Thr	Val	Asp	Pro	Asp	Leu	Arg
	690					695					700				
Trp	Trp	Ala	Leu	Thr	Ala	Leu	Ile	Ala	Arg	Gly	Asp	Ile	Glu	Ala	Val
705					710					715					720
Glu	Asp	Ala	Ile	Ala	Ala	Glu	Leu	Ser	Arg	Asp	Asn	Ser	Ser	Ala	Ser
				725					730					735	
Phe	Leu	Ala	Ser	Leu	Arg	Ala	Gly	Ala	Ala	Val	Asn	Thr	Glu	Glu	Val
			740				745						750		
Lys	Ala	Ala	Ala	Tyr	Lys	His	Val	Thr	Ala	Val	Asp	Ser	Gly	Leu	Ser
		755					760					765			
Asn	Leu	Glu	Leu	Arg	His	Lys	Ile	Glu	Gly	Leu	Thr	Phe	Thr	Gly	Ser
	770					775					780				
Ser	Glu	Leu	Leu	Gln	Ala	Tyr	Asn	Glu	Gln	Tyr	Phe	Glu	Ile	Leu	Asp
785					790					795					800
Asp	Val	Trp	Ala	Asn	Phe	Ser	Gly	Glu	Met	Ala	Gln	Gln	Ile	Val	Leu
				805					810					815	
Gly	Leu	Phe	Pro	Ser	Trp	Asn	Val	Ser	Glu	Glu	Gly	Leu	Lys	Arg	Thr
			820					825					830		
Asp	Glu	Phe	Leu	Asp	Gly	Glu	His	Val	Ala	Gly	Ile	Lys	Arg	Ile	Val
		835					840					845			
Ser	Glu	Ser	Leu	Asp	Arg	Thr	Ala	Arg	Ala	Leu	Arg	Asn	Arg	Ala	Ala
	850					855					860				

Asp Ala Ala
865

<210> 153

<211> 1578

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(1578)

<223> FRXA01014

<400> 153

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Asp Asp Leu Trp Leu Asn Glu Ser Phe Ala Thr Trp Ser Ala Ala Ile	
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tct cag gct gag gaa act gaa tac aac act gca tgg gtg act ttc gcc	96
Ser Gln Ala Glu Thr Glu Tyr Asn Thr Ala Trp Val Thr Phe Ala	
20 25 30	
aat gtg gag aag tcg tgg gcg tac cag cag gat cag ctg cct tcc acc	144
Asn Val Glu Lys Ser Trp Ala Tyr Gln Gln Asp Gln Leu Pro Ser Thr	
35 40 45	
cac ccg gtg ttc tct gac gga tac gac att gag act gtc gac cag aac	192
His Pro Val Phe Ser Asp Gly Tyr Asp Ile Glu Thr Val Asp Gln Asn	
50 55 60	
ttc gac ggc atc acc tac gca aag ggc gcc tcg gtg ctc aag cag ctg	240
Phe Asp Gly Ile Thr Tyr Ala Lys Gly Ala Ser Val Leu Lys Gln Leu	
65 70 75 80	
cag gca tac gtt ggc cgt gag gaa ttc ctg gca ggc gta cgc agg cac	288
Gln Ala Tyr Val Gly Arg Glu Glu Phe Leu Ala Gly Val Arg Arg His	
85 90 95	
ttt gcc aac cac gca tgg ggc aac gcc agc ttt gat gat ctg ctc ggc	336
Phe Ala Asn His Ala Trp Gly Asn Ala Ser Phe Asp Asp Leu Leu Gly	
100 105 110	
gcc ctc gag cag tcc tcc ggc cgc gac ctc tcc gac tgg gca aac cag	384
Ala Leu Glu Gln Ser Ser Gly Arg Asp Leu Ser Asp Trp Ala Asn Gln	
115 120 125	
tgg ctc aag acc acc ggc atc aac acc ctc ggc gca aag ttc acc acc	432
Trp Leu Lys Thr Thr Gly Ile Asn Thr Leu Gly Ala Lys Phe Thr Thr	
130 135 140	
gac aac ggc aaa tac acc tcc ttc tcc gtc acc cag acc ggc gcc gcg	480
Asp Asn Gly Lys Tyr Thr Ser Phe Ser Val Thr Gln Thr Gly Ala Ala	
145 150 155 160	
ccg ggt gcc ggt gag ctg cgg act cac cgc atc gcg gtg ggt ctt tat	528
Pro Gly Ala Gly Glu Leu Arg Thr His Arg Ile Ala Val Gly Leu Tyr	
165 170 175	
aag ctt gtc gac gga tcc ctc aac cgc tac gca cga gta gaa ctt gac	576
Lys Leu Val Asp Gly Ser Leu Asn Arg Tyr Ala Arg Val Glu Leu Asp	
180 185 190	
tgc agt ggc gcg tcg aca agc gtt gaa gag atc gtt gga ctt gag cag	624
Cys Ser Gly Ala Ser Thr Ser Val Glu Glu Ile Val Gly Leu Glu Gln	
195 200 205	

gct gac ttc gtg ctg gtc aac gat gat gat ctg acg tat gcg ctg ctg	672
Ala Asp Phe Val Leu Val Asn Asp Asp Asp Leu Thr Tyr Ala Leu Leu	
210 215 220	
gat ctg gat gat gat tca cgc aat ttt gtc atc gac aat att gat aag	720
Asp Leu Asp Asp Asp Ser Arg Asn Phe Val Ile Asp Asn Ile Asp Lys	
225 230 235 240	
ttc agc gac cct atg cct cgc acg ctg gtg tgg tcc gct gcg tgg gag	768
Phe Ser Asp Pro Met Pro Arg Thr Leu Val Trp Ser Ala Ala Trp Glu	
245 250 255	
atg act cgc gct ggt cag atg aag gct cgt gat ttc atc gcg ctg gtt	816
Met Thr Arg Ala Gly Gln Met Lys Ala Arg Asp Phe Ile Ala Leu Val	
260 265 270	
gct cgt ggc gct gct gcg gaa act gaa att gct gtg ctg gag cgc att	864
Ala Arg Gly Ala Ala Ala Glu Thr Glu Ile Ala Val Leu Glu Arg Ile	
275 280 285	
ctc gcg cag gct acc tct gcg ctg aag agc tac gcc gac cca gcg tgg	912
Leu Ala Gln Ala Thr Ser Ala Leu Lys Ser Tyr Ala Asp Pro Ala Trp	
290 295 300	
gca gaa gca act gga aat gac ctg ctg gcc gat gct ttc ctt gag ggt	960
Ala Glu Ala Thr Gly Asn Asp Leu Leu Ala Asp Ala Phe Leu Glu Gly	
305 310 315 320	
gct cgc tcc gca gaa cca gac tcc gac act cag ttg gcg ttc att cag	1008
Ala Arg Ser Ala Glu Pro Asp Ser Asp Thr Gln Leu Ala Phe Ile Gln	
325 330 335	
gct ctg gca aaa gca acg ctc aat gat gct gct gcc gat tac ttc cgc	1056
Ala Leu Ala Lys Ala Thr Leu Asn Asp Ala Ala Ala Asp Tyr Phe Arg	
340 345 350	
gac att ctt gcc ggc aac gtc gaa ggc ctg acc gtg gat cct gac ctg	1104
Asp Ile Leu Ala Gly Asn Val Glu Gly Leu Thr Val Asp Pro Asp Leu	
355 360 365	
cgt tgg tgg gca ctg act gcg ctt atc gcc cgt ggt gac atc gag gct	1152
Arg Trp Trp Ala Leu Thr Ala Leu Ile Ala Arg Gly Asp Ile Glu Ala	
370 375 380	
gtc gaa gat gca atc gcc gct gaa ctt tcc cgc gac aac tcc agt gcc	1200
Val Glu Asp Ala Ile Ala Ala Glu Leu Ser Arg Asp Asn Ser Ser Ala	
385 390 395 400	
tcc ttc ctc gca tca ctt cga gcc ggt gcc gct gtg aac act gaa gaa	1248
Ser Phe Leu Ala Ser Leu Arg Ala Gly Ala Ala Val Asn Thr Glu Glu	
405 410 415	
gtg aag gct gct gca tac aag cat gtc ccg gca gtt gat agt ggc cta	1296
Val Lys Ala Ala Ala Tyr Lys His Val Pro Ala Val Asp Ser Gly Leu	
420 425 430	
tcc aac ctg gag ctg cgc cac aag att gaa ggc ctc aca ttc act ggc	1344
Ser Asn Leu Glu Leu Arg His Lys Ile Glu Gly Leu Thr Phe Thr Gly	
435 440 445	

tct ttt gaa ctg ctg caa gcc tac aac gag cag tac ttc gaa atc ctt 1392
 Ser Phe Glu Leu Leu Gln Ala Tyr Asn Glu Gln Tyr Phe Glu Ile Leu
 450 455 460

gat gat gtg tgg gcg aac ttc tcc ggc gaa atg gca cag cag atc gtc 1440
 Asp Asp Val Trp Ala Asn Phe Ser Gly Glu Met Ala Gln Gln Ile Val
 465 470 475 480

ctc gga ctg ttc cct tca tgg aac gtt tcc gaa gag ggt ctc aag cgt 1488
 Leu Gly Leu Phe Pro Ser Trp Asn Val Ser Glu Glu Gly Leu Lys Arg
 485 490 495

acc gac gag ttt ctt gat ggc gaa cat gtc gca ggc atc aag cga att 1536
 Thr Asp Glu Phe Leu Asp Gly Glu His Val Ala Gly Ile Lys Arg Ile
 500 505 510

gtt tcc gaa tcc ctc gac cgc act gcc cgt gct ctg cgc aac 1578
 Val Ser Glu Ser Leu Asp Arg Thr Ala Arg Ala Leu Arg Asn
 515 520 525

<210> 154

<211> 526

<212> PRT

<213> Corynebacterium glutamicum

<400> 154

Asp Asp Leu Trp Leu Asn Glu Ser Phe Ala Thr Trp Ser Ala Ala Ile
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Ser Gln Ala Glu Glu Thr Glu Tyr Asn Thr Ala Trp Val Thr Phe Ala
 20 25 30

Asn Val Glu Lys Ser Trp Ala Tyr Gln Gln Asp Gln Leu Pro Ser Thr
 35 40 45

His Pro Val Phe Ser Asp Gly Tyr Asp Ile Glu Thr Val Asp Gln Asn
 50 55 60

Phe Asp Gly Ile Thr Tyr Ala Lys Gly Ala Ser Val Leu Lys Gln Leu
 65 70 75 80

Gln Ala Tyr Val Gly Arg Glu Glu Phe Leu Ala Gly Val Arg Arg His
 85 90 95

Phe Ala Asn His Ala Trp Gly Asn Ala Ser Phe Asp Asp Leu Leu Gly
 100 105 110

Ala Leu Glu Gln Ser Ser Gly Arg Asp Leu Ser Asp Trp Ala Asn Gln
 115 120 125

Trp Leu Lys Thr Thr Gly Ile Asn Thr Leu Gly Ala Lys Phe Thr Thr
 130 135 140

Asp Asn Gly Lys Tyr Thr Ser Phe Ser Val Thr Gln Thr Gly Ala Ala
 145 150 155 160

Pro Gly Ala Gly Glu Leu Arg Thr His Arg Ile Ala Val Gly Leu Tyr
 165 170 175

Lys Leu Val Asp Gly Ser Leu Asn Arg Tyr Ala Arg Val Glu Leu Asp

180					185					190					
Cys	Ser	Gly	Ala	Ser	Thr	Ser	Val	Glu	Glu	Ile	Val	Gly	Leu	Glu	Gln
		195					200					205			
Ala	Asp	Phe	Val	Leu	Val	Asn	Asp	Asp	Asp	Leu	Thr	Tyr	Ala	Leu	Leu
	210					215					220				
Asp	Leu	Asp	Asp	Asp	Ser	Arg	Asn	Phe	Val	Ile	Asp	Asn	Ile	Asp	Lys
225					230					235					240
Phe	Ser	Asp	Pro	Met	Pro	Arg	Thr	Leu	Val	Trp	Ser	Ala	Ala	Trp	Glu
				245					250					255	
Met	Thr	Arg	Ala	Gly	Gln	Met	Lys	Ala	Arg	Asp	Phe	Ile	Ala	Leu	Val
			260					265					270		
Ala	Arg	Gly	Ala	Ala	Ala	Glu	Thr	Glu	Ile	Ala	Val	Leu	Glu	Arg	Ile
		275					280					285			
Leu	Ala	Gln	Ala	Thr	Ser	Ala	Leu	Lys	Ser	Tyr	Ala	Asp	Pro	Ala	Trp
	290					295					300				
Ala	Glu	Ala	Thr	Gly	Asn	Asp	Leu	Leu	Ala	Asp	Ala	Phe	Leu	Glu	Gly
305					310					315					320
Ala	Arg	Ser	Ala	Glu	Pro	Asp	Ser	Asp	Thr	Gln	Leu	Ala	Phe	Ile	Gln
				325					330					335	
Ala	Leu	Ala	Lys	Ala	Thr	Leu	Asn	Asp	Ala	Ala	Ala	Asp	Tyr	Phe	Arg
			340					345					350		
Asp	Ile	Leu	Ala	Gly	Asn	Val	Glu	Gly	Leu	Thr	Val	Asp	Pro	Asp	Leu
	355						360					365			
Arg	Trp	Trp	Ala	Leu	Thr	Ala	Leu	Ile	Ala	Arg	Gly	Asp	Ile	Glu	Ala
	370					375					380				
Val	Glu	Asp	Ala	Ile	Ala	Ala	Glu	Leu	Ser	Arg	Asp	Asn	Ser	Ser	Ala
385					390					395					400
Ser	Phe	Leu	Ala	Ser	Leu	Arg	Ala	Gly	Ala	Ala	Val	Asn	Thr	Glu	Glu
				405					410					415	
Val	Lys	Ala	Ala	Ala	Tyr	Lys	His	Val	Pro	Ala	Val	Asp	Ser	Gly	Leu
			420					425				430			
Ser	Asn	Leu	Glu	Leu	Arg	His	Lys	Ile	Glu	Gly	Leu	Thr	Phe	Thr	Gly
		435					440					445			
Ser	Phe	Glu	Leu	Leu	Gln	Ala	Tyr	Asn	Glu	Gln	Tyr	Phe	Glu	Ile	Leu
	450					455					460				
Asp	Asp	Val	Trp	Ala	Asn	Phe	Ser	Gly	Glu	Met	Ala	Gln	Gln	Ile	Val
465					470					475					480
Leu	Gly	Leu	Phe	Pro	Ser	Trp	Asn	Val	Ser	Glu	Glu	Gly	Leu	Lys	Arg
				485					490					495	
Thr	Asp	Glu	Phe	Leu	Asp	Gly	Glu	His	Val	Ala	Gly	Ile	Lys	Arg	Ile
			500					505					510		

Val Ser Glu Ser Leu Asp Arg Thr Ala Arg Ala Leu Arg Asn
 515 520 525

<210> 155

<211> 964

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(964)

<223> FRXA01018

<400> 155

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tctaagggta gcgccccctc aaatttcaag gagcattaaa ttg acg tcc act aat 115
 Leu Thr Ser Thr Asn
 1 5

ctc acc cga cag gaa gct tcg gat cgt tcg agg tta ctg agt gta gaa 163
 Leu Thr Arg Gln Glu Ala Ser Asp Arg Ser Arg Leu Leu Ser Val Glu
 10 15 20

aac tat gac att gca ctt gat ctc aac aac ggt gat gag ttt ttt agt 211
 Asn Tyr Asp Ile Ala Leu Asp Leu Asn Asn Gly Asp Glu Phe Phe Ser
 25 30 35

tcc tcc acc gtt gtc agc ttc act gtc agg aag gct ggc gat acc ttt 259
 Ser Ser Thr Val Val Ser Phe Thr Val Arg Lys Ala Gly Asp Thr Phe
 40 45 50

att gat ctc cgc gca gca agc gtt gag gag gtt cgc ctg gac aat gtg 307
 Ile Asp Leu Arg Ala Ala Ser Val Glu Glu Val Arg Leu Asp Asn Val
 55 60 65

tcc atc aaa gat gag gct cta acc ctt ggc aag aac ggc tac gac gag 355
 Ser Ile Lys Asp Glu Ala Leu Thr Leu Gly Lys Asn Gly Tyr Asp Glu
 70 75 80 85

acg ttc ggc atc gcc ctg aag ggt ctt act ccc ggc gcg cac acc ttg 403
 Thr Phe Gly Ile Ala Leu Lys Gly Leu Thr Pro Gly Ala His Thr Leu
 90 95 100

cgg gta acg gcg tct atc ccc tat tcc cgc acc ggt gaa ggc ctg cac 451
 Arg Val Thr Ala Ser Ile Pro Tyr Ser Arg Thr Gly Glu Gly Leu His
 105 110 115

cgc atg gtg gat cca gca gac aat gag gtg tat ttg tac acc cag ttt 499
 Arg Met Val Asp Pro Ala Asp Asn Glu Val Tyr Leu Tyr Thr Gln Phe
 120 125 130

gag acc gcc gat gcc aag cgt atg ttc gcg tgt ttc gat cag cca gac 547
 Glu Thr Ala Asp Ala Lys Arg Met Phe Ala Cys Phe Asp Gln Pro Asp
 135 140 145

ctc aag gct acc tat gat ctg aac atc aaa act cct aag ggt tgg aag 595
 Leu Lys Ala Thr Tyr Asp Arg Leu Asn Ile Lys Thr Pro Lys Gly Trp Lys
 150 155 160 165

atc att tcc aac tct gag cag cag gtt tcc act cag cac act gat tac 643
 Ile Ile Ser Asn Ser Glu Gln Gln Val Ser Thr Gln His Thr Asp Tyr
 170 175 180

gat acc cac att tcc cga gtg gac tat ccc ctc tcc acc tac ctg att 691
 Asp Thr His Ile Ser Arg Val Asp Tyr Pro Leu Ser Thr Tyr Leu Ile
 185 190 195

gcg gtg tgc gcg ggt cgt tac cac gag gtg tgc gat gtc tgg aag ggt 739
 Ala Val Cys Ala Gly Arg Tyr His Glu Val Cys Asp Val Trp Lys Gly
 200 205 210

acg ctc acc cac cat gca gaa aca cct gcc gat cag cca act gag ctg 787
 Thr Leu Thr His His Ala Glu Thr Pro Ala Asp Gln Pro Thr Glu Leu
 215 220 225

act gtt ccg ctt gct ctc tac tgc cgc agt tct ttg gct aaa gat ctt 835
 Thr Val Pro Leu Ala Leu Tyr Cys Arg Ser Ser Leu Ala Lys Asp Leu
 230 235 240 245

gat gcg gtg cgt ctg ttt acc gaa acg aag cag ggc ttt gat tgg tac 883
 Asp Ala Val Arg Leu Phe Thr Glu Thr Lys Gln Gly Phe Asp Trp Tyr
 250 255 260

cac cgc aac ttc ggt gtg gcg tac cca ttc ggc aag tac gat cag atc 931
 His Arg Asn Phe Gly Val Ala Tyr Pro Phe Gly Lys Tyr Asp Gln Ile
 265 270 275

ttc gtc cct gaa ttt aat gct ggc gcg atg gag 964
 Phe Val Pro Glu Phe Asn Ala Gly Ala Met Glu
 280 285

<210> 156

<211> 288

<212> PRT

<213> Corynebacterium glutamicum

<400> 156

Leu Thr Ser Thr Asn Leu Thr Arg Gln Glu Ala Ser Asp Arg Ser Arg
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Leu Leu Ser Val Glu Asn Tyr Asp Ile Ala Leu Asp Leu Asn Asn Gly
 20 25 30

Asp Glu Phe Phe Ser Ser Ser Thr Val Val Ser Phe Thr Val Arg Lys
 35 40 45

Ala Gly Asp Thr Phe Ile Asp Leu Arg Ala Ala Ser Val Glu Glu Val
 50 55 60

Arg Leu Asp Asn Val Ser Ile Lys Asp Glu Ala Leu Thr Leu Gly Lys
 65 70 75 80

Asn Gly Tyr Asp Glu Thr Phe Gly Ile Ala Leu Lys Gly Leu Thr Pro
 85 90 95

Gly Ala His Thr Leu Arg Val Thr Ala Ser Ile Pro Tyr Ser Arg Thr
 100 105 110

Gly	Glu	Gly	Leu	His	Arg	Met	Val	Asp	Pro	Ala	Asp	Asn	Glu	Val	Tyr
		115					120					125			
Leu	Tyr	Thr	Gln	Phe	Glu	Thr	Ala	Asp	Ala	Lys	Arg	Met	Phe	Ala	Cys
		130				135					140				
Phe	Asp	Gln	Pro	Asp	Leu	Lys	Ala	Thr	Tyr	Asp	Leu	Asn	Ile	Lys	Thr
145					150					155					160
Pro	Lys	Gly	Trp	Lys	Ile	Ile	Ser	Asn	Ser	Glu	Gln	Gln	Val	Ser	Thr
				165				170						175	
Gln	His	Thr	Asp	Tyr	Asp	Thr	His	Ile	Ser	Arg	Val	Asp	Tyr	Pro	Leu
			180					185					190		
Ser	Thr	Tyr	Leu	Ile	Ala	Val	Cys	Ala	Gly	Arg	Tyr	His	Glu	Val	Cys
		195					200					205			
Asp	Val	Trp	Lys	Gly	Thr	Leu	Thr	His	His	Ala	Glu	Thr	Pro	Ala	Asp
		210				215					220				
Gln	Pro	Thr	Glu	Leu	Thr	Val	Pro	Leu	Ala	Leu	Tyr	Cys	Arg	Ser	Ser
225					230					235					240
Leu	Ala	Lys	Asp	Leu	Asp	Ala	Val	Arg	Leu	Phe	Thr	Glu	Thr	Lys	Gln
				245					250					255	
Gly	Phe	Asp	Trp	Tyr	His	Arg	Asn	Phe	Gly	Val	Ala	Tyr	Pro	Phe	Gly
			260					265					270		
Lys	Tyr	Asp	Gln	Ile	Phe	Val	Pro	Glu	Phe	Asn	Ala	Gly	Ala	Met	Glu
		275					280					285			

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<210> 157
<211> 1902
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(1879)  
<223> RXN01046
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<400> 157
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Met Ile Pro Phe Pro
1 5

ggg caa ccg cag cag caa agc gca ccc aat gac gag acc cgt ttc atc 163
Gly Gln Pro Gln Gln Gln Ser Ala Pro Asn Asp Glu Thr Arg Phe Ile
10 15 20

gac ctt aac gaa cgt cat aaa gat gat gaa cca gcc ctg ttt cgc gat—211
Asp Leu Asn Glu Arg His Lys Asp Asp Glu Pro Ala Leu Phe Arg Asp
25 30 35

gat gtt att gat caa act ctc gct att ttg atc agt aaa aat aag ccc 259
Asp Val Ile Asp Gln Thr Leu Ala Ile Leu Ile Ser Lys Asn Lys Pro

40	45	50	
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gaa gat att gcg cgc cgc ctt gcc aat gat gac gta tct att ccc gat Glu Asp Ile Ala Arg Arg Leu Ala Asn Asp Asp Val Ser Ile Pro Asp 70 75 80 85			355
cag ctt gtc ggc cac cgt att ctt gat gtc tcc att gca gag ctt gtt Gln Leu Val Gly His Arg Ile Leu Asp Val Ser Ile Ala Glu Leu Val 90 95 100			403
gct ggt gct ggc gtt gtt ggt cag ctc aag aaa cgc att ctg gat ctc Ala Gly Ala Gly Val Val Gly Gln Leu Lys Lys Arg Ile Leu Asp Leu 105 110 115			451
atc aag tat gcg acc gac ccg agt aac aaa gtc att atc ttt att gac Ile Lys Tyr Ala Thr Asp Pro Ser Asn Lys Val Ile Ile Phe Ile Asp 120 125 130			499
gag att cac caa att gct ggt gat cag tcc agt cac agt gga tcg caa Glu Ile His Gln Ile Ala Gly Asp Gln Ser Ser His Ser Gly Ser Gln 135 140 145			547
gcc aaa gtt gct cag att ctc aaa ccc tat ctt gcc cgt ggt gac ctt Ala Lys Val Ala Gln Ile Leu Lys Pro Tyr Leu Ala Arg Gly Asp Leu 150 155 160 165			595
cgt gtt att ggt gcc acc acc acc cag gaa gct cgt gac ttc gat cat Arg Val Ile Gly Ala Thr Thr Thr Gln Glu Ala Arg Asp Phe Asp His 170 175 180			643
gat cca gcc ctc aaa cgc cgt ttt agc aga gta aat gtc gat gaa ttt Asp Pro Ala Leu Lys Arg Arg Phe Ser Arg Val Asn Val Asp Glu Phe 185 190 195			691
gat cga gat caa acg ctc act att ctt cat gct gca cgt gat ggt tac Asp Arg Asp Gln Thr Leu Thr Ile Leu His Ala Ala Arg Asp Gly Tyr 200 205 210			739
ctc aaa cat ttc aac aac gct gtc acg gta tct gac gac gta ctg ggc Leu Lys His Phe Asn Asn Ala Val Thr Val Ser Asp Asp Val Leu Gly 215 220 225			787
tat gtc tac acc tac tcg cag caa ttc aac cca ggc aat aca gca caa Tyr Val Tyr Thr Tyr Ser Gln Gln Phe Asn Pro Gly Asn Thr Ala Gln 230 235 240 245			835
cct gat gca gca ctg acg ctg ttt gat aag gcg ttg gct tcc cta act Pro Asp Ala Ala Leu Thr Leu Phe Asp Lys Ala Leu Ala Ser Leu Thr 250 255 260			883
atg gag aaa cag cgt ctg atc aac aac cat gtc att gcg ccg tcg ctc Met Glu Lys Gln Arg Leu Ile Asn Asn His Val Ile Ala Pro Ser Leu 265 270 275			931
aag ttc cct gtg tca gaa agg cac atc cat aac acc gct cgc aaa ctt Lys Phe Pro Val Ser Glu Arg His Ile His Asn Thr Ala Arg Lys Leu 280 285 290			979

gcc ttt ggc tct caa gtg cca gcc tcc atc aat act gat gat gct cgt	1027
Ala Phe Gly Ser Gln Val Pro Ala Ser Ile Asn Thr Asp Asp Ala Arg	
295 300 305	
gac aaa ctc gaa acg ttg ttt ggt caa gat cat att att gag cca gta	1075
Asp Lys Leu Glu Thr Leu Phe Gly Gln Asp His Ile Ile Glu Pro Val	
310 315 320 325	
ctc acc gct atc aag cgt gaa cag ctt ggt att ttc cct cgc acc aaa	1123
Leu Thr Ala Ile Lys Arg Glu Gln Leu Gly Ile Phe Pro Arg Thr Lys	
330 335 340	
cca ttg agc tgg gtg ttt gct ggt tca tct ggt gtg ggt aaa aca gaa	1171
Pro Leu Ser Trp Val Phe Ala Gly Ser Ser Gly Val Gly Lys Thr Glu	
345 350 355	
atg gcg cgt att ctc tct cgc gcc att aat ggc ggc gat ccc atc att	1219
Met Ala Arg Ile Leu Ser Arg Ala Ile Asn Gly Gly Asp Pro Ile Ile	
360 365 370	
atc aat ggt ccc gaa tac att agt cct gag tcc att act ggc ctt atc	1267
Ile Asn Gly Pro Glu Tyr Ile Ser Pro Glu Ser Ile Thr Gly Leu Ile	
375 380 385	
gga tca tcc gat ggc tat atc ggc tct aat tct aag cgt gct aaa cca	1315
Gly Ser Ser Asp Gly Tyr Ile Gly Ser Asn Ser Lys Arg Ala Lys Pro	
390 395 400 405	
ctc gac ccg ctg att tct aat ccg cgt cag gtg att gtg ctc gat gaa	1363
Leu Asp Pro Leu Ile Ser Asn Pro Arg Gln Val Ile Val Leu Asp Glu	
410 415 420	
ttt gag aag tct cac cct cat ttc cag caa ttg ttc atg gca gct ctt	1411
Phe Glu Lys Ser His Pro His Phe Gln Gln Leu Phe Met Ala Ala Leu	
425 430 435	
gat aca ggc act atg gcg atg gct aat ggc acg aca ttg aat ttc tct	1459
Asp Thr Gly Thr Met Ala Met Ala Asn Gly Thr Thr Leu Asn Phe Ser	
440 445 450	
cag gcc att atc att gcc acc acc aat gca gcc cgc gac aaa atc ggt	1507
Gln Ala Ile Ile Ile Ala Thr Thr Asn Ala Ala Arg Asp Lys Ile Gly	
455 460 465	
cgt gac agc ttt gga ttc gat tca gat aat tca ggt gtc ctc ggt tct	1555
Arg Asp Ser Phe Gly Phe Asp Ser Asp Asn Ser Gly Val Leu Gly Ser	
470 475 480 485	
gct caa gca gca act gat ccg cgt gca cag gaa cgc ctc aag tca ctg	1603
Ala Gln Ala Ala Thr Asp Pro Arg Ala Gln Glu Arg Leu Lys Ser Leu	
490 495 500	
atg tcc aag gat ttc ctg ttg aac tgc tca acc gtt tcc aga ata tct	1651
Met Ser Lys Asp Phe Leu Leu Asn Cys Ser Thr Val Ser Arg Ile Ser	
505 510 515	
ttg cct tca acc gca ttg atg cag gca cct acc gtg aga ttc tgg aca	1699
Leu Pro Ser Thr Ala Leu Met Gln Ala Pro Thr Val Arg Phe Trp Thr	
520 525 530	

atc tct acc agc gtc gcc gtg acg ccg tgc tgc tta gcc acc ccg cat 1747
 Ile Ser Thr Ser Val Ala Val Thr Pro Cys Cys Leu Ala Thr Pro His
 535 540 545

tac gca gca cag atc cct gca gat att gat tca gac act ctt gat cag 1795
 Tyr Ala Ala Gln Ile Pro Ala Asp Ile Asp Ser Asp Thr Leu Asp Gln
 550 555 560 565

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 Leu Val Glu Thr Thr Phe Ile Ser Asp Phe Gly Ala Arg Pro Ala Ala
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<213> Corynebacterium glutamicum

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Ser Lys Asn Lys Pro Asn Ala Leu Leu Val Gly Pro Ala Gly Thr Gly
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Lys Ser Arg Ile Ala Glu Asp Ile Ala Arg Arg Leu Ala Asn Asp Asp
 65 70 75 80

Val Ser Ile Pro Asp Gln Leu Val Gly His Arg Ile Leu Asp Val Ser
 85 90 95

Ile Ala Glu Leu Val Ala Gly Ala Gly Val Val Gly Gln Leu Lys Lys
 100 105 110

Arg Ile Leu Asp Leu Ile Lys Tyr Ala Thr Asp Pro Ser Asn Lys Val
 115 120 125

Ile Ile Phe Ile Asp Glu Ile His Gln Ile Ala Gly Asp Gln Ser Ser
 130 135 140

His Ser Gly Ser Gln Ala Lys Val Ala Gln Ile Leu Lys Pro Tyr Leu
 145 150 155 160

Ala Arg Gly Asp Leu Arg Val Ile Gly Ala Thr Thr Thr Gln Glu Ala
 165 170 175

Arg Asp Phe Asp His Asp Pro Ala Leu Lys Arg Arg Phe Ser Arg Val
 180 185 190

Asn Val Asp Glu Phe Asp Arg Asp Gln Thr Leu Thr Ile Leu His Ala
 195 200 205
 Ala Arg Asp Gly Tyr Leu Lys His Phe Asn Asn Ala Val Thr Val Ser
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 Asp Asp Val Leu Gly Tyr Val Tyr Thr Tyr Ser Gln Gln Phe Asn Pro
 225 230 235 240
 Gly Asn Thr Ala Gln Pro Asp Ala Ala Leu Thr Leu Phe Asp Lys Ala
 245 250 255
 Leu Ala Ser Leu Thr Met Glu Lys Gln Arg Leu Ile Asn Asn His Val
 260 265 270
 Ile Ala Pro Ser Leu Lys Phe Pro Val Ser Glu Arg His Ile His Asn
 275 280 285
 Thr Ala Arg Lys Leu Ala Phe Gly Ser Gln Val Pro Ala Ser Ile Asn
 290 295 300
 Thr Asp Asp Ala Arg Asp Lys Leu Glu Thr Leu Phe Gly Gln Asp His
 305 310 315 320
 Ile Ile Glu Pro Val Leu Thr Ala Ile Lys Arg Glu Gln Leu Gly Ile
 325 330 335
 Phe Pro Arg Thr Lys Pro Leu Ser Trp Val Phe Ala Gly Ser Ser Gly
 340 345 350
 Val Gly Lys Thr Glu Met Ala Arg Ile Leu Ser Arg Ala Ile Asn Gly
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 Gly Asp Pro Ile Ile Ile Asn Gly Pro Glu Tyr Ile Ser Pro Glu Ser
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 Ile Thr Gly Leu Ile Gly Ser Ser Asp Gly Tyr Ile Gly Ser Asn Ser
 385 390 395 400
 Lys Arg Ala Lys Pro Leu Asp Pro Leu Ile Ser Asn Pro Arg Gln Val
 405 410 415
 Ile Val Leu Asp Glu Phe Glu Lys Ser His Pro His Phe Gln Gln Leu
 420 425 430
 Phe Met Ala Ala Leu Asp Thr Gly Thr Met Ala Met Ala Asn Gly Thr
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 Thr Leu Asn Phe Ser Gln Ala Ile Ile Ile Ala Thr Thr Asn Ala Ala
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 Arg Asp Lys Ile Gly Arg Asp Ser Phe Gly Phe Asp Ser Asp Asn Ser
 465 470 475 480
 Gly Val Leu Gly Ser Ala Gln Ala Ala Thr Asp Pro Arg Ala Gln Glu
 485 490 495
 Arg Leu Lys Ser Leu Met Ser Lys Asp Phe Leu Leu Asn Cys Ser Thr
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 Val Ser Arg Ile Ser Leu Pro Ser Thr Ala Leu Met Gln Ala Pro Thr

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Asp	Thr	Leu	Asp	Gln	Leu	Val	Glu	Thr	Thr	Phe	Ile	Ser	Asp	Phe	Gly
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<223> RXN01974
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Met Thr Gln Val Val															
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Ala Gly Thr Leu Val Gly Glu Ser Ile Asn Arg Glu Ile Asp Glu Asp															
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Lys Tyr Pro Tyr Leu Ser Ser Tyr Ala Ala Pro Val Ala Val Pro Val															
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Arg Glu Ile Ile Gly Arg Glu Glu Glu Val Asn Lys Ile Met Ala Ala															
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Leu Met Arg Pro Glu Ile Ser Asn Val Met Leu Val Gly Pro Ala Gly															
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Ser Gly Lys Thr Thr Leu Val Gln Gln Ala Leu Val Lys Asp Pro Glu															
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Arg Asn Tyr Ile Glu Val Asp Val Ala Lys Met Val Ala Asp Leu Ser															
90 95 100															
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Thr Pro Ala Gln Met Ala Ala Arg Ile Lys Gly Val Phe Glu Asp Ala															

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Ile Ala Tyr Arg Lys His Glu Gly His Glu Leu Val Leu Phe Val Asp																			
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gag ttt cac caa att gtg cag ctg tct aat gct gcg gta gag gca atc																			547
Glu Phe His Gln Ile Val Gln Leu Ser Asn Ala Ala Val Glu Ala Ile																			
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Lys Pro Ile Leu Ala Met Ser Gly Val Leu Gly Val Arg Val Ile Ala																			
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gcg aca act ctc gaa gaa ttt cac gaa cac atc agg ccg aac caa gca																			643
Ala Thr Thr Leu Glu Glu Phe His Glu His Ile Arg Pro Asn Gln Ala																			
170						175						180							
ttg acg gag cgt ttg cag gaa att cga cta acg ccg acc gat cag aag																			691
Leu Thr Glu Arg Leu Gln Glu Ile Arg Leu Thr Pro Thr Asp Gln Lys																			
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Thr Thr Val Ala Ile Leu Arg Gly Met Ala Asp Arg Tyr Gly Val Ser																			
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Asp Gln Phe Tyr Asp Asp His Val Phe Glu Gln Ile Tyr Ser Thr Thr																			
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Glu Arg Phe Met Pro Ser Ser Val Gln Pro Arg Lys Ser Ile Arg Val																			
230						235						240						245	
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Leu Asp Ala Met Val Gly Trp His Arg Leu Ser Gly Lys Pro Met Asp																			
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Met Asp Leu Leu Gly Asp Val Leu His Asp Ala Ile Gly Val Asp Ile																			
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Ala Phe Lys Val Asp Gly Thr Ser Ile Lys Asp Lys Leu Asp Glu Lys																			
280						285						290							
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Val Met Ala Gln Ser Leu Ala Thr Thr Val Val Ala Arg Arg Leu Gln																			
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Leu Val Val Ala Asp Leu His Asp Lys Ser Arg Pro Leu Ser Asn Phe																			
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Leu Phe Thr Gly Pro Thr Gly Val Gly Lys Thr Glu Leu Val Lys Gln																			
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Leu Ala Arg Val Leu Phe Gly Asp Asp Thr Gly Arg Leu Ile Arg Phe																			
345						350						355							

gac atg tca gag ttc gcc tta gaa tca agt ctt gac ctt ttc agg tct	1219
Asp Met Ser Glu Phe Ala Leu Glu Ser Ser Leu Asp Leu Phe Arg Ser	
360 365 370	
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Glu Leu Thr Arg Arg Val Ala Asp Gln Gly Asn Ala Ile Val Leu Leu	
375 380 385	
gat gag gtt gag aaa gct gat cga gct att gcg cgg ttg tta ctg cag	1315
Asp Glu Val Glu Lys Ala Asp Arg Ala Ile Ala Arg Leu Leu Leu Gln	
390 395 400 405	
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Val Leu Asp Asp Gly Arg Leu Ser Asp Asp Tyr Asn Arg Glu Val Ser	
410 415 420	
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Phe Leu Asn Thr Tyr Ile Val Met Thr Thr Asn Ala Gly Ser Glu Ile	
425 430 435	
ttc gag aca att tcg aac tat gcc act gat gac acg ggc gat ggt cgg	1459
Phe Glu Thr Ile Ser Asn Tyr Ala Thr Asp Asp Thr Gly Asp Gly Arg	
440 445 450	
gcg atc aaa gac ttt gtg aaa aac att cac acg tcg atc aag aat aag	1507
Ala Ile Lys Asp Phe Val Lys Asn Ile His Thr Ser Ile Lys Asn Lys	
455 460 465	
ggg ttt cca cct gag ctt ctt ggt cgt gta gat gaa att gtg cct ttt	1555
Gly Phe Pro Pro Glu Leu Leu Gly Arg Val Asp Glu Ile Val Pro Phe	
470 475 480 485	
caa ccg ctg tcg gag acg aca cag gac agg att att agc aag aag ctg	1603
Gln Pro Leu Ser Glu Thr Thr Gln Asp Arg Ile Ile Ser Lys Lys Leu	
490 495 500	
cag gat gtg gct act gag gtc tat gaa cgc cac ggc gtg aaa ctg cac	1651
Gln Asp Val Ala Thr Glu Val Tyr Glu Arg His Gly Val Lys Leu His	
505 510 515	
tgt tca caa aag gtt atg gag ttt ctg ctt gtg gat cag gtg gag gaa	1699
Cys Ser Gln Lys Val Met Glu Phe Leu Leu Val Asp Gln Val Glu Glu	
520 525 530	
agt gct gaa tct ggt ggt gcc cgt ggt gcg gtg cgg tct ttg cag cgg	1747
Ser Ala Glu Ser Gly Gly Ala Arg Gly Ala Val Arg Ser Leu Gln Arg	
535 540 545	
gaa gtg gtc act gaa gtg gcg acc ttt att aat acc tac cca gaa gtg	1795
Glu Val Val Thr Glu Val Ala Thr Phe Ile Asn Thr Tyr Pro Glu Val	
550 555 560 565	
cgt gac att tac gtt gat gtc gat ggt cag atg cgt aat aag act aac	1843
Arg Asp Ile Tyr Val Asp Val Asp Gly Gln Met Arg Asn Lys Thr Asn	
570 575 580	
cgt gtg tct acg gcc cgt gtg gtg ata aag cgt gtc gaa ggt	1885
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1908

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<212> PRT

<213> Corynebacterium glutamicum

<400> 160

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Val Ala Val Pro Val Arg Glu Ile Ile Gly Arg Glu Glu Glu Val Asn
 35 40 45

Lys Ile Met Ala Ala Leu Met Arg Pro Glu Ile Ser Asn Val Met Leu
 50 55 60

Val Gly Pro Ala Gly Ser Gly Lys Thr Thr Leu Val Gln Gln Ala Leu
 65 70 75 80

Val Lys Asp Pro Glu Arg Asn Tyr Ile Glu Val Asp Val Ala Lys Met
 85 90 95

Val Ala Asp Leu Ser Thr Pro Ala Gln Met Ala Ala Arg Ile Lys Gly
 100 105 110

Val Phe Glu Asp Ala Ile Ala Tyr Arg Lys His Glu Gly His Glu Leu
 115 120 125

Val Leu Phe Val Asp Glu Phe His Gln Ile Val Gln Leu Ser Asn Ala
 130 135 140

Ala Val Glu Ala Ile Lys Pro Ile Leu Ala Met Ser Gly Val Leu Gly
 145 150 155 160

Val Arg Val Ile Ala Ala Thr Thr Leu Glu Glu Phe His Glu His Ile
 165 170 175

Arg Pro Asn Gln Ala Leu Thr Glu Arg Leu Gln Glu Ile Arg Leu Thr
 180 185 190

Pro Thr Asp Gln Lys Thr Thr Val Ala Ile Leu Arg Gly Met Ala Asp
 195 200 205

Arg Tyr Gly Val Ser Asp Gln Phe Tyr Asp Asp His Val Phe Glu Gln
 210 215 220

Ile Tyr Ser Thr Thr Glu Arg Phe Met Pro Ser Ser Val Gln Pro Arg
 225 230 235 240

Lys Ser Ile Arg Val Leu Asp Ala Met Val Gly Trp His Arg Leu Ser
 245 250 255

Gly Lys Pro Met Asp Met Asp Leu Leu Gly Asp Val Leu His Asp Ala
 260 265 270

Ile Gly Val Asp Ile Ala Phe Lys Val Asp Gly Thr Ser Ile Lys Asp

275					280					285					
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Pro	Leu	Ser	Asn	Phe	Leu	Phe	Thr	Gly	Pro	Thr	Gly	Val	Gly	Lys	Thr
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Glu	Leu	Val	Lys	Gln	Leu	Ala	Arg	Val	Leu	Phe	Gly	Asp	Asp	Thr	Gly
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Arg	Leu	Leu	Leu	Gln	Val	Leu	Asp	Asp	Gly	Arg	Leu	Ser	Asp	Asp	Tyr
				405					410					415	
Asn	Arg	Glu	Val	Ser	Phe	Leu	Asn	Thr	Tyr	Ile	Val	Met	Thr	Thr	Asn
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Ala	Gly	Ser	Glu	Ile	Phe	Glu	Thr	Ile	Ser	Asn	Tyr	Ala	Thr	Asp	Asp
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Thr	Gly	Asp	Gly	Arg	Ala	Ile	Lys	Asp	Phe	Val	Lys	Asn	Ile	His	Thr
	450					455					460				
Ser	Ile	Lys	Asn	Lys	Gly	Phe	Pro	Pro	Glu	Leu	Leu	Gly	Arg	Val	Asp
465					470					475					480
Glu	Ile	Val	Pro	Phe	Gln	Pro	Leu	Ser	Glu	Thr	Thr	Gln	Asp	Arg	Ile
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Ile	Ser	Lys	Lys	Leu	Gln	Asp	Val	Ala	Thr	Glu	Val	Tyr	Glu	Arg	His
			500				505						510		
Gly	Val	Lys	Leu	His	Cys	Ser	Gln	Lys	Val	Met	Glu	Phe	Leu	Leu	Val
		515					520				525				
Asp	Gln	Val	Glu	Glu	Ser	Ala	Glu	Ser	Gly	Gly	Ala	Arg	Gly	Ala	Val
	530					535					540				
Arg	Ser	Leu	Gln	Arg	Glu	Val	Val	Thr	Glu	Val	Ala	Thr	Phe	Ile	Asn
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Thr	Tyr	Pro	Glu	Val	Arg	Asp	Ile	Tyr	Val	Asp	Val	Asp	Gly	Gln	Met
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Arg	Asn	Lys	Thr	Asn	Arg	Val	Ser	Thr	Ala	Arg	Val	Val	Ile	Lys	Arg
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gaa agc gcc gat ctg ctc aaa tgt tcc ttc tgc gga aag agc caa aag																163	
Glu Ser Ala Asp	Leu Leu Lys Cys	Ser Phe Cys Gly	Lys Ser	Gln Lys													
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cag gta aaa aaa ctc atc gcg ggt ggc gcc gta tat atc tgt gat gag																211	
Gln Val Lys Lys	Leu Ile Ala Gly	Gly Ala Val Tyr	Ile Cys Asp	Glu													
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Cys Ile Glu Leu Cys Asn Glu Ile Ile Glu Glu Glu	Leu Gly Gln Ala																
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caa cac gac gag cag gag cgc aac gag ctc ccc aag ccg tcg gag att																307	
Gln His Asp Glu Gln Glu Arg Asn Glu Leu Pro Lys Pro Ser Glu Ile																	
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tca gcc ttc ctt gat act tat gtc atc ggg cag gac cca gca aaa cgt																355	
Ser Ala Phe Leu Asp Thr Tyr Val Ile Gly Gln Asp Pro Ala Lys Arg																	
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atc ctg tcg gtt gcg gtg tac aac cat tac aag cgt ctc cgc gca tcg																403	
Ile Leu Ser Val Ala Val Tyr Asn His Tyr Lys Arg Leu Arg Ala Ser																	
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gaa acc atc ggt cgt cgc agg aat gac gag cct gaa acc gaa ctg gtt																451	
Glu Thr Ile Gly Arg Arg Arg Asn Asp Glu Pro Glu Thr Glu Leu Val																	
																105 110 115	
aag tcc aat att ttg atg ctc ggc ccc act ggc tcc ggc aag act ttc																499	
Lys Ser Asn Ile Leu Met Leu Gly Pro Thr Gly Ser Gly Lys Thr Phe																	
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Leu Ala Gln Thr Leu Ala Lys Leu Leu Asp Val Pro Phe Ala Ile Ala																	
																135 140 145	
gat gcc acc tca ctg acc gag gct ggt tat gtg ggc gag gat gtg gaa																595	
Asp Ala Thr Ser Leu Thr Glu Ala Gly Tyr Val Gly Glu Asp Val Glu																	
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Asn Ile Leu Leu Lys Leu Leu Gln Ala Ala Asp Phe Asp Val Glu Arg																	

170								175				180				
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Ala	Gln	Arg	Gly	Ile	Ile	Tyr	Ile	Asp	Glu	Val	Asp	Lys	Ile	Ser	Arg	
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aag	tct	gaa	aac	cca	tcg	atc	act	cgc	gat	gtt	tcc	ggc	gaa	ggc	gtg	739
Lys	Ser	Glu	Asn	Pro	Ser	Ile	Thr	Arg	Asp	Val	Ser	Gly	Glu	Gly	Val	
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cag	cag	gca	ctg	ctg	aaa	att	ttg	gaa	ggc	act	gtc	gcc	gca	atc	cca	787
Gln	Gln	Ala	Leu	Leu	Lys	Ile	Leu	Glu	Gly	Thr	Val	Ala	Ala	Ile	Pro	
		215				220					225					
ccg	cag	gga	gga	cgc	aag	cac	ccc	aac	cag	gat	ttc	atc	cag	ctg	gat	835
Pro	Gln	Gly	Gly	Arg	Lys	His	Pro	Asn	Gln	Asp	Phe	Ile	Gln	Leu	Asp	
230					235					240					245	
acc	acc	aac	att	ttg	ttc	atc	gtt	gct	ggc	gcg	ttc	tct	ggc	ctg	gag	883
Thr	Thr	Asn	Ile	Leu	Phe	Ile	Val	Ala	Gly	Ala	Phe	Ser	Gly	Leu	Glu	
				250					255					260		
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Lys	Val	Ile	Ala	Asp	Arg	Asn	Gly	Lys	Lys	Gly	Leu	Gly	Phe	Gly	Val	
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gag	gtc	tct	tcc	aag	aag	gaa	gaa	gcc	aac	att	gtg	gat	atc	ttc	aag	979
Glu	Val	Ser	Ser	Lys	Lys	Glu	Glu	Ala	Asn	Ile	Val	Asp	Ile	Phe	Lys	
			280				285					290				
gat	gtc	ctc	cct	gag	gac	ctg	gtg	aag	ttt	ggc	ctc	atc	cca	gaa	ttc	1027
Asp	Val	Leu	Pro	Glu	Asp	Leu	Val	Lys	Phe	Gly	Leu	Ile	Pro	Glu	Phe	
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att	ggg	cgt	ctg	cca	gtc	gtt	gcc	acc	gta	tcc	aac	ctg	gat	cag	aaa	1075
Ile	Gly	Arg	Leu	Pro	Val	Val	Ala	Thr	Val	Ser	Asn	Leu	Asp	Gln	Lys	
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Tyr	Arg	Arg	Leu	Phe	Glu	Met	Asp	Asp	Ala	Val	Leu	Thr	Phe	Thr	Asp	
			345					350					355			
gat	gct	ttg	gag	gag	atc	gct	aat	cag	gca	ctc	gag	cgc	aaa	act	ggc	1219
Asp	Ala	Leu	Glu	Glu	Ile	Ala	Asn	Gln	Ala	Leu	Glu	Arg	Lys	Thr	Gly	
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gcc	cgt	ggc	ctg	cgc	gcg	atc	atg	gaa	gag	atc	ctg	gtt	ccg	atc	atg	1267
Ala	Arg	Gly	Leu	Arg	Ala	Ile	Met	Glu	Glu	Ile	Leu	Val	Pro	Ile	Met	
			375			380					385					
tat	gac	ctc	cca	gac	cgt	aaa	gac	gtt	ggc	gaa	gtc	atc	atc	aac	ggc	1315
Tyr	Asp	Leu	Pro	Asp	Arg	Lys	Asp	Val	Gly	Glu	Val	Ile	Ile	Asn	Gly	
390					395				400						405	
gcc	gtt	gcc	cgt	ggc	gaa	gcc	gaa	cca	gag	atg	ttg	gaa	gct	gtc	gca	1363
Ala	Val	Ala	Arg	Gly	Glu	Ala	Glu	Pro	Glu	Met	Leu	Glu	Ala	Val	Ala	
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 425

1401

<210> 162

<211> 426

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 162

Met Ala Arg Met Gln Glu Ser Ala Asp Leu Leu Lys Cys Ser Phe Cys
 1 5 10 15

Gly Lys Ser Gln Lys Gln Val Lys Lys Leu Ile Ala Gly Gly Ala Val
 20 25 30

Tyr Ile Cys Asp Glu Cys Ile Glu Leu Cys Asn Glu Ile Ile Glu Glu
 35 40 45

Glu Leu Gly Gln Ala Gln His Asp Glu Gln Glu Arg Asn Glu Leu Pro
 50 55 60

Lys Pro Ser Glu Ile Ser Ala Phe Leu Asp Thr Tyr Val Ile Gly Gln
 65 70 75 80

Asp Pro Ala Lys Arg Ile Leu Ser Val Ala Val Tyr Asn His Tyr Lys
 85 90 95

Arg Leu Arg Ala Ser Glu Thr Ile Gly Arg Arg Arg Asn Asp Glu Pro
 100 105 110

Glu Thr Glu Leu Val Lys Ser Asn Ile Leu Met Leu Gly Pro Thr Gly
 115 120 125

Ser Gly Lys Thr Phe Leu Ala Gln Thr Leu Ala Lys Leu Leu Asp Val
 130 135 140

Pro Phe Ala Ile Ala Asp Ala Thr Ser Leu Thr Glu Ala Gly Tyr Val
 145 150 155 160

Gly Glu Asp Val Glu Asn Ile Leu Leu Lys Leu Leu Gln Ala Ala Asp
 165 170 175

Phe Asp Val Glu Arg Ala Gln Arg Gly Ile Ile Tyr Ile Asp Glu Val
 180 185 190

Asp Lys Ile Ser Arg Lys Ser Glu Asn Pro Ser Ile Thr Arg Asp Val
 195 200 205

Ser Gly Glu Gly Val Gln Gln Ala Leu Leu Lys Ile Leu Glu Gly Thr
 210 215 220

Val Ala Ala Ile Pro Pro Gln Gly Gly Arg Lys His Pro Asn Gln Asp
 225 230 235 240

Phe Ile Gln Leu Asp Thr Thr Asn Ile Leu Phe Ile Val Ala Gly Ala
 245 250 255

Phe Ser Gly Leu Glu Lys Val Ile Ala Asp Arg Asn Gly Lys Lys Gly

260										265					270				
Leu	Gly	Phe	Gly	Val	Glu	Val	Ser	Ser	Lys	Lys	Glu	Glu	Ala	Asn	Ile				
275										280					285				
Val	Asp	Ile	Phe	Lys	Asp	Val	Leu	Pro	Glu	Asp	Leu	Val	Lys	Phe	Gly				
290										295					300				
Leu	Ile	Pro	Glu	Phe	Ile	Gly	Arg	Leu	Pro	Val	Val	Ala	Thr	Val	Ser				
305										310					315				
Asn	Leu	Asp	Gln	Lys	Ser	Leu	Val	Lys	Val	Leu	Thr	Glu	Pro	Arg	Asn				
325										330					335				
Ser	Leu	Val	Lys	Gln	Tyr	Arg	Arg	Leu	Phe	Glu	Met	Asp	Asp	Ala	Val				
340										345					350				
Leu	Thr	Phe	Thr	Asp	Asp	Ala	Leu	Glu	Glu	Ile	Ala	Asn	Gln	Ala	Leu				
355										360					365				
Glu	Arg	Lys	Thr	Gly	Ala	Arg	Gly	Leu	Arg	Ala	Ile	Met	Glu	Glu	Ile				
370										375					380				
Leu	Val	Pro	Ile	Met	Tyr	Asp	Leu	Pro	Asp	Arg	Lys	Asp	Val	Gly	Glu				
385										390					395				
Val	Ile	Ile	Asn	Gly	Ala	Val	Ala	Arg	Gly	Glu	Ala	Glu	Pro	Glu	Met				
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420										425									

<210> 163

<211> 1401

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1378)

<223> FRXA01120

<400> 163

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												Met	Ala	Arg	Met	Gln			
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gaa	agc	gcc	gat	ctg	ctc	aaa	tgt	tcc	ttc	tgc	gga	aag	agc	caa	aag	163						
Glu	Ser	Ala	Asp	Leu	Leu	Lys	Cys	Ser	Phe	Cys	Gly	Lys	Ser	Gln	Lys							
												10					15			20		

cag	gta	aaa	aaa	ctc	atc	gcg	ggt	ggc	gcc	gta	tat	atc	tgt	gat	gag	211								
Gln	Val	Lys	Lys	Leu	Ile	Ala	Gly	Gly	Ala	Val	Tyr	Ile	Cys	Asp	Glu									
												25					30					35		

tgc	att	gag	ctg	tgc	aac	gag	att	att	gaa	gaa	gaa	ctc	ggt	caa	gct	259								
Cys	Ile	Glu	Leu	Cys	Asn	Glu	Ile	Ile	Glu	Glu	Glu	Leu	Gly	Gln	Ala									
												40					45					50		

caa cac gac gag cag gag cgc aac gag ctc ccc aag ccg tcg gag att	307
Gln His Asp Glu Gln Glu Arg Asn Glu Leu Pro Lys Pro Ser Glu Ile	
55 60 65	
tca gcc ttc ctt gat act tat gtc atc ggg cag gac cca gca aaa cgt	355
Ser Ala Phe Leu Asp Thr Tyr Val Ile Gly Gln Asp Pro Ala Lys Arg	
70 75 80 85	
atc ctg tcg gtt gcg gtg tac aac cat tac aag cgt ctc cgc gca tcg	403
Ile Leu Ser Val Ala Val Tyr Asn His Tyr Lys Arg Leu Arg Ala Ser	
90 95 100	
gaa acc atc ggt cgt cgc agg aat gac gag cct gaa acc gaa ctg gtt	451
Glu Thr Ile Gly Arg Arg Arg Asn Asp Glu Pro Glu Thr Glu Leu Val	
105 110 115	
aag tcc aat att ttg atg ctc ggc ccc act ggc tcc ggc aag act ttc	499
Lys Ser Asn Ile Leu Met Leu Gly Pro Thr Gly Ser Gly Lys Thr Phe	
120 125 130	
ctt gcc cag act ttg gca aag ctg ctg gat gtt cct ttt gct atc gcg	547
Leu Ala Gln Thr Leu Ala Lys Leu Leu Asp Val Pro Phe Ala Ile Ala	
135 140 145	
gat gcc acc tca ctg acc gag gct ggt tat gtg ggc gag gat gtg gaa	595
Asp Ala Thr Ser Leu Thr Glu Ala Gly Tyr Val Gly Glu Asp Val Glu	
150 155 160 165	
aac atc ttg ctc aag ctg ctt cag gct gct gat ttt gat gtg gaa cgt	643
Asn Ile Leu Leu Lys Leu Leu Gln Ala Ala Asp Phe Asp Val Glu Arg	
170 175 180	
gca cag cgc ggc atc att tac atc gat gaa gtg gac aag att tcc cgc	691
Ala Gln Arg Gly Ile Ile Tyr Ile Asp Glu Val Asp Lys Ile Ser Arg	
185 190 195	
aag tct gaa aac cca tcg atc act cgc gat gtt tcc ggt gaa ggc gtg	739
Lys Ser Glu Asn Pro Ser Ile Thr Arg Asp Val Ser Gly Glu Gly Val	
200 205 210	
cag cag gca ctg ctg aaa att ttg gaa ggc act gtc gcc gca atc cca	787
Gln Gln Ala Leu Leu Lys Ile Leu Glu Gly Thr Val Ala Ala Ile Pro	
215 220 225	
ccg cag gga gga cgc aag cac ccc aac cag gat ttc atc cag ctg gat	835
Pro Gln Gly Gly Arg Lys His Pro Asn Gln Asp Phe Ile Gln Leu Asp	
230 235 240 245	
acc acc aac att ttg ttc atc gtt gct ggt gcg ttc tct ggt ctg gag	883
Thr Thr Asn Ile Leu Phe Ile Val Ala Gly Ala Phe Ser Gly Leu Glu	
250 255 260	
aag gtc atc gcg gac cgc aat ggc aag aaa ggc ttg ggc ttc ggt gtg	931
Lys Val Ile Ala Asp Arg Asn Gly Lys Lys Gly Leu Gly Phe Gly Val	
265 270 275	
gag gtc tct tcc aag aag gaa gaa gcc aac att gtg gat atc ttc aag	979
Glu Val Ser Ser Lys Lys Glu Glu Ala Asn Ile Val Asp Ile Phe Lys	
280 285 290	

gat gtc ctc cct gag gac ctg gtg aag ttt ggt ctc atc cca gaa ttc 1027
 Asp Val Leu Pro Glu Asp Leu Val Lys Phe Gly Leu Ile Pro Glu Phe
 295 300 305

 att ggg cgt ctg cca gtc gtt gcc acc gta tcc aac ctg gat cag aaa 1075
 Ile Gly Arg Leu Pro Val Val Ala Thr Val Ser Asn Leu Asp Gln Lys
 310 315 320 325

 tct ctg gtc aag gtt ctc acg gag cct cgt aac tca ttg gtg aag cag 1123
 Ser Leu Val Lys Val Leu Thr Glu Pro Arg Asn Ser Leu Val Lys Gln
 330 335 340

 tat cga cgt ctg ttt gaa atg gat gac gct gtg ttg acc ttt act gat 1171
 Tyr Arg Arg Leu Phe Glu Met Asp Asp Ala Val Leu Thr Phe Thr Asp
 345 350 355

 gat gct ttg gag gag atc gct aat cag gca ctc gag cgc aaa act ggc 1219
 Asp Ala Leu Glu Glu Ile Ala Asn Gln Ala Leu Glu Arg Lys Thr Gly
 360 365 370

 gcc cgt ggc ctg cgc gcg atc atg gaa gag atc ctg gtt ccg atc atg 1267
 Ala Arg Gly Leu Arg Ala Ile Met Glu Glu Ile Leu Val Pro Ile Met
 375 380 385

 tat gac ctc cca gac cgt aaa gac gtt ggc gaa gtc atc atc aac ggt 1315
 Tyr Asp Leu Pro Asp Arg Lys Asp Val Gly Glu Val Ile Ile Asn Gly
 390 395 400 405

 gcc gtt gcc cgt ggc gaa gcc gaa cca gag atg ttg gaa gct gtc gca 1363
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 gaa gaa aag acc gcg tagttggcag gagttatcac cgg 1401
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<210> 164

<211> 426

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 164

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 20 25 30

 Tyr Ile Cys Asp Glu Cys Ile Glu Leu Cys Asn Glu Ile Ile Glu Glu
 35 40 45

 Glu Leu Gly Gln Ala Gln His Asp Glu Gln Glu Arg Asn Glu Leu Pro
 50 55 60

 Lys Pro Ser Glu Ile Ser Ala Phe Leu Asp Thr Tyr Val Ile Gly Gln
 65 70 75 80

 Asp Pro Ala Lys Arg Ile Leu Ser Val Ala Val Tyr Asn His Tyr Lys
 85 90 95

Arg Leu Arg Ala Ser Glu Thr Ile Gly Arg Arg Arg Asn Asp Glu Pro
 100 105 110
 Glu Thr Glu Leu Val Lys Ser Asn Ile Leu Met Leu Gly Pro Thr Gly
 115 120 125
 Ser Gly Lys Thr Phe Leu Ala Gln Thr Leu Ala Lys Leu Leu Asp Val
 130 135 140
 Pro Phe Ala Ile Ala Asp Ala Thr Ser Leu Thr Glu Ala Gly Tyr Val
 145 150 155 160
 Gly Glu Asp Val Glu Asn Ile Leu Leu Lys Leu Leu Gln Ala Ala Asp
 165 170 175
 Phe Asp Val Glu Arg Ala Gln Arg Gly Ile Ile Tyr Ile Asp Glu Val
 180 185 190
 Asp Lys Ile Ser Arg Lys Ser Glu Asn Pro Ser Ile Thr Arg Asp Val
 195 200 205
 Ser Gly Glu Gly Val Gln Gln Ala Leu Leu Lys Ile Leu Glu Gly Thr
 210 215 220
 Val Ala Ala Ile Pro Pro Gln Gly Gly Arg Lys His Pro Asn Gln Asp
 225 230 235 240
 Phe Ile Gln Leu Asp Thr Thr Asn Ile Leu Phe Ile Val Ala Gly Ala
 245 250 255
 Phe Ser Gly Leu Glu Lys Val Ile Ala Asp Arg Asn Gly Lys Lys Gly
 260 265 270
 Leu Gly Phe Gly Val Glu Val Ser Ser Lys Lys Glu Glu Ala Asn Ile
 275 280 285
 Val Asp Ile Phe Lys Asp Val Leu Pro Glu Asp Leu Val Lys Phe Gly
 290 295 300
 Leu Ile Pro Glu Phe Ile Gly Arg Leu Pro Val Val Ala Thr Val Ser
 305 310 315 320
 Asn Leu Asp Gln Lys Ser Leu Val Lys Val Leu Thr Glu Pro Arg Asn
 325 330 335
 Ser Leu Val Lys Gln Tyr Arg Arg Leu Phe Glu Met Asp Asp Ala Val
 340 345 350
 Leu Thr Phe Thr Asp Asp Ala Leu Glu Glu Ile Ala Asn Gln Ala Leu
 355 360 365
 Glu Arg Lys Thr Gly Ala Arg Gly Leu Arg Ala Ile Met Glu Glu Ile
 370 375 380
 Leu Val Pro Ile Met Tyr Asp Leu Pro Asp Arg Lys Asp Val Gly Glu
 385 390 395 400

 Val Ile Ile Asn Gly Ala Val Ala Arg Gly Glu Ala Glu Pro Glu Met
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 Leu Glu Ala Val Ala Glu Glu Lys Thr Ala

425

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<220>
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<222> (101)..(901)
<223> RXN00397
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Gly Glu Ile Ile Pro Ile Gln Thr Lys Leu Gly His Trp Arg Asp Val
10 15 20

cgg gat tcc gaa gat ctg cca ttc caa gta atc gca tcg cgc acc aac 211
Arg Asp Ser Glu Asp Leu Pro Phe Gln Val Ile Ala Ser Arg Thr Asn
25 30 35

gtg acc att atg gaa aac acc ctg gaa tgg acc aac agc cgc ctt gag 259
Val Thr Ile Met Glu Asn Thr Leu Glu Trp Thr Asn Ser Arg Leu Glu
40 45 50

cgt ggc gaa gag ttc acc gag ctc gac att tat gct cac tac ttg gaa 307
Arg Gly Glu Glu Phe Thr Glu Leu Asp Ile Tyr Ala His Tyr Leu Glu
55 60 65

gag ttg gaa gat tac gcc ctc caa ttc acc ttc gat gtc gag ccc tac 355
Glu Leu Glu Asp Tyr Ala Leu Gln Phe Thr Phe Asp Val Glu Pro Tyr
70 75 80 85

ttc	acc	aac	ctg	cac	tcc	tcc	aac	aga	atg	ctc	ttc	cct	gga	cct	cct	403
Phe	Thr	Asn	Leu	His	Ser	Ser	Asn	Arg	Met	Leu	Phe	Pro	Gly	Pro	Pro	
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gtg gat ttc ccg atc aac gca gaa acc cga tgc att cag ctc gac gcc 451
Val Asp Phe Pro Ile Asn Ala Glu Thr Arg Cys Ile Gln Leu Asp Ala
105 110 115

ggt gtt gca gta aag aag gac ggc gtg gtg ctg ggt acc tca gat atg 499
Gly Val Ala Val Lys Lys Asp Gly Val Val Leu Gly Thr Ser Asp Met
120 125 130

gcg agg tcc ctg cct cga acc gcc gct ggc caa gaa gcc tat gag tac 547
Ala Arg Ser Leu Pro Arg Thr Ala Ala Gly Gln Glu Ala Tyr Glu Tyr
135 140 145

ttc	ttc	aag	gtg	gtt	cgt	gaa	ggc	atc	atc	ggg	cag	ctg	cgc	ccg	ggc	595
Phe	Phe	Lys	Val	Val	Arg	Glu	Gly	Ile	Ile	Gly	Gln	Leu	Arg	Pro	Gly	
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gtg atc tgc gct gac gtg cac gaa gca acc ctt gat tac cta agc ccg 643

Val Ile Cys Ala Asp Val His Glu Ala Thr Leu Asp Tyr Leu Ser Pro
 170 175 180

cag cta cct cgc atg att gac atc gga atg ctg ggt gcc gac acc gat 691
 Gln Leu Pro Arg Met Ile Asp Ile Gly Met Leu Gly Ala Asp Thr Asp
 185 190 195

ttc aac acc atc tac cgc aag cgc aat gtt ggc cac ctg atg ggc aag 739
 Phe Asn Thr Ile Tyr Arg Lys Arg Asn Val Gly His Leu Met Gly Lys
 200 205 210

cag gaa tcc ttt gcc aat gag ctt cgc cct gga tac aag cac att ctt 787
 Gln Glu Ser Phe Ala Asn Glu Leu Arg Pro Gly Tyr Lys His Ile Leu
 215 220 225

cac cac ggc tcc tat ggt gcc gcg gag atc cct tgg cgc tac aac ggt 835
 His His Gly Ser Tyr Gly Ala Ala Glu Ile Pro Trp Arg Tyr Asn Gly
 230 235 240 245

gta gcc att ggt acc gag gat ctg tgg tac atc ggc gca gac aag acc 883
 Val Ala Ile Gly Thr Glu Asp Leu Trp Tyr Ile Gly Ala Asp Lys Thr
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tac att ttg agc cag cgc taaggagaac ccagtgcacag aaa 924
 Tyr Ile Leu Ser Gln Arg
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<210> 166

<211> 267

<212> PRT

<213> Corynebacterium glutamicum

<400> 166

Leu Ser Leu Thr Glu Gly Glu Ile Ile Pro Ile Gln Thr Lys Leu Gly
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His Trp Arg Asp Val Arg Asp Ser Glu Asp Leu Pro Phe Gln Val Ile
 20 25 30

Ala Ser Arg Thr Asn Val Thr Ile Met Glu Asn Thr Leu Glu Trp Thr
 35 40 45

Asn Ser Arg Leu Glu Arg Gly Glu Glu Phe Thr Glu Leu Asp Ile Tyr
 50 55 60

Ala His Tyr Leu Glu Glu Leu Glu Asp Tyr Ala Leu Gln Phe Thr Phe
 65 70 75 80

Asp Val Glu Pro Tyr Phe Thr Asn Leu His Ser Ser Asn Arg Met Leu
 85 90 95

Phe Pro Gly Pro Pro Val Asp Phe Pro Ile Asn Ala Glu Thr Arg Cys
 100 105 110

Ile Gln Leu Asp Ala Gly Val Ala Val Lys Lys Asp Gly Val Val Leu
 115 120 125

Gly Thr Ser Asp Met Ala Arg Ser Leu Pro Arg Thr Ala Ala Gly Gln
 130 135 140

Glu Ala Tyr Glu Tyr Phe Phe Lys Val Val Arg Glu Gly Ile Ile Gly
 145 150 155 160
 Gln Leu Arg Pro Gly Val Ile Cys Ala Asp Val His Glu Ala Thr Leu
 165 170 175
 Asp Tyr Leu Ser Pro Gln Leu Pro Arg Met Ile Asp Ile Gly Met Leu
 180 185 190
 Gly Ala Asp Thr Asp Phe Asn Thr Ile Tyr Arg Lys Arg Asn Val Gly
 195 200 205
 His Leu Met Gly Lys Gln Glu Ser Phe Ala Asn Glu Leu Arg Pro Gly
 210 215 220
 Tyr Lys His Ile Leu His His Gly Ser Tyr Gly Ala Ala Glu Ile Pro
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 Gly Ala Asp Lys Thr Tyr Ile Leu Ser Gln Arg
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 <211> 2049
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(2026)
 <223> RXN01868

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 Met Lys Asp Leu Tyr
 1 5

cgc ttt gtc aat ggc ctg tgg ctt gac acc cac atc att ccc gac gat 163
 Arg Phe Val Asn Gly Leu Trp Leu Asp Thr His Ile Ile Pro Asp Asp
 10 15 20

cgc gcg gtg gac ggc acg ttc cac aag ctg cgc gat gat gct gaa gaa 211
 Arg Ala Val Asp Gly Thr Phe His Lys Leu Arg Asp Asp Ala Glu Glu
 25 30 35

gac gtc cat gag atc gtc aag gaa gac act gga cgc gca ggc aca ctt 259
 Asp Val His Glu Ile Val Lys Glu Asp Thr Gly Arg Ala Gly Thr Leu
 40 45 50

tat gcc tca ttt atg gat act gac gcc atc aac gct gct ggt gtt gca 307
 Tyr Ala Ser Phe Met Asp Thr Asp Ala Ile Asn Ala Ala Gly Val Ala
 55 60 65

ccg ctc gat gcg gat ctg aac agg ctg tct gtt gct aac tca tcg ttt 355
 Pro Leu Asp Ala Asp Leu Asn Arg Leu Ser Val Ala Asn Ser Ser Phe
 70 75 80 85

ttc gca gct gct ctc ggc gaa ctg gac cgt gaa ggc gtt ggc gcg cca	403
Phe Ala Ala Ala Leu Gly Glu Leu Asp Arg Glu Gly Val Gly Ala Pro	
90 95 100	
gta ggt ttc tgg gtg gag aag gat tct tcc tcc aac gaa tcc gtc gcc	451
Val Gly Phe Trp Val Glu Lys Asp Ser Ser Ser Asn Glu Ser Val Ala	
105 110 115	
tat gtc atc cag tcc ggc ctc ggc ctg ccc gat gag gct tat tac cgc	499
Tyr Val Ile Gln Ser Gly Leu Gly Leu Pro Asp Glu Ala Tyr Tyr Arg	
120 125 130	
gag gag gca cac gcc gaa act ctc gcg gcc tac aaa gag cac gtt gag	547
Glu Glu Ala His Ala Glu Thr Leu Ala Ala Tyr Lys Glu His Val Glu	
135 140 145	
cgc atg ctc ggc tac ttg gat aac agc cgc ctc ttc ggt ctg tcg gct	595
Arg Met Leu Gly Tyr Leu Asp Asn Ser Arg Leu Phe Gly Leu Ser Ala	
150 155 160 165	
gct tcc gct gcc gca cga att gtc gcc ctg gaa acg gaa atc gct gct	643
Ala Ser Ala Ala Ala Arg Ile Val Ala Leu Glu Thr Glu Ile Ala Ala	
170 175 180	
ggc cac tgg gat gtc gtg aag acc cgc gac gcc gta gcc acc tac aac	691
Gly His Trp Asp Val Val Lys Thr Arg Asp Ala Val Ala Thr Tyr Asn	
185 190 195	
ccc acc gaa ctc ggc gcg ctg cca cca aag gtc cgc acg ctg ctc agt	739
Pro Thr Glu Leu Gly Ala Leu Pro Pro Lys Val Arg Thr Leu Leu Ser	
200 205 210	
tcc gca ggc ctc ccg gac cag cgc ctg gta tcg atg atg ccg tca tac	787
Ser Ala Gly Leu Pro Asp Gln Arg Leu Val Ser Met Met Pro Ser Tyr	
215 220 225	
ctc gac cac ctc aac ggc ttg ctt gtc gac gac cgc ctc ccc gat tgg	835
Leu Asp His Leu Asn Gly Leu Leu Val Asp Asp Arg Leu Pro Asp Trp	
230 235 240 245	
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Gln Leu Trp Ala Thr Trp His Ile Leu Arg Ser Arg Ala Gly Leu Leu	
250 255 260	
acc gag gaa att agc caa gca aac ttc gac ttc tat ggc acc aaa ctg	931
Thr Glu Glu Ile Ser Gln Ala Asn Phe Asp Phe Tyr Gly Thr Lys Leu	
265 270 275	
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Ser Gly Ala Thr Glu Gln Lys Asp Arg Trp Lys Arg Ala Val Gly Leu	
280 285 290	
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Ala Glu Arg Met Val Gly Glu Glu Ile Gly Gln Arg Phe Val Glu Arg	
295 300 305	
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His Phe Pro Ala Ser Ser Lys Glu His Met Leu Glu Leu Val Asp Tyr	
310 315 320 325	

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Leu Val Ala Ala Tyr Arg Asp Arg Ile Ser Asn Leu Glu Trp Met Thr	
330 335 340	
ccc gcc acc cgc gag cgt gcc ctg gaa aag ttg ggc aaa ttc aac gcg	1171
Pro Ala Thr Arg Glu Arg Ala Leu Glu Lys Leu Gly Lys Phe Asn Ala	
345 350 355	
aaa atc ggc tac ccc gac aag tgg cgc tcc tac gaa ggc ctc gaa ttc	1219
Lys Ile Gly Tyr Pro Asp Lys Trp Arg Ser Tyr Glu Gly Leu Glu Phe	
360 365 370	
ggc tcc gac ctg gtg gac aac tcc cgc aag ggc tcc gcg ttc ctc cat	1267
Gly Ser Asp Leu Val Asp Asn Ser Arg Lys Gly Ser Ala Phe Leu His	
375 380 385	
gac tat gag ctg ggc aag atc ggc aaa cca gcc gac cgc gac gaa tgg	1315
Asp Tyr Glu Leu Gly Lys Ile Gly Lys Pro Ala Asp Arg Asp Glu Trp	
390 395 400 405	
gtc acc acc cca caa acc gtc aac gcc ttc tac aac ccc gtg gtc aac	1363
Val Thr Thr Pro Gln Thr Val Asn Ala Phe Tyr Asn Pro Val Val Asn	
410 415 420	
gac atc acc ttc ccc gca gcc atc ctg cgc gca cca ttc ttc gac ccc	1411
Asp Ile Thr Phe Pro Ala Ala Ile Leu Arg Ala Pro Phe Phe Asp Pro	
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gaa gca gaa gcc gca gaa aac ttc ggt gca atc ggt gct gtg atc gga	1459
Glu Ala Glu Ala Ala Glu Asn Phe Gly Ala Ile Gly Ala Val Ile Gly	
440 445 450	
cac gaa atc ggc cac ggc ttt gac gat caa ggc agc caa tac gac ggc	1507
His Glu Ile Gly His Gly Phe Asp Asp Gln Gly Ser Gln Tyr Asp Gly	
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gac ggc aac ctc aac tcc tgg tgg acc gac gaa gac cgc tcc gca ttc	1555
Asp Gly Asn Leu Asn Ser Trp Trp Thr Asp Glu Asp Arg Ser Ala Phe	
470 475 480 485	
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Glu Gln Leu Thr Ser Arg Leu Val Thr Gln Phe Ser Gly Leu Val Pro	
490 495 500	
gcc gtc ctg acc tct gaa gga atc gac acc gac ggc gtc aac ggt gaa	1651
Ala Val Leu Thr Ser Glu Gly Ile Asp Thr Asp Gly Val Asn Gly Glu	
505 510 515	
ttc act ctc ggc gaa aac atc ggt gac ctc ggc gga ttg ggc atc gct	1699
Phe Thr Leu Gly Glu Asn Ile Gly Asp Leu Gly Gly Leu Gly Ile Ala	
520 525 530	
gtc gtt gcc tac gaa aag tac ctc gca gac cgt ggc caa acc ttt gaa	1747
Val Val Ala Tyr Glu Lys Tyr Leu Ala Asp Arg Gly Gln Thr Phe Glu	
535 540 545	
acc tca cca gtc caa aaa ttc gaa gca gaa ggc gcc gag gaa ggc ctg	1795
Thr Ser Pro Val Gln Lys Phe Glu Ala Glu Gly Ala Glu Glu Gly Leu	
550 555 560 565	
gcc gag caa gaa ttc aac ggt ctc caa cgc ctc ttc ctg tcc tgg gct	1843

Ala Glu Gln Glu Phe Asn Gly Leu Gln Arg Leu Phe Leu Ser Trp Ala
 570 575 580

cgc gtg tgg cgc acc aaa atc cgc cca cag atg gcc gtc caa tac ctg 1891
 Arg Val Trp Arg Thr Lys Ile Arg Pro Gln Met Ala Val Gln Tyr Leu
 585 590 595

gcc atc gac cca cac tcc cct gca gaa ttc cgc tgc aat gtc atc gcc 1939
 Ala Ile Asp Pro His Ser Pro Ala Glu Phe Arg Cys Asn Val Ile Ala
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 Gly Asn Val Ala Glu Phe Tyr Glu Ala Phe Asp Val Pro Glu Asp Ala
 615 620 625

cct gtg tac atc aag cca gaa gag cgc cta gct atc tgg tagttgtag 2036
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 630 635 640

tttgtattga aaa 2049

<210> 168

<211> 642

<212> PRT

<213> Corynebacterium glutamicum

<400> 168

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Ile Ile Pro Asp Asp Arg Ala Val Asp Gly Thr Phe His Lys Leu Arg
 20 25 30

Asp Asp Ala Glu Glu Asp Val His Glu Ile Val Lys Glu Asp Thr Gly
 35 40 45

Arg Ala Gly Thr Leu Tyr Ala Ser Phe Met Asp Thr Asp Ala Ile Asn
 50 55 60

Ala Ala Gly Val Ala Pro Leu Asp Ala Asp Leu Asn Arg Leu Ser Val
 65 70 75 80

Ala Asn Ser Ser Phe Phe Ala Ala Ala Leu Gly Glu Leu Asp Arg Glu
 85 90 95

Gly Val Gly Ala Pro Val Gly Phe Trp Val Glu Lys Asp Ser Ser Ser
 100 105 110

Asn Glu Ser Val Ala Tyr Val Ile Gln Ser Gly Leu Gly Leu Pro Asp
 115 120 125

Glu Ala Tyr Tyr Arg Glu Glu Ala His Ala Glu Thr Leu Ala Ala Tyr
 130 135 140

~~Lys Glu His Val Glu Arg Met Leu Gly Tyr Leu Asp Asn Ser Arg Leu~~
~~145 150 155 160~~

Phe Gly Leu Ser Ala Ala Ser Ala Ala Ala Arg Ile Val Ala Leu Glu
 165 170 175

Thr Glu Ile Ala Ala Gly His Trp Asp Val Val Lys Thr Arg Asp Ala
 180 185 190
 Val Ala Thr Tyr Asn Pro Thr Glu Leu Gly Ala Leu Pro Pro Lys Val
 195 200 205
 Arg Thr Leu Leu Ser Ser Ala Gly Leu Pro Asp Gln Arg Leu Val Ser
 210 215 220
 Met Met Pro Ser Tyr Leu Asp His Leu Asn Gly Leu Leu Val Asp Asp
 225 230 235 240
 Arg Leu Pro Asp Trp Gln Leu Trp Ala Thr Trp His Ile Leu Arg Ser
 245 250 255
 Arg Ala Gly Leu Leu Thr Glu Glu Ile Ser Gln Ala Asn Phe Asp Phe
 260 265 270
 Tyr Gly Thr Lys Leu Ser Gly Ala Thr Glu Gln Lys Asp Arg Trp Lys
 275 280 285
 Arg Ala Val Gly Leu Ala Glu Arg Met Val Gly Glu Glu Ile Gly Gln
 290 295 300
 Arg Phe Val Glu Arg His Phe Pro Ala Ser Ser Lys Glu His Met Leu
 305 310 315 320
 Glu Leu Val Asp Tyr Leu Val Ala Ala Tyr Arg Asp Arg Ile Ser Asn
 325 330 335
 Leu Glu Trp Met Thr Pro Ala Thr Arg Glu Arg Ala Leu Glu Lys Leu
 340 345 350
 Gly Lys Phe Asn Ala Lys Ile Gly Tyr Pro Asp Lys Trp Arg Ser Tyr
 355 360 365
 Glu Gly Leu Glu Phe Gly Ser Asp Leu Val Asp Asn Ser Arg Lys Gly
 370 375 380
 Ser Ala Phe Leu His Asp Tyr Glu Leu Gly Lys Ile Gly Lys Pro Ala
 385 390 395 400
 Asp Arg Asp Glu Trp Val Thr Thr Pro Gln Thr Val Asn Ala Phe Tyr
 405 410 415
 Asn Pro Val Val Asn Asp Ile Thr Phe Pro Ala Ala Ile Leu Arg Ala
 420 425 430
 Pro Phe Phe Asp Pro Glu Ala Glu Ala Ala Glu Asn Phe Gly Ala Ile
 435 440 445
 Gly Ala Val Ile Gly His Glu Ile Gly His Gly Phe Asp Asp Gln Gly
 450 455 460
 Ser Gln Tyr Asp Gly Asp Gly Asn Leu Asn Ser Trp Trp Thr Asp Glu
 465 470 475 480
 Asp Arg Ser Ala Phe Glu Gln Leu Thr Ser Arg Leu Val Thr Gln Phe
 485 490 495
 Ser Gly Leu Val Pro Ala Val Leu Thr Ser Glu Gly Ile Asp Thr Asp

500								505				510			
Gly	Val	Asn	Gly	Glu	Phe	Thr	Leu	Gly	Glu	Asn	Ile	Gly	Asp	Leu	Gly
515								520				525			
Gly	Leu	Gly	Ile	Ala	Val	Val	Ala	Tyr	Glu	Lys	Tyr	Leu	Ala	Asp	Arg
530								535				540			
Gly	Gln	Thr	Phe	Glu	Thr	Ser	Pro	Val	Gln	Lys	Phe	Glu	Ala	Glu	Gly
545								550				555			
Ala	Glu	Glu	Gly	Leu	Ala	Glu	Gln	Glu	Phe	Asn	Gly	Leu	Gln	Arg	Leu
565								570				575			
Phe	Leu	Ser	Trp	Ala	Arg	Val	Trp	Arg	Thr	Lys	Ile	Arg	Pro	Gln	Met
580								585				590			
Ala	Val	Gln	Tyr	Leu	Ala	Ile	Asp	Pro	His	Ser	Pro	Ala	Glu	Phe	Arg
595								600				605			
Cys	Asn	Val	Ile	Ala	Gly	Asn	Val	Ala	Glu	Phe	Tyr	Glu	Ala	Phe	Asp
610								615				620			
Val	Pro	Glu	Asp	Ala	Pro	Val	Tyr	Ile	Lys	Pro	Glu	Glu	Arg	Leu	Ala
625								630				635			
												640			
Ile Trp															

<210> 169
 <211> 1734
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1711)
 <223> FRXA01868

<400> 169
 atgcggatct gaacaggctg tctgttgcta actcatcggt ttcgcagctg ctctcggcga 60

actggaccgt gaaggcggtg gcgcgccagt aggtttctgg gtg gag aag gat tct 115
 Val Glu Lys Asp Ser
 1 5

tcc tcc aac gaa tcc gtc gcc tat gtc atc cag tcc ggc ctc ggc ctg 163
 Ser Ser Asn Glu Ser Val Ala Tyr Val Ile Gln Ser Gly Leu Gly Leu
 10 15 20

ccc gat gag gct tat tac cgc gag gag gca cac gcc gaa act ctc gcg 211
 Pro Asp Glu Ala Tyr Tyr Arg Glu Glu Ala His Ala Glu Thr Leu Ala
 25 30 35

~~gcc tac aaa gag cac gtt gag cgc atg ctc ggc tac ttg gat aac agc 259~~
 Ala Tyr Lys Glu His Val Glu Arg Met Leu Gly Tyr Leu Asp Asn Ser
 40 45 50

cgc ctc ttc ggt ctg tcg gct gct tcc gct gcc gca cga att gtc gcc 307
 Arg Leu Phe Gly Leu Ser Ala Ala Ser Ala Ala Arg Ile Val Ala

55	60	65	
ctg gaa acg gaa atc gct gct ggc cac tgg gat gtc gtg aag acc cgc			355
Leu Glu Thr Glu Ile Ala Ala Gly His Trp Asp Val Val Lys Thr Arg			
70	75	80	85
gac gcc gta gcc acc tac aac ccc acc gaa ctc ggc gcg ctg cca cca			403
Asp Ala Val Ala Thr Tyr Asn Pro Thr Glu Leu Gly Ala Leu Pro Pro			
	90	95	100
aag gtc cgc acg ctg ctc agt tcc gca ggc ctc ccg gac cag cgc ctg			451
Lys Val Arg Thr Leu Leu Ser Ser Ala Gly Leu Pro Asp Gln Arg Leu			
	105	110	115
gta tcg atg atg ccg tca tac ctc gac cac ctc aac ggc ttg ctt gtc			499
Val Ser Met Met Pro Ser Tyr Leu Asp His Leu Asn Gly Leu Leu Val			
	120	125	130
gac gac cgc ctc ccc gat tgg cag cta tgg gca acc tgg cac atc ttg			547
Asp Asp Arg Leu Pro Asp Trp Gln Leu Trp Ala Thr Trp His Ile Leu			
	135	140	145
agg tct cga gca gga ctg ttg acc gag gaa att agc caa gca aac ttc			595
Arg Ser Arg Ala Gly Leu Leu Thr Glu Glu Ile Ser Gln Ala Asn Phe			
150	155	160	165
gac ttc tat ggc acc aaa ctg tcc ggc gcc acc gag caa aaa gat cga			643
Asp Phe Tyr Gly Thr Lys Leu Ser Gly Ala Thr Glu Gln Lys Asp Arg			
	170	175	180
tgg aag cgt gct gtc ggc ctg gca gag cgc atg gtg ggc gag gaa atc			691
Trp Lys Arg Ala Val Gly Leu Ala Glu Arg Met Val Gly Glu Glu Ile			
	185	190	195
ggg caa cga ttc gtc gaa agg cat ttt cct gca agc tcc aag gag cac			739
Gly Gln Arg Phe Val Glu Arg His Phe Pro Ala Ser Ser Lys Glu His			
	200	205	210
atg ctt gag ctc gtc gac tac ctg gtt gcc gcc tac cgt gat cgc att			787
Met Leu Glu Leu Val Asp Tyr Leu Val Ala Ala Tyr Arg Asp Arg Ile			
	215	220	225
tcc aac ctc gaa tgg atg acg ccc gcc acc cgc gag cgt gcc ctg gaa			835
Ser Asn Leu Glu Trp Met Thr Pro Ala Thr Arg Glu Arg Ala Leu Glu			
230	235	240	245
aag ttg ggc aaa ttc aac gcg aaa atc ggc tac ccc gac aag tgg cgc			883
Lys Leu Gly Lys Phe Asn Ala Lys Ile Gly Tyr Pro Asp Lys Trp Arg			
	250	255	260
tcc tac gaa ggc ctc gaa ttc ggc tcc gac ctg gtg gac aac tcc cgc			931
Ser Tyr Glu Gly Leu Glu Phe Gly Ser Asp Leu Val Asp Asn Ser Arg			
	265	270	275
aag ggc tcc gcg ttc ctc cat gac tat gag ctg ggc aag atc ggc aaa			979
Lys Gly Ser Ala Phe Leu His Asp Tyr Glu Leu Gly Lys Ile Gly Lys			
280	285	290	
cca gcc gac cgc gac gaa tgg gtc acc acc cca caa acc gtc aac gcc			1027
Pro Ala Asp Arg Asp Glu Trp Val Thr Thr Pro Gln Thr Val Asn Ala			
295	300	305	

ttc tac aac ccc gtg gtc aac gac atc acc ttc ccc gca gcc atc ctg	1075
Phe Tyr Asn Pro Val Val Asn Asp Ile Thr Phe Pro Ala Ala Ile Leu	
310 315 320 325	
cgc gca cca ttc ttc gac ccc gaa gca gaa gcc gca gaa aac ttc ggt	1123
Arg Ala Pro Phe Phe Asp Pro Glu Ala Glu Ala Ala Glu Asn Phe Gly	
330 335 340	
gca atc ggt gct gtg atc gga cac gaa atc ggc cac ggc ttt gac gat	1171
Ala Ile Gly Ala Val Ile Gly His Glu Ile Gly His Gly Phe Asp Asp	
345 350 355	
caa ggc agc caa tac gac ggc gac ggc aac ctc aac tcc tgg tgg acc	1219
Gln Gly Ser Gln Tyr Asp Gly Asp Gly Asn Leu Asn Ser Trp Trp Thr	
360 365 370	
gac gaa gac cgc tcc gca ttc gag cag ctc acc tca cgt ctg gtc acc	1267
Asp Glu Asp Arg Ser Ala Phe Glu Gln Leu Thr Ser Arg Leu Val Thr	
375 380 385	
caa ttc agc gga ctc gtc cct gcc gtc ctg acc tct gaa gga atc gac	1315
Gln Phe Ser Gly Leu Val Pro Ala Val Leu Thr Ser Glu Gly Ile Asp	
390 395 400 405	
acc gac ggc gtc aac ggt gaa ttc act ctc ggc gaa aac atc ggt gac	1363
Thr Asp Gly Val Asn Gly Glu Phe Thr Leu Gly Glu Asn Ile Gly Asp	
410 415 420	
ctc ggc gga ttg ggc atc gct gtc gtt gcc tac gaa aag tac ctc gca	1411
Leu Gly Gly Leu Gly Ile Ala Val Val Ala Tyr Glu Lys Tyr Leu Ala	
425 430 435	
gac cgt ggc caa acc ttt gaa acc tca cca gtc caa aaa ttc gaa gca	1459
Asp Arg Gly Gln Thr Phe Glu Thr Ser Pro Val Gln Lys Phe Glu Ala	
440 445 450	
gaa ggc gcc gag gaa ggc ctg gcc gag caa gaa ttc aac ggt ctc caa	1507
Glu Gly Ala Glu Glu Gly Leu Ala Glu Gln Glu Phe Asn Gly Leu Gln	
455 460 465	
cgc ctc ttc ctg tcc tgg gct cgc gtg tgg cgc acc aaa atc cgc cca	1555
Arg Leu Phe Leu Ser Trp Ala Arg Val Trp Arg Thr Lys Ile Arg Pro	
470 475 480 485	
cag atg gcc gtc caa tac ctg gcc atc gac cca cac tcc cct gca gaa	1603
Gln Met Ala Val Gln Tyr Leu Ala Ile Asp Pro His Ser Pro Ala Glu	
490 495 500	
ttc cgc tgc aat gtc atc gcc gga aac gtc gct gaa ttc tac gaa gca	1651
Phe Arg Cys Asn Val Ile Ala Gly Asn Val Ala Glu Phe Tyr Glu Ala	
505 510 515	
ttc gac gtc ccc gaa gat gca cct gtg tac atc aag cca gaa gag cgc	1699
Phe Asp Val Pro Glu Asp Ala Pro Val Tyr Ile Lys Pro Glu Glu Arg	
520 525 530	
cta gct atc tgg tagttgttag ttggtattga aaa	1734
Leu Ala Ile Trp	
535	

<210> 170

<211> 537

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 170

Val Glu Lys Asp Ser Ser Ser Asn Glu Ser Val Ala Tyr Val Ile Gln
 1 5 10 15

Ser Gly Leu Gly Leu Pro Asp Glu Ala Tyr Tyr Arg Glu Glu Ala His
 20 25 30

Ala Glu Thr Leu Ala Ala Tyr Lys Glu His Val Glu Arg Met Leu Gly
 35 40 45

Tyr Leu Asp Asn Ser Arg Leu Phe Gly Leu Ser Ala Ala Ser Ala Ala
 50 55 60

Ala Arg Ile Val Ala Leu Glu Thr Glu Ile Ala Ala Gly His Trp Asp
 65 70 75 80

Val Val Lys Thr Arg Asp Ala Val Ala Thr Tyr Asn Pro Thr Glu Leu
 85 90 95

Gly Ala Leu Pro Pro Lys Val Arg Thr Leu Leu Ser Ser Ala Gly Leu
 100 105 110

Pro Asp Gln Arg Leu Val Ser Met Met Pro Ser Tyr Leu Asp His Leu
 115 120 125

Asn Gly Leu Leu Val Asp Asp Arg Leu Pro Asp Trp Gln Leu Trp Ala
 130 135 140

Thr Trp His Ile Leu Arg Ser Arg Ala Gly Leu Leu Thr Glu Glu Ile
 145 150 155 160

Ser Gln Ala Asn Phe Asp Phe Tyr Gly Thr Lys Leu Ser Gly Ala Thr
 165 170 175

Glu Gln Lys Asp Arg Trp Lys Arg Ala Val Gly Leu Ala Glu Arg Met
 180 185 190

Val Gly Glu Glu Ile Gly Gln Arg Phe Val Glu Arg His Phe Pro Ala
 195 200 205

Ser Ser Lys Glu His Met Leu Glu Leu Val Asp Tyr Leu Val Ala Ala
 210 215 220

Tyr Arg Asp Arg Ile Ser Asn Leu Glu Trp Met Thr Pro Ala Thr Arg
 225 230 235 240

Glu Arg Ala Leu Glu Lys Leu Gly Lys Phe Asn Ala Lys Ile Gly Tyr
 245 250 255

Pro Asp Lys Trp Arg Ser Tyr Glu Gly Leu Glu Phe Gly Ser Asp Leu
 260 265 270

Val Asp Asn Ser Arg Lys Gly Ser Ala Phe Leu His Asp Tyr Glu Leu
 275 280 285

Gly Lys Ile Gly Lys Pro Ala Asp Arg Asp Glu Trp Val Thr Thr Pro
 290 295 300
 Gln Thr Val Asn Ala Phe Tyr Asn Pro Val Val Asn Asp Ile Thr Phe
 305 310 315 320
 Pro Ala Ala Ile Leu Arg Ala Pro Phe Phe Asp Pro Glu Ala Glu Ala
 325 330 335
 Ala Glu Asn Phe Gly Ala Ile Gly Ala Val Ile Gly His Glu Ile Gly
 340 345 350
 His Gly Phe Asp Asp Gln Gly Ser Gln Tyr Asp Gly Asp Gly Asn Leu
 355 360 365
 Asn Ser Trp Trp Thr Asp Glu Asp Arg Ser Ala Phe Glu Gln Leu Thr
 370 375 380
 Ser Arg Leu Val Thr Gln Phe Ser Gly Leu Val Pro Ala Val Leu Thr
 385 390 395 400
 Ser Glu Gly Ile Asp Thr Asp Gly Val Asn Gly Glu Phe Thr Leu Gly
 405 410 415
 Glu Asn Ile Gly Asp Leu Gly Gly Leu Gly Ile Ala Val Val Ala Tyr
 420 425 430
 Glu Lys Tyr Leu Ala Asp Arg Gly Gln Thr Phe Glu Thr Ser Pro Val
 435 440 445
 Gln Lys Phe Glu Ala Glu Gly Ala Glu Glu Gly Leu Ala Glu Gln Glu
 450 455 460
 Phe Asn Gly Leu Gln Arg Leu Phe Leu Ser Trp Ala Arg Val Trp Arg
 465 470 475 480
 Thr Lys Ile Arg Pro Gln Met Ala Val Gln Tyr Leu Ala Ile Asp Pro
 485 490 495
 His Ser Pro Ala Glu Phe Arg Cys Asn Val Ile Ala Gly Asn Val Ala
 500 505 510
 Glu Phe Tyr Glu Ala Phe Asp Val Pro Glu Asp Ala Pro Val Tyr Ile
 515 520 525
 Lys Pro Glu Glu Arg Leu Ala Ile Trp
 530 535

<210> 171

<211> 426

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(403)

<223> FRXA01869

<400> 171

tgacaggcta ccttctgggg ttgacatgat cccaacgct caaccactt gtggcaccaa 60

ccacaaaccc tgtggcggta aatcccctag agtaggccac atg aag gat ctt tat 115
Met Lys Asp Leu Tyr
1 5

cgc ttt gtc aat ggc ctg tgg ctt gac acc cac atc att ccc gac gat 163
Arg Phe Val Asn Gly Leu Trp Leu Asp Thr His Ile Ile Pro Asp Asp
10 15 20

cgc gcg gtg gac ggc acg ttc cac aag ctg cgc gat gat gct gaa gaa 211
Arg Ala Val Asp Gly Thr Phe His Lys Leu Arg Asp Asp Ala Glu Glu
25 30 35

gac gtc cat gag atc gtc aag gaa gac act gga cgc gca ggc aca ctt 259
Asp Val His Glu Ile Val Lys Glu Asp Thr Gly Arg Ala Gly Thr Leu
40 45 50

tat gcc tca ttt atg gat act gac gcc atc aac gct gct ggt gtt gca 307
Tyr Ala Ser Phe Met Asp Thr Asp Ala Ile Asn Ala Ala Gly Val Ala
55 60 65

ccg ctc gat gcg gat ctg aac agg ctg tct gtt gct aac tca tcg ttt 355
Pro Leu Asp Ala Asp Leu Asn Arg Leu Ser Val Ala Asn Ser Ser Phe
70 75 80 85

tcg cag ctg ctc tcg gcg aac tgg acc gtg aag gcg ttg gcg cgc cag 403
Ser Gln Leu Leu Ser Ala Asn Trp Thr Val Lys Ala Leu Ala Arg Gln
90 95 100

taggtttctg ggtggagaag gat 426

<210> 172

<211> 101

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 172

Met Lys Asp Leu Tyr Arg Phe Val Asn Gly Leu Trp Leu Asp Thr His
1 5 10 15

Ile Ile Pro Asp Asp Arg Ala Val Asp Gly Thr Phe His Lys Leu Arg
20 25 30

Asp Asp Ala Glu Glu Asp Val His Glu Ile Val Lys Glu Asp Thr Gly
35 40 45

Arg Ala Gly Thr Leu Tyr Ala Ser Phe Met Asp Thr Asp Ala Ile Asn
50 55 60

Ala Ala Gly Val Ala Pro Leu Asp Ala Asp Leu Asn Arg Leu Ser Val
65 70 75 80

Ala Asn Ser Ser Phe Ser Gln Leu Leu Ser Ala Asn Trp Thr Val Lys
85 90 95

Ala Leu Ala Arg Gln
100

<210> 173

<211> 1404
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1381)
 <223> RXN00499

<400> 173

tgccaacagg ggatatgcca ctgtgtaccc cacggcgatg atcggtaaaa tcctcggcgc 60

gcagatatgtg ttcttgctgc tctaagggtga tttttgggca gtg gtg ggg gtg gtg 115
 Val Val Gly Val Val
 1 5

tcc acc cct gcg cgt aac ctg gga agc atg act aaa aca ctt ggt tcc 163
 Ser Thr Pro Ala Arg Asn Leu Gly Ser Met Thr Lys Thr Leu Gly Ser
 10 15 20

ctt cag ctg gaa gaa atc acg ctg acc ctc cct ctg act gaa gat gtg 211
 Leu Gln Leu Glu Glu Ile Thr Leu Thr Leu Pro Leu Thr Glu Asp Val
 25 30 35

gcc gat gaa cgc acc att gat gtg ttc gca cgc att gcc aca cgc gtc 259
 Ala Asp Glu Arg Thr Ile Asp Val Phe Ala Arg Ile Ala Thr Arg Val
 40 45 50

ggt ggg gaa gac ctt cca tat tta gta ttc ctg cag ggt ggg cct ggc 307
 Gly Gly Glu Asp Leu Pro Tyr Leu Val Phe Leu Gln Gly Gly Pro Gly
 55 60 65

aat gaa gct cca cgt cca agc ctt aat ccc ctc aac ccc aat tgg ttg 355
 Asn Glu Ala Pro Arg Pro Ser Leu Asn Pro Leu Asn Pro Asn Trp Leu
 70 75 80 85

ggc gtg gcc ttg gag gaa tac cgc gtg gtc atg ttg gat caa cgt ggc 403
 Gly Val Ala Leu Glu Glu Tyr Arg Val Val Met Leu Asp Gln Arg Gly
 90 95 100

acc ggc cgt tcc acc cca gtg ggt aat gat att ttg gaa aaa ccc aca 451
 Thr Gly Arg Ser Thr Pro Val Gly Asn Asp Ile Leu Glu Lys Pro Thr
 105 110 115

gca gaa gta gtg gag tac tta tcc cac ctg cgc gca gat ggc att gtg 499
 Ala Glu Val Val Glu Tyr Leu Ser His Leu Arg Ala Asp Gly Ile Val
 120 125 130

cga gat gct gaa gcc ctg cgt aag cat ttg ggt gtg aat cag tgg aac 547
 Arg Asp Ala Glu Ala Leu Arg Lys His Leu Gly Val Asn Gln Trp Asn
 135 140 145

ctt tta ggc cag tcc ttc gga ggt ttc acc acc ctg cat tac ttg tcc 595
 Leu Leu Gly Gln Ser Phe Gly Gly Phe Thr Thr Leu His Tyr Leu Ser
 150 155 160 165

cgg cac gcc gat tcc ttg gac aac gtg ttt att acc ggc ggt ctc agc 643
 Arg His Ala Asp Ser Leu Asp Asn Val Phe Ile Thr Gly Gly Leu Ser
 170 175 180

gct att gat cgc cca gca gaa gac gtg tat gcc aac tgt tac aac cgc 691

Ala	Ile	Asp	Arg	Pro	Ala	Glu	Asp	Val	Tyr	Ala	Asn	Cys	Tyr	Asn	Arg	
			185					190					195			
atg	cgc	cga	aac	tct	gag	gaa	ttc	tac	cgt	cgc	ttc	ccg	caa	tta	cgg	739
Met	Arg	Arg	Asn	Ser	Glu	Glu	Phe	Tyr	Arg	Arg	Phe	Pro	Gln	Leu	Arg	
		200					205					210				
gaa	act	ttc	cga	ggg	ttg	gtt	aat	cgt	gct	cgc	gcc	ggg	gag	att	gtg	787
Glu	Thr	Phe	Arg	Gly	Leu	Val	Asn	Arg	Ala	Arg	Ala	Gly	Glu	Ile	Val	
	215					220					225					
ctt	ccc	acc	ggc	gaa	gtt	gtg	tca	gaa	acc	agg	ctg	cga	tcc	ctt	ggt	835
Leu	Pro	Thr	Gly	Glu	Val	Val	Ser	Glu	Thr	Arg	Leu	Arg	Ser	Leu	Gly	
230					235					240					245	
cac	ttg	ttg	ggt	agc	aat	gac	ggc	tgg	ttt	gat	ctg	tac	aac	ctg	ctg	883
His	Leu	Leu	Gly	Ser	Asn	Asp	Gly	Trp	Phe	Asp	Leu	Tyr	Asn	Leu	Leu	
				250					255					260		
gaa	tta	gat	ccc	acc	tcc	aac	gct	ttt	gtc	cat	gac	ctg	gca	gga	ctt	931
Glu	Leu	Asp	Pro	Thr	Ser	Asn	Ala	Phe	Val	His	Asp	Leu	Ala	Gly	Leu	
			265					270					275			
ttg	cct	ttc	ggc	aac	cgc	aac	cca	att	tat	tac	gtg	ctc	cat	gag	tcc	979
Leu	Pro	Phe	Gly	Asn	Arg	Asn	Pro	Ile	Tyr	Tyr	Val	Leu	His	Glu	Ser	
		280					285					290				
tct	tac	gcc	gac	ggt	gtg	gtg	aca	aat	tgg	gca	gca	gag	cgt	gtg	ctt	1027
Ser	Tyr	Ala	Asp	Gly	Val	Val	Thr	Asn	Trp	Ala	Ala	Glu	Arg	Val	Leu	
	295				300						305					
cca	gag	gat	ttc	cgc	gag	gat	cca	aca	ctg	ctc	acc	ggt	gag	cac	gtg	1075
Pro	Glu	Asp	Phe	Arg	Glu	Asp	Pro	Thr	Leu	Leu	Thr	Gly	Glu	His	Val	
310					315					320					325	
ttc	cag	gag	tgg	aca	gac	acc	gtg	ccg	tcg	ctc	aag	ccg	tgg	aag	gac	1123
Phe	Gln	Glu	Trp	Thr	Asp	Thr	Val	Pro	Ser	Leu	Lys	Pro	Trp	Lys	Asp	
				330				335						340		
gtt	gcc	ctg	gca	ttg	gct	cag	cag	gaa	tgg	ccc	aag	ctt	tat	gat	gcg	1171
Val	Ala	Leu	Ala	Leu	Ala	Gln	Gln	Glu	Trp	Pro	Lys	Leu	Tyr	Asp	Ala	
			345					350					355			
aag	gca	ttg	gaa	aac	tca	cag	gcc	aag	ggc	gct	gca	gca	gtg	tat	gcc	1219
Lys	Ala	Leu	Glu	Asn	Ser	Gln	Ala	Lys	Gly	Ala	Ala	Ala	Val	Tyr	Ala	
		360					365					370				
aat	gac	gtt	ttc	gtc	cca	gtg	gat	tac	tct	ctg	gaa	acc	gca	caa	cac	1267
Asn	Asp	Val	Phe	Val	Pro	Val	Asp	Tyr	Ser	Leu	Glu	Thr	Ala	Gln	His	
		375				380					385					
ctg																

425

<210> 174

<211> 427

<212> PRT

<213> Corynebacterium glutamicum

<400> 174

Val Val Gly Val Val Ser Thr Pro Ala Arg Asn Leu Gly Ser Met Thr
 1 5 10 15

Lys Thr Leu Gly Ser Leu Gln Leu Glu Glu Ile Thr Leu Thr Leu Pro
 20 25 30

Leu Thr Glu Asp Val Ala Asp Glu Arg Thr Ile Asp Val Phe Ala Arg
 35 40 45

Ile Ala Thr Arg Val Gly Gly Glu Asp Leu Pro Tyr Leu Val Phe Leu
 50 55 60

Gln Gly Gly Pro Gly Asn Glu Ala Pro Arg Pro Ser Leu Asn Pro Leu
 65 70 75 80

Asn Pro Asn Trp Leu Gly Val Ala Leu Glu Glu Tyr Arg Val Val Met
 85 90 95

Leu Asp Gln Arg Gly Thr Gly Arg Ser Thr Pro Val Gly Asn Asp Ile
 100 105 110

Leu Glu Lys Pro Thr Ala Glu Val Val Glu Tyr Leu Ser His Leu Arg
 115 120 125

Ala Asp Gly Ile Val Arg Asp Ala Glu Ala Leu Arg Lys His Leu Gly
 130 135 140

Val Asn Gln Trp Asn Leu Leu Gly Gln Ser Phe Gly Gly Phe Thr Thr
 145 150 155 160

Leu His Tyr Leu Ser Arg His Ala Asp Ser Leu Asp Asn Val Phe Ile
 165 170 175

Thr Gly Gly Leu Ser Ala Ile Asp Arg Pro Ala Glu Asp Val Tyr Ala
 180 185 190

Asn Cys Tyr Asn Arg Met Arg Arg Asn Ser Glu Glu Phe Tyr Arg Arg
 195 200 205

Phe Pro Gln Leu Arg Glu Thr Phe Arg Gly Leu Val Asn Arg Ala Arg
 210 215 220

Ala Gly Glu Ile Val Leu Pro Thr Gly Glu Val Val Ser Glu Thr Arg
 225 230 235 240

Leu Arg Ser Leu Gly His Leu Leu Gly Ser Asn Asp Gly Trp Phe Asp
 245 250 255

Leu Tyr Asn Leu Leu Glu Leu Asp Pro Thr Ser Asn Ala Phe Val His
 260 265 270

Asp Leu Ala Gly Leu Leu Pro Phe Gly Asn Arg Asn Pro Ile Tyr Tyr

275	280	285
Val Leu His Glu Ser Ser Tyr Ala Asp Gly Val Val Thr Asn Trp Ala 290 295 300		
Ala Glu Arg Val Leu Pro Glu Asp Phe Arg Glu Asp Pro Thr Leu Leu 305 310 315 320		
Thr Gly Glu His Val Phe Gln Glu Trp Thr Asp Thr Val Pro Ser Leu 325 330 335		
Lys Pro Trp Lys Asp Val Ala Leu Ala Leu Ala Gln Gln Glu Trp Pro 340 345 350		
Lys Leu Tyr Asp Ala Lys Ala Leu Glu Asn Ser Gln Ala Lys Gly Ala 355 360 365		
Ala Ala Val Tyr Ala Asn Asp Val Phe Val Pro Val Asp Tyr Ser Leu 370 375 380		
Glu Thr Ala Gln His Leu Pro Gly Val Gln Leu Phe Ile Thr Ser Gln 385 390 395 400		
His Glu His Asn Gly Leu Arg Ala Ser Ser Gly Ala Val Leu Lys His 405 410 415		
Leu Phe Asp Leu Ala His Gly Arg Glu Val Arg 420 425		

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<211> 980

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(957)

<223> FRXA00499

<400> 175

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tcc cac ctg cgc gca gat ggc att gtg cga gat gct gaa gcc ctg cgt Ser His Leu Arg Ala Asp Gly Ile Val Arg Asp Ala Glu Ala Leu Arg 20 25 30 96	
aag cat ttg ggt gtg aat cag tgg aac ctt tta ggc cag tcc ttc gga Lys His Leu Gly Val Asn Gln Trp Asn Leu Leu Gly Gln Ser Phe Gly 35 40 45 144	
ggt ttc acc acc ctg cat tac ttg tcc cgg cac gcc gat tcc ttg gac Gly Phe Thr Thr Leu His Tyr Leu Ser Arg His Ala Asp Ser Leu Asp 50 55 60 192	
aac gtg ttt att acc ggc ggt ctc agc gct att gat cgc cca gca gaa Asn Val Phe Ile Thr Gly Gly Leu Ser Ala Ile Asp Arg Pro Ala Glu 65 70 75 80 240	

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<211> 319

<212> PRT

<213> Corynebacterium glutamicum

<400> 176

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Ser His Leu Arg Ala Asp Gly Ile Val Arg Asp Ala Glu Ala Leu Arg
 20 25 30

Lys His Leu Gly Val Asn Gln Trp Asn Leu Leu Gly Gln Ser Phe Gly
 35 40 45

Gly Phe Thr Thr Leu His Tyr Leu Ser Arg His Ala Asp Ser Leu Asp
 50 55 60

Asn Val Phe Ile Thr Gly Gly Leu Ser Ala Ile Asp Arg Pro Ala Glu
 65 70 75 80

Asp Val Tyr Ala Asn Cys Tyr Asn Arg Met Arg Arg Asn Ser Glu Glu
 85 90 95

Phe Tyr Arg Arg Phe Pro Gln Leu Arg Glu Thr Phe Arg Gly Leu Val
 100 105 110

Asn Arg Ala Arg Ala Gly Glu Ile Val Leu Pro Thr Gly Glu Val Val
 115 120 125

Ser Glu Thr Arg Leu Arg Ser Leu Gly His Leu Leu Gly Ser Asn Asp
 130 135 140

Gly Trp Phe Asp Leu Tyr Asn Leu Leu Glu Leu Asp Pro Thr Ser Asn
 145 150 155 160

Ala Phe Val His Asp Leu Ala Gly Leu Leu Pro Phe Gly Asn Arg Asn
 165 170 175

Pro Ile Tyr Tyr Val Leu His Glu Ser Ser Tyr Ala Asp Gly Val Val
 180 185 190

Thr Asn Trp Ala Ala Glu Arg Val Leu Pro Glu Asp Phe Arg Glu Asp
 195 200 205

Pro Thr Leu Leu Thr Gly Glu His Val Phe Gln Glu Trp Thr Asp Thr
 210 215 220

Val Pro Ser Leu Lys Pro Trp Lys Asp Val Ala Leu Ala Leu Ala Gln
 225 230 235 240

Gln Glu Trp Pro Lys Leu Tyr Asp Ala Lys Ala Leu Glu Asn Ser Gln
 245 250 255

Ala Lys Gly Ala Ala Ala Val Tyr Ala Asn Asp Val Phe Val Pro Val
 260 265 270

Asp Tyr Ser Leu Glu Thr Ala Gln His Leu Pro Gly Val Gln Leu Phe
 275 280 285

Ile Thr Ser Gln His Glu His Asn Gly Leu Arg Ala Ser Ser Gly Ala
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Val Leu Lys His Leu Phe Asp Leu Ala His Gly Arg Glu Val Arg
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<210> 177

<211> 2127

<212> DNA

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<220>

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<222> (101)..(2104)

<223> RXN01277

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 Met Thr Asp Tyr Thr
 1 5

ttc ctc gaa gac att gac acc ccg gaa gcg ctc gcg tgg gcg gaa aaa 163
 Phe Leu Glu Asp Ile Asp Thr Pro Glu Ala Leu Ala Trp Ala Glu Lys
 10 15 20

tgg tcg ggg gaa agc gtc gaa aag cta aaa agc cca gcc aag gac gcc 211
 Trp Ser Gly Glu Ser Val Glu Lys Leu Lys Ser Pro Ala Lys Asp Ala
 25 30 35

ctg gaa gcc agg ctg ctg gct gcg ttg gac acc gat gat cgc att gcc 259
 Leu Glu Ala Arg Leu Leu Ala Ala Leu Asp Thr Asp Asp Arg Ile Ala
 40 45 50

tac gtg agc cgg cgc ggt gag aag ctg tac aac ttt tgg cgg gac gcg 307
 Tyr Val Ser Arg Arg Gly Glu Lys Leu Tyr Asn Phe Trp Arg Asp Ala
 55 60 65

cag cat ccg cgt gga gtg tgg cgc acg acc acg ttg gag tcg tat gaa 355
 Gln His Pro Arg Gly Val Trp Arg Thr Thr Leu Glu Ser Tyr Glu
 70 75 80 85

agt gac cag ccg gag tgg gac gtg ctc att gat gtg gat gcg ttg gcg 403
 Ser Asp Gln Pro Glu Trp Asp Val Leu Ile Asp Val Asp Ala Leu Ala
 90 95 100

gag gat gag ggc gaa aac tgg gta tgg aag ggc gcg gtt gtg cgc tcg 451
 Glu Asp Glu Gly Glu Asn Trp Val Trp Lys Gly Ala Val Val Arg Ser
 105 110 115

ccg gag ttt gat cgg gcg ttg gtg aag ttc tcg cgg ggc ggg gct gat 499
 Pro Glu Phe Asp Arg Ala Leu Val Lys Phe Ser Arg Gly Gly Ala Asp
 120 125 130

gcg acg gtg att agg gag ttt gat ctg gcc acg gct gct ttc gtg gat 547
 Ala Thr Val Ile Arg Glu Phe Asp Leu Ala Thr Ala Ala Phe Val Asp
 135 140 145

gat tcg ccg ttt gaa ttg aag gag gcg aag tcc gat gtc acg tgg gtt Asp Ser Pro Phe Glu Leu Lys Glu Ala Lys Ser Asp Val Thr Trp Val 150 155 160 165	595
gat ctg gat acg ttg ctg gtg ggc acg gat acc ggc gag ggg tca ctg Asp Leu Asp Thr Leu Leu Val Gly Thr Asp Thr Gly Glu Gly Ser Leu 170 175 180	643
acg gat tct ggg tac ccg gcg cgg gtg ctc acg tgg aag cgt ggg act Thr Asp Ser Gly Tyr Pro Ala Arg Val Leu Thr Trp Lys Arg Gly Thr 185 190 195	691
ccg ctt gag cag gcg gag ttg ttc ttt gag ggg tcg cgt cag gat gtg Pro Leu Glu Gln Ala Glu Leu Phe Phe Glu Gly Ser Arg Gln Asp Val 200 205 210	739
gcg act cat gcg tgg cgg gat tca aca cct ggt ttt gag cgg acg ttt Ala Thr His Ala Trp Arg Asp Ser Thr Pro Gly Phe Glu Arg Thr Phe 215 220 225	787
gtg tca agg tcg ttg gat ttc tat aat tcg gag acg tcg ctg gaa acc Val Ser Arg Ser Leu Asp Phe Tyr Asn Ser Glu Thr Ser Leu Glu Thr 230 235 240 245	835
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gtg aag aag cag tgg att ttt gtg agt cct cgg acg gat ttc gct ggg Val Lys Lys Gln Trp Ile Phe Val Ser Pro Arg Thr Asp Phe Ala Gly 265 270 275	931
att cca gca ggt ggc ttg gga gtg ctg ctg tta aag gag ttc ctt gag Ile Pro Ala Gly Gly Leu Gly Val Leu Leu Lys Glu Phe Leu Glu 280 285 290	979
ggc ggg cgc gat ttt cag cct gtg ttt acg cct act gag tcg acg tcg Gly Gly Arg Asp Phe Gln Pro Val Phe Thr Pro Thr Glu Ser Thr Ser 295 300 305	1027
ctg cag gga ttg gcc acg aca aag aat ttc ctg gtt tta acg ctc ctt Leu Gln Gly Leu Ala Thr Lys Asn Phe Leu Val Leu Thr Leu Leu 310 315 320 325	1075
aat aat gtc tcc aca gaa atc gtc aca gtg ccg ctc aat gat ccg aca Asn Asn Val Ser Thr Glu Ile Val Thr Val Pro Leu Asn Asp Pro Thr 330 335 340	1123
acg gag cat gaa cac att gac ctc cca gag cat gtc acc gcg cat gtg Thr Glu His Glu His Ile Asp Leu Pro Glu His Val Thr Ala His Val 345 350 355	1171
gtt gct acc tcc ccg ttg gat ggc gat gaa att tgg gtg cag gca gcg Val Ala Thr Ser Pro Leu Asp Gly Asp Glu Ile Trp Val Gln Ala Ala 360 365 370	1219
agt ttc acc gaa gcg cca acg ttg ctg cgt gcg gag ctg cct ggt gcg Ser Phe Thr Glu Ala Pro Thr Leu Leu Arg Ala Glu Leu Pro Gly Ala 375 380 385	1267
ctt gag gct gtg aag aag gcg ccg ttg cag ttt gaa aat gct ggt cag	1315

Leu	Glu	Ala	Val	Lys	Lys	Ala	Pro	Leu	Gln	Phe	Glu	Asn	Ala	Gly	Gln			
390					395					400					405			
gag	act	cgt	cag	cat	tgg	gca	acc	tcg	gcg	gat	gga	acg	aag	att	ccg			1363
Glu	Thr	Arg	Gln	His	Trp	Ala	Thr	Ser	Ala	Asp	Gly	Thr	Lys	Ile	Pro			
				410					415					420				
tac	ttt	att	aca	gga	gcc	ttc	gag	gag	gaa	cca	caa	aac	acc	ctg	gtc			1411
Tyr	Phe	Ile	Thr	Gly	Ala	Phe	Glu	Glu	Glu	Pro	Gln	Asn	Thr	Leu	Val			
			425					430					435					
cac	gcc	tac	ggc	ggc	ttc	gag	gtt	tcc	ctt	acc	cca	agc	cac	tcc	ccg			1459
His	Ala	Tyr	Gly	Gly	Phe	Glu	Val	Ser	Leu	Thr	Pro	Ser	His	Ser	Pro			
		440					445					450						
acc	cgc	ggc	atc	gca	tgg	ttg	gaa	aag	ggc	tac	tac	ttt	gtg	gaa	gcc			1507
Thr	Arg	Gly	Ile	Ala	Trp	Leu	Glu	Lys	Gly	Tyr	Tyr	Phe	Val	Glu	Ala			
	455					460						465						
aac	ctg	cgt	ggt	ggc	ggt	gaa	ttc	ggt	ccg	gaa	tgg	cat	tcg	cag	gca			1555
Asn	Leu	Arg	Gly	Gly	Gly	Glu	Phe	Gly	Pro	Glu	Trp	His	Ser	Gln	Ala			
470					475					480					485			
acc	aag	ctg	aac	cgc	atg	aag	gtg	tgg	gag	gat	cac	cgc	gcg	gtg	ctc			1603
Thr	Lys	Leu	Asn	Arg	Met	Lys	Val	Trp	Glu	Asp	His	Arg	Ala	Val	Leu			
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gcc	gac	ctt	gtg	gag	cgc	ggc	tac	gca	acg	ccg	gag	cag	att	gcg	att			1651
Ala	Asp	Leu	Val	Glu	Arg	Gly	Tyr	Ala	Thr	Pro	Glu	Gln	Ile	Ala	Ile			
			505					510					515					
cgt	ggc	gga	tcc	aac	ggt	ggt	ttg	ctg	aca	agt	ggc	gcg	tta	act	cag			1699
Arg	Gly	Gly	Ser	Asn	Gly	Gly	Leu	Leu	Thr	Ser	Gly	Ala	Leu	Thr	Gln			
		520					525					530						
tac	cca	gaa	gca	ttc	ggt	gcg	gca	gtt	gtg	cag	gtg	ccg	ttg	gct	gat			1747
Tyr	Pro	Glu	Ala	Phe	Gly	Ala	Ala	Val	Val	Gln	Val	Pro	Leu	Ala	Asp			
	535					540					545							
atg	ttg	cgc	tat	cac	acc	tgg	tca	gcg	ggt	gct	tcg	tgg	atg	gcg	gag			1795
Met	Leu	Arg	Tyr	His	Thr	Trp	Ser	Ala	Gly	Ala	Ser	Trp	Met	Ala	Glu			
550					555					560					565			
tac	ggc	aac	cct	gac	gat	ccg	gag	gaa	cgg	gcg	gtg	att	gag	cag	tac			1843
Tyr	Gly	Asn	Pro	Asp	Asp	Pro	Glu	Glu	Arg	Ala	Val	Ile	Glu	Gln	Tyr			
				570					575					580				
tcg	ccg	gtg	cag	gcg	gtg	gtg	ggc	gtc	gag	aag	cga	att	tat	cca	ccc			1891
Ser	Pro	Val	Gln	Ala	Val	Val	Gly	Val	Glu	Lys	Arg	Ile	Tyr	Pro	Pro			
			585					590					595					
gca	ttg	gtg	acg	acc	tca	acc	cgg	gac	gac	cgc	gtc	cac	ccc	gcg	cac			1939
Ala	Leu	Val	Thr	Thr	Ser	Thr	Arg	Asp	Asp	Arg	Val	His	Pro	Ala	His			
		600					605					610						
gcg	cgc	ctt	ttt	gct	caa	gct	ttg	ctt	gat	gcg	ggc	cag	gcc	gtg	gat			1987
Ala	Arg	Leu	Phe	Ala	Gln	Ala	Leu	Leu	Asp	Ala	Gly	Gln	Ala	Val	Asp			
		615				620					625							
tac	tac	gaa	aac	acc	gag	ggc	ggc	cat	gcc	ggc	gcg	gcg	gat	aac	aag			2035
Tyr	Tyr	Glu	Asn	Thr	Glu	Gly	Gly	His	Ala	Gly	Ala	Ala	Asp	Asn	Lys			

630 635 640 645
 cag acc gcg ttt gtg gaa tcg ctg atc tac acc tgg atc gag aag act 2083
 Gln Thr Ala Phe Val Glu Ser Leu Ile Tyr Thr Trp Ile Glu Lys Thr
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 Leu Asp Gln Gln Gly Ser Ile
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<210> 178

<211> 668

<212> PRT

<213> Corynebacterium glutamicum

<400> 178

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Pro Ala Lys Asp Ala Leu Glu Ala Arg Leu Leu Ala Ala Leu Asp Thr
 35 40 45

Asp Asp Arg Ile Ala Tyr Val Ser Arg Arg Gly Glu Lys Leu Tyr Asn
 50 55 60

Phe Trp Arg Asp Ala Gln His Pro Arg Gly Val Trp Arg Thr Thr Thr
 65 70 75 80

Leu Glu Ser Tyr Glu Ser Asp Gln Pro Glu Trp Asp Val Leu Ile Asp
 85 90 95

Val Asp Ala Leu Ala Glu Asp Glu Gly Glu Asn Trp Val Trp Lys Gly
 100 105 110

Ala Val Val Arg Ser Pro Glu Phe Asp Arg Ala Leu Val Lys Phe Ser
 115 120 125

Arg Gly Gly Ala Asp Ala Thr Val Ile Arg Glu Phe Asp Leu Ala Thr
 130 135 140

Ala Ala Phe Val Asp Asp Ser Pro Phe Glu Leu Lys Glu Ala Lys Ser
 145 150 155 160

Asp Val Thr Trp Val Asp Leu Asp Thr Leu Leu Val Gly Thr Asp Thr
 165 170 175

Gly Glu Gly Ser Leu Thr Asp Ser Gly Tyr Pro Ala Arg Val Leu Thr
 180 185 190

Trp Lys Arg Gly Thr Pro Leu Glu Gln Ala Glu Leu Phe Phe Glu Gly
 195 200 205

Ser Arg Gln Asp Val Ala Thr His Ala Trp Arg Asp Ser Thr Pro Gly
 210 215 220

Phe Glu Arg Thr Phe Val Ser Arg Ser Leu Asp Phe Tyr Asn Ser Glu
 225 230 235 240

Thr Ser Leu Glu Thr Glu Gly Gly Leu Val Lys Leu Asp Val Pro Thr
 245 250 255
 Asp Cys Asp Val Ile Val Lys Lys Gln Trp Ile Phe Val Ser Pro Arg
 260 265 270
 Thr Asp Phe Ala Gly Ile Pro Ala Gly Gly Leu Gly Val Leu Leu Leu
 275 280 285
 Lys Glu Phe Leu Glu Gly Gly Arg Asp Phe Gln Pro Val Phe Thr Pro
 290 295 300
 Thr Glu Ser Thr Ser Leu Gln Gly Leu Ala Thr Thr Lys Asn Phe Leu
 305 310 315 320
 Val Leu Thr Leu Leu Asn Asn Val Ser Thr Glu Ile Val Thr Val Pro
 325 330 335
 Leu Asn Asp Pro Thr Thr Glu His Glu His Ile Asp Leu Pro Glu His
 340 345 350
 Val Thr Ala His Val Val Ala Thr Ser Pro Leu Asp Gly Asp Glu Ile
 355 360 365
 Trp Val Gln Ala Ala Ser Phe Thr Glu Ala Pro Thr Leu Leu Arg Ala
 370 375 380
 Glu Leu Pro Gly Ala Leu Glu Ala Val Lys Lys Ala Pro Leu Gln Phe
 385 390 395 400
 Glu Asn Ala Gly Gln Glu Thr Arg Gln His Trp Ala Thr Ser Ala Asp
 405 410 415
 Gly Thr Lys Ile Pro Tyr Phe Ile Thr Gly Ala Phe Glu Glu Glu Pro
 420 425 430
 Gln Asn Thr Leu Val His Ala Tyr Gly Gly Phe Glu Val Ser Leu Thr
 435 440 445
 Pro Ser His Ser Pro Thr Arg Gly Ile Ala Trp Leu Glu Lys Gly Tyr
 450 455 460
 Tyr Phe Val Glu Ala Asn Leu Arg Gly Gly Gly Glu Phe Gly Pro Glu
 465 470 475 480
 Trp His Ser Gln Ala Thr Lys Leu Asn Arg Met Lys Val Trp Glu Asp
 485 490 495
 His Arg Ala Val Leu Ala Asp Leu Val Glu Arg Gly Tyr Ala Thr Pro
 500 505 510
 Glu Gln Ile Ala Ile Arg Gly Gly Ser Asn Gly Gly Leu Leu Thr Ser
 515 520 525
 Gly Ala Leu Thr Gln Tyr Pro Glu Ala Phe Gly Ala Ala Val Val Gln
 530 535 540
 Val Pro Leu Ala Asp Met Leu Arg Tyr His Thr Trp Ser Ala Gly Ala
 545 550 555 560

Ser Trp Met Ala Glu Tyr Gly Asn Pro Asp Asp Pro Glu Glu Arg Ala
 565 570 575

Val Ile Glu Gln Tyr Ser Pro Val Gln Ala Val Val Gly Val Glu Lys
 580 585 590

Arg Ile Tyr Pro Pro Ala Leu Val Thr Thr Ser Thr Arg Asp Asp Arg
 595 600 605

Val His Pro Ala His Ala Arg Leu Phe Ala Gln Ala Leu Leu Asp Ala
 610 615 620

Gly Gln Ala Val Asp Tyr Tyr Glu Asn Thr Glu Gly Gly His Ala Gly
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Ala Ala Asp Asn Lys Gln Thr Ala Phe Val Glu Ser Leu Ile Tyr Thr
 645 650 655

Trp Ile Glu Lys Thr Leu Asp Gln Gln Gly Ser Ile
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<222> (101)..(1789)

<223> FRXA01277

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 Phe Leu Glu Asp Ile Asp Thr Pro Glu Ala Leu Ala Trp Ala Glu Lys
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tgg tcg ggg gaa agc gtc gaa aag cta aaa agc cca gcc aag gac gcc 211
 Trp Ser Gly Glu Ser Val Glu Lys Leu Lys Ser Pro Ala Lys Asp Ala
 25 30 35

ctg gaa gcc agg ctg ctg gct gcg ttg gac acc gat gat cgc att gcc 259
 Leu Glu Ala Arg Leu Leu Ala Ala Leu Asp Thr Asp Asp Arg Ile Ala
 40 45 50

tac gtg agc cgg cgc ggt gag aag ctg tac aac ttt tgg cgg gac gcg 307
 Tyr Val Ser Arg Arg Gly Glu Lys Leu Tyr Asn Phe Trp Arg Asp Ala
 55 60 65

cag cat ccg cgt gga gtg tgg cgc acg acc acg ttg gag tcg tat gaa 355
 Gln His Pro Arg Gly Val Trp Arg Thr Thr Thr Leu Glu Ser Tyr Glu
 70 75 80 85

agt gac cag ccg gag tgg gac gtg ctc att gat gtg gat gcg ttg gcg 403
 Ser Asp Gln Pro Glu Trp Asp Val Leu Ile Asp Val Asp Ala Leu Ala

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Glu	Asp	Glu	Gly	Glu	Asn	Trp	Val	Trp	Lys	Gly	Ala	Val	Val	Arg	Ser	
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ccg	gag	ttt	gat	cgg	gcg	ttg	gtg	aag	ttc	tcg	cgg	ggc	ggg	gct	gat	499
Pro	Glu	Phe	Asp	Arg	Ala	Leu	Val	Lys	Phe	Ser	Arg	Gly	Gly	Ala	Asp	
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Ala	Thr	Val	Ile	Arg	Glu	Phe	Asp	Leu	Ala	Thr	Ala	Ala	Phe	Val	Asp	
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gat	tcg	ccg	ttt	gaa	ttg	aag	gag	gcg	aag	tcc	gat	gtc	acg	tgg	gtt	595
Asp	Ser	Pro	Phe	Glu	Leu	Lys	Glu	Ala	Lys	Ser	Asp	Val	Thr	Trp	Val	
150				155								160				165
gat	ctg	gat	acg	ttg	ctg	gtg	ggc	acg	gat	acc	ggc	gag	ggg	tca	ctg	643
Asp	Leu	Asp	Thr	Leu	Leu	Val	Gly	Thr	Asp	Thr	Gly	Glu	Gly	Ser	Leu	
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acg	gat	tct	ggg	tac	ccg	gcg	cgg	gtg	ctc	acg	tgg	aag	cgt	ggg	act	691
Thr	Asp	Ser	Gly	Tyr	Pro	Ala	Arg	Val	Leu	Thr	Trp	Lys	Arg	Gly	Thr	
185								190				195				
ccg	ctt	gag	cag	gcg	gag	ttg	ttc	ttt	gag	ggg	tcg	cgt	cag	gat	gtg	739
Pro	Leu	Glu	Gln	Ala	Glu	Leu	Phe	Phe	Glu	Gly	Ser	Arg	Gln	Asp	Val	
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gcg	act	cat	gcg	tgg	cgg	gat	tca	aca	cct	ggt	ttt	gag	cgg	acg	ttt	787
Ala	Thr	His	Ala	Trp	Arg	Asp	Ser	Thr	Pro	Gly	Phe	Glu	Arg	Thr	Phe	
215				220								225				
gtg	tca	agg	tcg	ttg	gat	ttc	tat	aat	tcg	gag	acg	tcg	ctg	gaa	acc	835
Val	Ser	Arg	Ser	Leu	Asp	Phe	Tyr	Asn	Ser	Glu	Thr	Ser	Leu	Glu	Thr	
230				235				240				245				
gag	ggt	ggc	ctg	gtc	aag	ctt	gat	gtg	ccg	acc	gat	tgc	gat	gtc	att	883
Glu	Gly	Gly	Leu	Val	Lys	Leu	Asp	Val	Pro	Thr	Asp	Cys	Asp	Val	Ile	
				250				255				260				
gtg	aag	aag	cag	tgg	att	ttt	gtg	agt	cct	cgg	acg	gat	ttc	gct	ggg	931
Val	Lys	Lys	Gln	Trp	Ile	Phe	Val	Ser	Pro	Arg	Thr	Asp	Phe	Ala	Gly	
265								270				275				
att	cca	gca	ggt	ggc	ttg	gga	gtg	ctg	ctg	tta	aag	gag	ttc	ctt	gag	979
Ile	Pro	Ala	Gly	Gly	Leu	Gly	Val	Leu	Leu	Leu	Lys	Glu	Phe	Leu	Glu	
280				285								290				
ggc	ggg	cgc	gat	ttt	cag	cct	gtg	ttt	acg	cct	act	gag	tcg	acg	tcg	1027
Gly	Gly	Arg	Asp	Phe	Gln	Pro	Val	Phe	Thr	Pro	Thr	Glu	Ser	Thr	Ser	
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Leu	Gln	Gly	Leu	Ala	Thr	Thr										

acg gag cat gaa cac att gac ctc cca gag cat gtc acc gcg cat gtg	1171
Thr Glu His Glu His Ile Asp Leu Pro Glu His Val Thr Ala His Val	
345 350 355	
gtt gct acc tcc ccg ttg gat ggc gat gaa att tgg gtg cag gca gcg	1219
Val Ala Thr Ser Pro Leu Asp Gly Asp Glu Ile Trp Val Gln Ala Ala	
360 365 370	
agt ttc acc gaa gcg cca acg ttg ctg cgt gcg gag ctg cct ggt gcg	1267
Ser Phe Thr Glu Ala Pro Thr Leu Leu Arg Ala Glu Leu Pro Gly Ala	
375 380 385	
ctt gag gct gtg aag aag gcg ccg ttg cag ttt gaa aat gct ggt cag	1315
Leu Glu Ala Val Lys Lys Ala Pro Leu Gln Phe Glu Asn Ala Gly Gln	
390 395 400 405	
gag act cgt cag cat tgg gca acc tcg gcg gat gga acg aag att ccg	1363
Glu Thr Arg Gln His Trp Ala Thr Ser Ala Asp Gly Thr Lys Ile Pro	
410 415 420	
tac ttt att aca gga gcc ttc gag gag gaa cca caa aac acc ctg gtc	1411
Tyr Phe Ile Thr Gly Ala Phe Glu Glu Glu Pro Gln Asn Thr Leu Val	
425 430 435	
cac gcc tac ggc ggc ttc gag gtt tcc ctt acc cca agc cac tcc ccg	1459
His Ala Tyr Gly Gly Phe Glu Val Ser Leu Thr Pro Ser His Ser Pro	
440 445 450	
acc cgc ggc atc gca tgg ttg gaa aag ggc tac tac ttt gtg gaa gcc	1507
Thr Arg Gly Ile Ala Trp Leu Glu Lys Gly Tyr Tyr Phe Val Glu Ala	
455 460 465	
aac ctg cgt ggt ggc ggt gaa ttc ggt ccg gaa tgg cat tcg cag gca	1555
Asn Leu Arg Gly Gly Gly Glu Phe Gly Pro Glu Trp His Ser Gln Ala	
470 475 480 485	
acc aag ctg aac cgc atg aag gtg tgg gag gat cac cgc gcg gtg ctc	1603
Thr Lys Leu Asn Arg Met Lys Val Trp Glu Asp His Arg Ala Val Leu	
490 495 500	
gcc gac ctt gtg gag cgc ggc tac gca acg ccg gag cag att gcg att	1651
Ala Asp Leu Val Glu Arg Gly Tyr Ala Thr Pro Glu Gln Ile Ala Ile	
505 510 515	
cgt ggc gga tcc aac ggt ggt ttg ctg aca agt ggc gcg tta act cag	1699
Arg Gly Gly Ser Asn Gly Gly Leu Leu Thr Ser Gly Ala Leu Thr Gln	
520 525 530	
tac cca gaa gca ttc ggt gcg gca gtt gtg cag gtg ccg ttg gct gat	1747
Tyr Pro Glu Ala Phe Gly Ala Ala Val Val Gln Val Pro Leu Ala Asp	
535 540 545	
atg ttg cgc tat cac acc tgg tca gcg ggt acc tcg tgg atg	1789
Met Leu Arg Tyr His Thr Trp Ser Ala Gly Thr Ser Trp Met	
550 555 560	
taggtgtcgg caaccatggg aac	1812

<211> 563

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 180

Met	Thr	Asp	Tyr	Thr	Phe	Leu	Glu	Asp	Ile	Asp	Thr	Pro	Glu	Ala	Leu
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Ala	Trp	Ala	Glu	Lys	Trp	Ser	Gly	Glu	Ser	Val	Glu	Lys	Leu	Lys	Ser
			20					25					30		
Pro	Ala	Lys	Asp	Ala	Leu	Glu	Ala	Arg	Leu	Leu	Ala	Ala	Leu	Asp	Thr
		35					40					45			
Asp	Asp	Arg	Ile	Ala	Tyr	Val	Ser	Arg	Arg	Gly	Glu	Lys	Leu	Tyr	Asn
	50					55					60				
Phe	Trp	Arg	Asp	Ala	Gln	His	Pro	Arg	Gly	Val	Trp	Arg	Thr	Thr	Thr
65					70					75					80
Leu	Glu	Ser	Tyr	Glu	Ser	Asp	Gln	Pro	Glu	Trp	Asp	Val	Leu	Ile	Asp
				85					90					95	
Val	Asp	Ala	Leu	Ala	Glu	Asp	Glu	Gly	Glu	Asn	Trp	Val	Trp	Lys	Gly
			100					105					110		
Ala	Val	Val	Arg	Ser	Pro	Glu	Phe	Asp	Arg	Ala	Leu	Val	Lys	Phe	Ser
		115					120					125			
Arg	Gly	Gly	Ala	Asp	Ala	Thr	Val	Ile	Arg	Glu	Phe	Asp	Leu	Ala	Thr
	130					135					140				
Ala	Ala	Phe	Val	Asp	Asp	Ser	Pro	Phe	Glu	Leu	Lys	Glu	Ala	Lys	Ser
145					150					155					160
Asp	Val	Thr	Trp	Val	Asp	Leu	Asp	Thr	Leu	Leu	Val	Gly	Thr	Asp	Thr
				165					170					175	
Gly	Glu	Gly	Ser	Leu	Thr	Asp	Ser	Gly	Tyr	Pro	Ala	Arg	Val	Leu	Thr
			180					185					190		
Trp	Lys	Arg	Gly	Thr	Pro	Leu	Glu	Gln	Ala	Glu	Leu	Phe	Phe	Glu	Gly
		195					200					205			
Ser	Arg	Gln	Asp	Val	Ala	Thr	His	Ala	Trp	Arg	Asp	Ser	Thr	Pro	Gly
	210					215					220				
Phe	Glu	Arg	Thr	Phe	Val	Ser	Arg	Ser	Leu	Asp	Phe	Tyr	Asn	Ser	Glu
225					230					235					240
Thr	Ser	Leu	Glu	Thr	Glu	Gly	Gly	Leu	Val	Lys	Leu	Asp	Val	Pro	Thr
				245					250					255	
Asp	Cys	Asp	Val	Ile	Val	Lys	Lys	Gln	Trp	Ile	Phe	Val	Ser	Pro	Arg
			260					265					270		

Thr	Asp	Phe	Ala	Gly	Ile	Pro	Ala	Gly	Gly	Leu	Gly	Val	Leu	Leu	Leu
		275					280					285			
Lys	Glu	Phe	Leu	Glu	Gly	Gly	Arg	Asp	Phe	Gln	Pro	Val	Phe	Thr	Pro
	290					295					300				

Thr Glu Ser Thr Ser Leu Gln Gly Leu Ala Thr Thr Lys Asn Phe Leu
 305 310 315 320
 Val Leu Thr Leu Leu Asn Asn Val Ser Thr Glu Ile Val Thr Val Pro
 325 330 335
 Leu Asn Asp Pro Thr Thr Glu His Glu His Ile Asp Leu Pro Glu His
 340 345 350
 Val Thr Ala His Val Val Ala Thr Ser Pro Leu Asp Gly Asp Glu Ile
 355 360 365
 Trp Val Gln Ala Ala Ser Phe Thr Glu Ala Pro Thr Leu Leu Arg Ala
 370 375 380
 Glu Leu Pro Gly Ala Leu Glu Ala Val Lys Lys Ala Pro Leu Gln Phe
 385 390 395 400
 Glu Asn Ala Gly Gln Glu Thr Arg Gln His Trp Ala Thr Ser Ala Asp
 405 410 415
 Gly Thr Lys Ile Pro Tyr Phe Ile Thr Gly Ala Phe Glu Glu Glu Pro
 420 425 430
 Gln Asn Thr Leu Val His Ala Tyr Gly Gly Phe Glu Val Ser Leu Thr
 435 440 445
 Pro Ser His Ser Pro Thr Arg Gly Ile Ala Trp Leu Glu Lys Gly Tyr
 450 455 460
 Tyr Phe Val Glu Ala Asn Leu Arg Gly Gly Gly Glu Phe Gly Pro Glu
 465 470 475 480
 Trp His Ser Gln Ala Thr Lys Leu Asn Arg Met Lys Val Trp Glu Asp
 485 490 495
 His Arg Ala Val Leu Ala Asp Leu Val Glu Arg Gly Tyr Ala Thr Pro
 500 505 510
 Glu Gln Ile Ala Ile Arg Gly Gly Ser Asn Gly Gly Leu Leu Thr Ser
 515 520 525
 Gly Ala Leu Thr Gln Tyr Pro Glu Ala Phe Gly Ala Ala Val Val Gln
 530 535 540
 Val Pro Leu Ala Asp Met Leu Arg Tyr His Thr Trp Ser Ala Gly Thr
 545 550 555 560
 Ser Trp Met

<210> 181

<211> 915

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(892)

<223> RXN00675

<400> 181

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tggttttaac	agtttaattt	gaagaaagag	acgtggaagc	atg	ggt	ttc	cgt	tcc	115
				Met	Gly	Phe	Arg	Ser	
				1				5	

aag	aag	aag	gtt	att	gcg	gca	aag	acc	gcc	gct	gag	ctg	gac	gcg	atg	163
Lys	Lys	Lys	Val	Ile	Ala	Ala	Lys	Thr	Ala	Ala	Glu	Leu	Asp	Ala	Met	
			10						15					20		

cag	gcg	gcg	ggt	gag	atc	gtc	ggc	aag	gct	ttg	cag	gct	gtg	cgc	gct	211
Gln	Ala	Ala	Gly	Glu	Ile	Val	Gly	Lys	Ala	Leu	Gln	Ala	Val	Arg	Ala	
			25					30					35			

gag	gct	aaa	gct	ggc	atg	agc	acg	tgg	gat	ctg	gat	cag	atc	gcg	gag	259
Glu	Ala	Lys	Ala	Gly	Met	Ser	Thr	Trp	Asp	Leu	Asp	Gln	Ile	Ala	Glu	
		40					45					50				

cag	gtt	atc	cgc	gat	gct	ggc	gcc	gtt	cct	aca	ttc	ctg	ggt	tac	cag	307
Gln	Val	Ile	Arg	Asp	Ala	Gly	Ala	Val	Pro	Thr	Phe	Leu	Gly	Tyr	Gln	
	55					60					65					

ggt	ttt	ccg	gca	tca	gtg	tgc	gct	tcg	gtc	aat	gag	gtg	att	gtt	cac	355
Gly	Phe	Pro	Ala	Ser	Val	Cys	Ala	Ser	Val	Asn	Glu	Val	Ile	Val	His	
70					75					80					85	

ggc	att	cca	tcc	aag	gag	acc	atc	ttg	gag	gaa	ggc	gat	ctg	gtg	tcc	403
Gly	Ile	Pro	Ser	Lys	Glu	Thr	Ile	Leu	Glu	Glu	Gly	Asp	Leu	Val	Ser	
			90						95					100		

atc	gac	tgc	ggc	gca	acc	ttt	gat	ggt	tgg	gtc	ggc	gat	tcc	gcg	tgg	451
Ile	Asp	Cys	Gly	Ala	Thr	Phe	Asp	Gly	Trp	Val	Gly	Asp	Ser	Ala	Trp	
			105					110					115			

agc	ttc	ggc	atc	ggc	gag	ctg	gac	gag	gac	gtc	cag	ggt	ctc	aac	ttg	499
Ser	Phe	Gly	Ile	Gly	Glu	Leu	Asp	Glu	Asp	Val	Gln	Gly	Leu	Asn	Leu	
		120					125					130				

gct	acc	gag	tgg	gtc	ctc	atg	gaa	ggc	atg	aag	gcc	atg	gtt	cca	ggc	547
Ala	Thr	Glu	Trp	Val	Leu	Met	Glu	Gly	Met	Lys	Ala	Met	Val	Pro	Gly	
	135					140					145					

aac	cgt	ttg	acc	gat	gtc	tcc	cac	gct	ctc	gag	gtc	gca	acc	cgc	aag	595
Asn	Arg	Leu	Thr	Asp	Val	Ser	His	Ala	Leu	Glu	Val	Ala	Thr	Arg	Lys	
150					155					160					165	

gct	gag	tcc	aag	ttc	ggc	gtc	gcg	ctc	ggc	atc	gtc	gat	ggc	tac	ggc	643
Ala	Glu	Ser	Lys	Phe	Gly	Val	Ala	Leu	Gly	Ile	Val	Asp	Gly	Tyr	Gly	
			170						175					180		

gga	cac	ggc	att	ggc	cgc	cac	atg	cac	gag	gag	cca	tac	ttg	gct	aat	691
Gly	His	Gly	Ile	Gly	Arg	His	Met	His	Glu	Glu	Pro	Tyr	Leu	Ala	Asn	
			185					190					195			

gag	ggc	aag	gcc	ggc	aag	ggc	cct	gtg	att	cag	gag	ggc	tcc	gtg	ctc	739
Glu	Gly	Lys	Ala	Gly	Lys	Gly	Pro	Val	Ile	Gln	Glu	Gly	Ser	Val	Leu	
		200					205					210				

gcc att gag cct atg ctc acc ctc ggc acc gaa gat tcc gca gtg ctg 787
 Ala Ile Glu Pro Met Leu Thr Leu Gly Thr Glu Asp Ser Ala Val Leu
 215 220 225

gaa gat gat tgg act gtc gtg act ctc gac ggt tca tgg gca tca cac 835
 Glu Asp Asp Trp Thr Val Val Thr Leu Asp Gly Ser Trp Ala Ser His
 230 235 240 245

tgg gag cac acc gtt gca gcc acc aag ggc ggc ccg cgc atc ctc acg 883
 Trp Glu His Thr Val Ala Ala Thr Lys Gly Gly Pro Arg Ile Leu Thr
 250 255 260

ccg cgt tat taaaatgatg cttttcgcacg cat 915
 Pro Arg Tyr

<210> 182

<211> 264

<212> PRT

<213> Corynebacterium glutamicum

<400> 182

Met Gly Phe Arg Ser Lys Lys Lys Val Ile Ala Ala Lys Thr Ala Ala
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Glu Leu Asp Ala Met Gln Ala Ala Gly Glu Ile Val Gly Lys Ala Leu
 20 25 30

Gln Ala Val Arg Ala Glu Ala Lys Ala Gly Met Ser Thr Trp Asp Leu
 35 40 45

Asp Gln Ile Ala Glu Gln Val Ile Arg Asp Ala Gly Ala Val Pro Thr
 50 55 60

Phe Leu Gly Tyr Gln Gly Phe Pro Ala Ser Val Cys Ala Ser Val Asn
 65 70 75 80

Glu Val Ile Val His Gly Ile Pro Ser Lys Glu Thr Ile Leu Glu Glu
 85 90 95

Gly Asp Leu Val Ser Ile Asp Cys Gly Ala Thr Phe Asp Gly Trp Val
 100 105 110

Gly Asp Ser Ala Trp Ser Phe Gly Ile Gly Glu Leu Asp Glu Asp Val
 115 120 125

Gln Gly Leu Asn Leu Ala Thr Glu Trp Val Leu Met Glu Gly Met Lys
 130 135 140

Ala Met Val Pro Gly Asn Arg Leu Thr Asp Val Ser His Ala Leu Glu
 145 150 155 160

Val Ala Thr Arg Lys Ala Glu Ser Lys Phe Gly Val Ala Leu Gly Ile
 165 170 175

Val Asp Gly Tyr Gly Gly His Gly Ile Gly Arg His Met His Glu Glu
 180 185 190

Pro Tyr Leu Ala Asn Glu Gly Lys Ala Gly Lys Gly Pro Val Ile Gln
 195 200 205

Glu Gly Ser Val Leu Ala Ile Glu Pro Met Leu Thr Leu Gly Thr Glu
 210 215 220

Asp Ser Ala Val Leu Glu Asp Asp Trp Thr Val Val Thr Leu Asp Gly
 225 230 235 240

Ser Trp Ala Ser His Trp Glu His Thr Val Ala Ala Thr Lys Gly Gly
 245 250 255

Pro Arg Ile Leu Thr Pro Arg Tyr
 260

<210> 183
 <211> 506
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(483)
 <223> FRXA00675

<400> 183
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 Cys Gly Ala Thr Phe Asp Gly Trp Val Gly Asp Ser Ala Trp Ser Phe
 1 5 10 15

ggc atc ggc gag ctg gac gag gac gtc cag ggt ctc aac ttg gct acc 96
 Gly Ile Gly Glu Leu Asp Glu Asp Val Gln Gly Leu Asn Leu Ala Thr
 20 25 30

gag tgg gtc ctc atg gaa ggc atg aag gcc atg gtt cca ggc aac cgt 144
 Glu Trp Val Leu Met Glu Gly Met Lys Ala Met Val Pro Gly Asn Arg
 35 40 45

ttg acc gat gtc tcc cac gct ctc gag gtc gca acc cgc aag gct gag 192
 Leu Thr Asp Val Ser His Ala Leu Glu Val Ala Thr Arg Lys Ala Glu
 50 55 60

tcc aag ttc ggc gtc gcg ctc ggc atc gtc gat ggc tac ggc gga cac 240
 Ser Lys Phe Gly Val Ala Leu Gly Ile Val Asp Gly Tyr Gly Gly His
 65 70 75 80

ggc att ggc cgc cac atg cac gag gag cca tac ttg gct aat gag ggc 288
 Gly Ile Gly Arg His Met His Glu Glu Pro Tyr Leu Ala Asn Glu Gly
 85 90 95

aag gcc ggc aag ggc cct gtg att cag gag ggc tcc gtg ctc gcc att 336
 Lys Ala Gly Lys Gly Pro Val Ile Gln Glu Gly Ser Val Leu Ala Ile
 100 105 110

gag cct atg ctc acc ctc ggc acc gaa gat tcc gca gtg ctg gaa gat 384
 Glu Pro Met Leu Thr Leu Gly Thr Glu Asp Ser Ala Val Leu Glu Asp
 115 120 125

gat tgg act gtc gtg act ctc gac ggt tca tgg gca tca cac tgg gag 432
 Asp Trp Thr Val Val Thr Leu Asp Gly Ser Trp Ala Ser His Trp Glu
 130 135 140

cac acc gtt gca gcc acc aag ggc ggc ccg cgc atc ctc acg ccg cgt 480
 His Thr Val Ala Ala Thr Lys Gly Gly Pro Arg Ile Leu Thr Pro Arg
 145 150 155 160

tat taaaatgatg cttttcgacg cat 506
 Tyr

<210> 184
 <211> 161
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 184
 Cys Gly Ala Thr Phe Asp Gly Trp Val Gly Asp Ser Ala Trp Ser Phe
 1 5 10 15
 Gly Ile Gly Glu Leu Asp Glu Asp Val Gln Gly Leu Asn Leu Ala Thr
 20 25 30
 Glu Trp Val Leu Met Glu Gly Met Lys Ala Met Val Pro Gly Asn Arg
 35 40 45
 Leu Thr Asp Val Ser His Ala Leu Glu Val Ala Thr Arg Lys Ala Glu
 50 55 60
 Ser Lys Phe Gly Val Ala Leu Gly Ile Val Asp Gly Tyr Gly Gly His
 65 70 75 80
 Gly Ile Gly Arg His Met His Glu Glu Pro Tyr Leu Ala Asn Glu Gly
 85 90 95
 Lys Ala Gly Lys Gly Pro Val Ile Gln Glu Gly Ser Val Leu Ala Ile
 100 105 110
 Glu Pro Met Leu Thr Leu Gly Thr Glu Asp Ser Ala Val Leu Glu Asp
 115 120 125
 Asp Trp Thr Val Val Thr Leu Asp Gly Ser Trp Ala Ser His Trp Glu
 130 135 140
 His Thr Val Ala Ala Thr Lys Gly Gly Pro Arg Ile Leu Thr Pro Arg
 145 150 155 160
 Tyr

<210> 185
 <211> 1788
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1765)
 <223> RXN00877

<400> 185
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gcagacatga tgaaaactct agcaactagt atcggtcact	atg act gtt gaa cac	115
	Met Thr Val Glu His	
	1 5	
ctg ctc aag ccc agc acc ttg ccc tac cag ctg ccc gat ttc gca gcg	163	
Leu Leu Lys Pro Ser Thr Leu Pro Tyr Gln Leu Pro Asp Phe Ala Ala		
	10 15 20	
atc aag gtg gct gat ttc ccg ccc gcc ttc gaa ctc gca tta gct gaa	211	
Ile Lys Val Ala Asp Phe Pro Pro Ala Phe Glu Leu Ala Leu Ala Glu		
	25 30 35	
cac gat gct gaa att aca gcg atc gct acc aat gag gac gct cct acc	259	
His Asp Ala Glu Ile Thr Ala Ile Ala Thr Asn Glu Asp Ala Pro Thr		
	40 45 50	
tgg gag aac acc att gag gcc ctg gaa cgc gca ggc ctg tcc ctc aac	307	
Trp Glu Asn Thr Ile Glu Ala Leu Glu Arg Ala Gly Leu Ser Leu Asn		
	55 60 65	
cgc gtc gcc gcc gta ttc ttc aac ttg cag ggc acc gat tcc tcc cct	355	
Arg Val Ala Ala Val Phe Phe Asn Leu Gln Gly Thr Asp Ser Ser Pro		
	70 75 80 85	
gaa atg gat gaa atc gca gcc act atc gcg ccg aaa ctc tcc gcg cat	403	
Glu Met Asp Glu Ile Ala Ala Thr Ile Ala Pro Lys Leu Ser Ala His		
	90 95 100	
tcg gat gcg att ttc cac aat gct gcg ctt ttc gcg cgc att gag gcc	451	
Ser Asp Ala Ile Phe His Asn Ala Ala Leu Phe Ala Arg Ile Glu Ala		
	105 110 115	
gta gaa gca ccg gcc gac gag gaa tcg caa cgc ctg ttg tcc cac acc	499	
Val Glu Ala Pro Ala Asp Glu Glu Ser Gln Arg Leu Leu Ser His Thr		
	120 125 130	
aag cgc gct ttt cga cgt cgc ggt gca gca ctc aac gcc gac ggc aag	547	
Lys Arg Ala Phe Arg Arg Arg Gly Ala Ala Leu Asn Ala Asp Gly Lys		
	135 140 145	
gcc cga ctg agc acc atc aac cag cgc cta tcg gca ctg tcc gaa cag	595	
Ala Arg Leu Ser Thr Ile Asn Gln Arg Leu Ser Ala Leu Ser Glu Gln		
	150 155 160 165	
ttc ggc cgc aac ctg ctt cag gac acc cgc gat ctg gcg gtc aac ttt	643	
Phe Gly Arg Asn Leu Leu Gln Asp Thr Arg Asp Leu Ala Val Asn Phe		
	170 175 180	
gaa gaa tct gaa ctt gcc ggt ttt agc gaa gcc cgc ata tcc gcc gcc	691	
Glu Glu Ser Glu Leu Ala Gly Phe Ser Glu Ala Arg Ile Ser Ala Ala		
	185 190 195	
gct gac tac gca gca gca gtt ggc acc gaa ggc tac gtg gtt cca ctg	739	
Ala Asp Tyr Ala Ala Ala Val Gly Thr Glu Gly Tyr Val Val Pro Leu		
	200 205 210	
gaa ctg ccc acc gtg cag tca gag cag gca gta tta acc gaa tcc gcc	787	
Glu Leu Pro Thr Val Gln Ser Glu Gln Ala Val Leu Thr Glu Ser Ala		
	215 220 225	

tcg cgt gca aag ctt tat gaa gcc tcc cag aag cgt ggc gcc agc ctg	835
Ser Arg Ala Lys Leu Tyr Glu Ala Ser Gln Lys Arg Gly Ala Ser Leu	
230 235 240 245	
aac aag gac gtg ctg ctc gaa acc gtg cgt ctg cgt gct gaa cgc gcc	883
Asn Lys Asp Val Leu Leu Glu Thr Val Arg Leu Arg Ala Glu Arg Ala	
250 255 260	
aca ctt tta ggc tac gac acc cac gcc gat tac gtc atc gaa gaa gaa	931
Thr Leu Leu Gly Tyr Asp Thr His Ala Asp Tyr Val Ile Glu Glu Glu	
265 270 275	
acc gcc gat gac gtc gca gcc gtg cgc gcc ttg ctt tat gat ctc gcc	979
Thr Ala Asp Asp Val Ala Ala Val Arg Ala Leu Leu Tyr Asp Leu Ala	
280 285 290	
cca gcc gcc tct gcc aat gcg aaa gcc gaa tac aaa ctc tcc gca gaa	1027
Pro Ala Ala Ser Ala Asn Ala Lys Ala Glu Tyr Lys Leu Ser Ala Glu	
295 300 305	
gaa gca gaa gaa cac ggc caa aaa gtc ggc gca gct gac tgg agc ttc	1075
Glu Ala Glu Glu His Gly Gln Lys Val Gly Ala Ala Asp Trp Ser Phe	
310 315 320 325	
tgg gaa gcc aaa gtc cgc gcc cgc gac tac gcc ctg gac gaa acc gaa	1123
Trp Glu Ala Lys Val Arg Ala Arg Asp Tyr Ala Leu Asp Glu Thr Glu	
330 335 340	
ctg cgc aac tac ttc cca ttg aac caa gta ctc cgt gac ggc gtc ttc	1171
Leu Arg Asn Tyr Phe Pro Leu Asn Gln Val Leu Arg Asp Gly Val Phe	
345 350 355	
ttc gct gct aac cgc ctc tac gga atc acc gtg gaa cca cgc cct gac	1219
Phe Ala Ala Asn Arg Leu Tyr Gly Ile Thr Val Glu Pro Arg Pro Asp	
360 365 370	
ctg cgc ggt tac gcc gag ggc gtg gac gtc tgg gaa gtc ctc gat tct	1267
Leu Arg Gly Tyr Ala Glu Gly Val Asp Val Trp Glu Val Leu Asp Ser	
375 380 385	
gac ggc tcc ggc atc ggc ctg atc ctt acc gac tac tac ggc cga cca	1315
Asp Gly Ser Gly Ile Gly Leu Ile Leu Thr Asp Tyr Tyr Gly Arg Pro	
390 395 400 405	
tcc aag cgg ggc ggc gct tgg atg tcc agc ttt gtc gac caa tcc gag	1363
Ser Lys Arg Gly Gly Ala Trp Met Ser Ser Phe Val Asp Gln Ser Glu	
410 415 420	
ctg cta ggc acc aag cca gtc gtg gtc aac gtt atg ggt att acc aaa	1411
Leu Leu Gly Thr Lys Pro Val Val Val Asn Val Met Gly Ile Thr Lys	
425 430 435	
cca acc acc ggc gaa gca cta ctc agc ctc gat gaa gta acc acc atc	1459
Pro Thr Thr Gly Glu Ala Leu Leu Ser Leu Asp Glu Val Thr Thr Ile	
440 445 450	
ttc cac gaa ttc ggc cac ggc ctg cac ggc ttg ctg tcc aag gtg cgc	1507
Phe His Glu Phe Gly His Gly Leu His Gly Leu Leu Ser Lys Val Arg	
455 460 465	
tac cca agc ttc tcc gga acc tcc gtg ccc cgc gac tac gta gaa ttc	1555

Tyr Pro Ser Phe Ser Gly Thr Ser Val Pro Arg Asp Tyr Val Glu Phe
 470 475 480 485
 ccc tcc cag atc aac gaa aac tgg gca ttc gac cct gca gta gtc cgc 1603
 Pro Ser Gln Ile Asn Glu Asn Trp Ala Phe Asp Pro Ala Val Val Arg
 490 495 500
 aac tac gcc cgc cac gtg gac acc ggc gac atc att cca gac tcc ctg 1651
 Asn Tyr Ala Arg His Val Asp Thr Gly Asp Ile Ile Pro Asp Ser Leu
 505 510 515
 ctt gag gca gtg gaa gca tgt ggc att tca gac aga gtg gtg gaa cat 1699
 Leu Glu Ala Val Glu Ala Cys Gly Ile Ser Asp Arg Val Val Glu His
 520 525 530
 gtg agt act tgt ccc cat cta tta tcg acc tgc cct gtc tct ccc tgt 1747
 Val Ser Thr Cys Pro His Leu Leu Ser Thr Cys Pro Val Ser Pro Cys
 535 540 545
 cca cag cgg atg ccg cac tagtcaatga cattgaccaa tta 1788
 Pro Gln Arg Met Pro His
 550 555

<210> 186

<211> 555

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 186

Met Thr Val Glu His Leu Leu Lys Pro Ser Thr Leu Pro Tyr Gln Leu
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 Pro Asp Phe Ala Ala Ile Lys Val Ala Asp Phe Pro Pro Ala Phe Glu
 20 25 30
 Leu Ala Leu Ala Glu His Asp Ala Glu Ile Thr Ala Ile Ala Thr Asn
 35 40 45
 Glu Asp Ala Pro Thr Trp Glu Asn Thr Ile Glu Ala Leu Glu Arg Ala
 50 55 60
 Gly Leu Ser Leu Asn Arg Val Ala Ala Val Phe Phe Asn Leu Gln Gly
 65 70 75 80
 Thr Asp Ser Ser Pro Glu Met Asp Glu Ile Ala Ala Thr Ile Ala Pro
 85 90 95
 Lys Leu Ser Ala His Ser Asp Ala Ile Phe His Asn Ala Ala Leu Phe
 100 105 110
 Ala Arg Ile Glu Ala Val Glu Ala Pro Ala Asp Glu Glu Ser Gln Arg
 115 120 125
 Leu Leu Ser His Thr Lys Arg Ala Phe Arg Arg Arg Gly Ala Ala Leu
 130 135 140
 Asn Ala Asp Gly Lys Ala Arg Leu Ser Thr Ile Asn Gln Arg Leu Ser
 145 150 155 160
 Ala Leu Ser Glu Gln Phe Gly Arg Asn Leu Leu Gln Asp Thr Arg Asp

165										170					175				
Leu	Ala	Val	Asn	Phe	Glu	Glu	Ser	Glu	Leu	Ala	Gly	Phe	Ser	Glu	Ala				
			180					185					190						
Arg	Ile	Ser	Ala	Ala	Ala	Asp	Tyr	Ala	Ala	Ala	Val	Gly	Thr	Glu	Gly				
		195					200					205							
Tyr	Val	Val	Pro	Leu	Glu	Leu	Pro	Thr	Val	Gln	Ser	Glu	Gln	Ala	Val				
	210					215					220								
Leu	Thr	Glu	Ser	Ala	Ser	Arg	Ala	Lys	Leu	Tyr	Glu	Ala	Ser	Gln	Lys				
225					230					235					240				
Arg	Gly	Ala	Ser	Leu	Asn	Lys	Asp	Val	Leu	Leu	Glu	Thr	Val	Arg	Leu				
				245					250					255					
Arg	Ala	Glu	Arg	Ala	Thr	Leu	Leu	Gly	Tyr	Asp	Thr	His	Ala	Asp	Tyr				
			260					265					270						
Val	Ile	Glu	Glu	Glu	Thr	Ala	Asp	Asp	Val	Ala	Ala	Val	Arg	Ala	Leu				
		275					280					285							
Leu	Tyr	Asp	Leu	Ala	Pro	Ala	Ala	Ser	Ala	Asn	Ala	Lys	Ala	Glu	Tyr				
	290					295				300									
Lys	Leu	Ser	Ala	Glu	Glu	Ala	Glu	Glu	His	Gly	Gln	Lys	Val	Gly	Ala				
305					310					315					320				
Ala	Asp	Trp	Ser	Phe	Trp	Glu	Ala	Lys	Val	Arg	Ala	Arg	Asp	Tyr	Ala				
				325					330					335					
Leu	Asp	Glu	Thr	Glu	Leu	Arg	Asn	Tyr	Phe	Pro	Leu	Asn	Gln	Val	Leu				
			340					345					350						
Arg	Asp	Gly	Val	Phe	Phe	Ala	Ala	Asn	Arg	Leu	Tyr	Gly	Ile	Thr	Val				
		355						360				365							
Glu	Pro	Arg	Pro	Asp	Leu	Arg	Gly	Tyr	Ala	Glu	Gly	Val	Asp	Val	Trp				
	370					375					380								
Glu	Val	Leu	Asp	Ser	Asp	Gly	Ser	Gly	Ile	Gly	Leu	Ile	Leu	Thr	Asp				
385					390					395					400				
Tyr	Tyr	Gly	Arg	Pro	Ser	Lys	Arg	Gly	Gly	Ala	Trp	Met	Ser	Ser	Phe				
				405					410					415					
Val	Asp	Gln	Ser	Glu	Leu	Leu	Gly	Thr	Lys	Pro	Val	Val	Val	Asn	Val				
			420					425					430						
Met	Gly	Ile	Thr	Lys	Pro	Thr	Thr	Gly	Glu	Ala	Leu	Leu	Ser	Leu	Asp				
		435					440					445							
Glu	Val	Thr	Thr	Ile	Phe	His	Glu	Phe	Gly	His	Gly	Leu	His	Gly	Leu				
	450					455					460								
Leu	Ser	Lys	Val	Arg	Tyr	Pro	Ser	Phe	Ser	Gly	Thr	Ser	Val	Pro	Arg				
465					470					475					480				
Asp	Tyr	Val	Glu	Phe	Pro	Ser	Gln	Ile	Asn	Glu	Asn	Trp	Ala	Phe	Asp				
				485					490					495					

Pro Ala Val Val Arg Asn Tyr Ala Arg His Val Asp Thr Gly Asp Ile
 500 505 510

Ile Pro Asp Ser Leu Leu Glu Ala Val Glu Ala Cys Gly Ile Ser Asp
 515 520 525

Arg Val Val Glu His Val Ser Thr Cys Pro His Leu Leu Ser Thr Cys
 530 535 540

Pro Val Ser Pro Cys Pro Gln Arg Met Pro His
 545 550 555

<210> 187
 <211> 1088
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(1065)
 <223> FRXA00877

<400> 187
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 Ala Ala Ala Val Gly Thr Glu Gly Tyr Val Val Pro Leu Glu Leu Pro
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acc gtg cag tca gag cag gca gta tta acc gaa tcc gcc tcg cgt gca 96
 Thr Val Gln Ser Glu Gln Ala Val Leu Thr Glu Ser Ala Ser Arg Ala
 20 25 30

aag ctt tat gaa gcc tcc cag aag cgt ggc gcc agc ctg aac aag gac 144
 Lys Leu Tyr Glu Ala Ser Gln Lys Arg Gly Ala Ser Leu Asn Lys Asp
 35 40 45

gtg ctg ctc gaa acc gtg cgt ctg cgt gct gaa cgc gcc aca ctt tta 192
 Val Leu Leu Glu Thr Val Arg Leu Arg Ala Glu Arg Ala Thr Leu Leu
 50 55 60

ggc tac gac acc cac gcc gat tac gtc atc gaa gaa gaa acc gcc gat 240
 Gly Tyr Asp Thr His Ala Asp Tyr Val Ile Glu Glu Glu Thr Ala Asp
 65 70 75 80

gac gtc gca gcc gtg cgc gcc ttg ctt tat gat ctc gcc cca gcc gcc 288
 Asp Val Ala Ala Val Arg Ala Leu Leu Tyr Asp Leu Ala Pro Ala Ala
 85 90 95

tct gcc aat gcg aaa gcc gaa tac aaa ctc tcc gca gaa gaa gca gaa 336
 Ser Ala Asn Ala Lys Ala Glu Tyr Lys Leu Ser Ala Glu Glu Ala Glu
 100 105 110

gaa cac ggc caa aaa gtc ggc gca gct gac tgg agc ttc tgg gaa gcc 384
 Glu His Gly Gln Lys Val Gly Ala Ala Asp Trp Ser Phe Trp Glu Ala
 115 120 125

aaa gtc cgc gcc cgc gac tac gcc ctg gac gaa acc gaa ctg cgc aac 432
 Lys Val Arg Ala Arg Asp Tyr Ala Leu Asp Glu Thr Glu Leu Arg Asn
 130 135 140

tac ttc cca ttg aac caa gta ctc cgt gac ggc gtc ttc ttc gct gct	480
Tyr Phe Pro Leu Asn Gln Val Leu Arg Asp Gly Val Phe Phe Ala Ala	
145 150 155 160	
aac cgc ctc tac gga atc acc gtg gaa cca cgc cct gac ctg cgc ggt	528
Asn Arg Leu Tyr Gly Ile Thr Val Glu Pro Arg Pro Asp Leu Arg Gly	
165 170 175	
tac gcc gag ggc gtg gac gtc tgg gaa gtc ctc gat tct gac ggc tcc	576
Tyr Ala Glu Gly Val Asp Val Trp Glu Val Leu Asp Ser Asp Gly Ser	
180 185 190	
ggc atc ggc ctg atc ctt acc gac tac tac ggc cga cca tcc aag cgg	624
Gly Ile Gly Leu Ile Leu Thr Asp Tyr Tyr Gly Arg Pro Ser Lys Arg	
195 200 205	
ggc ggc gct tgg atg tcc agc ttt gtc gac caa tcc gag ctg cta ggc	672
Gly Gly Ala Trp Met Ser Ser Phe Val Asp Gln Ser Glu Leu Leu Gly	
210 215 220	
acc aag cca gtc gtg gtc aac gtt atg ggt att acc aaa cca acc acc	720
Thr Lys Pro Val Val Val Asn Val Met Gly Ile Thr Lys Pro Thr Thr	
225 230 235 240	
ggc gaa gca cta ctc agc ctc gat gaa gta acc acc atc ttc cac gaa	768
Gly Glu Ala Leu Leu Ser Leu Asp Glu Val Thr Thr Ile Phe His Glu	
245 250 255	
ttc ggc cac ggc ctg cac ggc ttg ctg tcc aag gtg cgc tac cca agc	816
Phe Gly His Gly Leu His Gly Leu Leu Ser Lys Val Arg Tyr Pro Ser	
260 265 270	
ttc tcc gga acc tcc gtg ccc cgc gac tac gta gaa ttc ccc tcc cag	864
Phe Ser Gly Thr Ser Val Pro Arg Asp Tyr Val Glu Phe Pro Ser Gln	
275 280 285	
atc aac gaa aac tgg gca ttc gac cct gca gta gtc cgc aac tac gcc	912
Ile Asn Glu Asn Trp Ala Phe Asp Pro Ala Val Val Arg Asn Tyr Ala	
290 295 300	
cgc cac gtg gac acc ggc gac atc att cca gac tcc ctg ctt gag gca	960
Arg His Val Asp Thr Gly Asp Ile Ile Pro Asp Ser Leu Leu Glu Ala	
305 310 315 320	
gtg gaa gca tgt ggc att tca gac aga gtg gtg gaa cat gtg agt act	1008
Val Glu Ala Cys Gly Ile Ser Asp Arg Val Val Glu His Val Ser Thr	
325 330 335	
tgt ccc cat cta tta tcg acc tgc cct gtc tct ccc tgt cca cag cgg	1056
Cys Pro His Leu Leu Ser Thr Cys Pro Val Ser Pro Cys Pro Gln Arg	
340 345 350	
atg ccg cac tagtcaatga cattgaccaa tta	1088
Met Pro His	
355	

<210> 188

<211> 355

<212> PRT

<213> Corynebacterium glutamicum

<400> 188

Ala	Ala	Ala	Val	Gly	Thr	Glu	Gly	Tyr	Val	Val	Pro	Leu	Glu	Leu	Pro	1	5	10	15
Thr	Val	Gln	Ser	Glu	Gln	Ala	Val	Leu	Thr	Glu	Ser	Ala	Ser	Arg	Ala	20	25	30	
Lys	Leu	Tyr	Glu	Ala	Ser	Gln	Lys	Arg	Gly	Ala	Ser	Leu	Asn	Lys	Asp	35	40	45	
Val	Leu	Leu	Glu	Thr	Val	Arg	Leu	Arg	Ala	Glu	Arg	Ala	Thr	Leu	Leu	50	55	60	
Gly	Tyr	Asp	Thr	His	Ala	Asp	Tyr	Val	Ile	Glu	Glu	Glu	Thr	Ala	Asp	65	70	75	80
Asp	Val	Ala	Ala	Val	Arg	Ala	Leu	Leu	Tyr	Asp	Leu	Ala	Pro	Ala	Ala	85	90	95	
Ser	Ala	Asn	Ala	Lys	Ala	Glu	Tyr	Lys	Leu	Ser	Ala	Glu	Glu	Ala	Glu	100	105	110	
Glu	His	Gly	Gln	Lys	Val	Gly	Ala	Ala	Asp	Trp	Ser	Phe	Trp	Glu	Ala	115	120	125	
Lys	Val	Arg	Ala	Arg	Asp	Tyr	Ala	Leu	Asp	Glu	Thr	Glu	Leu	Arg	Asn	130	135	140	
Tyr	Phe	Pro	Leu	Asn	Gln	Val	Leu	Arg	Asp	Gly	Val	Phe	Phe	Ala	Ala	145	150	155	160
Asn	Arg	Leu	Tyr	Gly	Ile	Thr	Val	Glu	Pro	Arg	Pro	Asp	Leu	Arg	Gly	165	170	175	
Tyr	Ala	Glu	Gly	Val	Asp	Val	Trp	Glu	Val	Leu	Asp	Ser	Asp	Gly	Ser	180	185	190	
Gly	Ile	Gly	Leu	Ile	Leu	Thr	Asp	Tyr	Tyr	Gly	Arg	Pro	Ser	Lys	Arg	195	200	205	
Gly	Gly	Ala	Trp	Met	Ser	Ser	Phe	Val	Asp	Gln	Ser	Glu	Leu	Leu	Gly	210	215	220	
Thr	Lys	Pro	Val	Val	Val	Asn	Val	Met	Gly	Ile	Thr	Lys	Pro	Thr	Thr	225	230	235	240
Gly	Glu	Ala	Leu	Leu	Ser	Leu	Asp	Glu	Val	Thr	Thr	Ile	Phe	His	Glu	245	250	255	
Phe	Gly	His	Gly	Leu	His	Gly	Leu	Leu	Ser	Lys	Val	Arg	Tyr	Pro	Ser	260	265	270	
Phe	Ser	Gly	Thr	Ser	Val	Pro	Arg	Asp	Tyr	Val	Glu	Phe	Pro	Ser	Gln	275	280	285	
Ile	Asn	Glu	Asn	Trp	Ala	Phe	Asp	Pro	Ala	Val	Val	Arg	Asn	Tyr	Ala	290	295	300	
Arg	His	Val	Asp	Thr	Gly	Asp	Ile	Ile	Pro	Asp	Ser	Leu	Leu	Glu	Ala	305	310	315	320

Val Glu Ala Cys Gly Ile Ser Asp Arg Val Val Glu His Val Ser Thr
 325 330 335

Cys Pro His Leu Leu Ser Thr Cys Pro Val Ser Pro Cys Pro Gln Arg
 340 345 350

Met Pro His
 355

<210> 189

<211> 663

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(640)

<223> RXN01226

<400> 189

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tggcgggggcc tgtttttgct tgtggtggac tcatggttgg atg ggg gat gtg aat 115
 Met Gly Asp Val Asn
 1 5

aac tct ccc ctt tta gtt gtt ggc ctg gga aat ccc ggc ccg aaa tac 163
 Asn Ser Pro Leu Leu Val Val Gly Leu Gly Asn Pro Gly Pro Lys Tyr
 10 15 20

gtt ggc acc cgc cac aat att ggc ttt gag gtt gca gaa gaa cta gtg 211
 Val Gly Thr Arg His Asn Ile Gly Phe Glu Val Ala Glu Glu Leu Val
 25 30 35

tcg cgc agc ttt gga tca ttt agt gtg cac aag cgc tcc aac acc gat 259
 Ser Arg Ser Ser Phe Gly Ser Phe Ser Val His Lys Arg Ser Asn Thr Asp
 40 45 50

atc gcg cag ctt cct ggg cta att gtg gcc aag ccg cgc agc ttt atg 307
 Ile Ala Gln Leu Pro Gly Leu Ile Val Ala Lys Pro Arg Ser Phe Met
 55 60 65

aac ctg tcg gga act ccg att cgg gcg ctg tgt gac ttc ttt aag att 355
 Asn Leu Ser Gly Thr Pro Ile Arg Ala Leu Cys Asp Phe Phe Lys Ile
 70 75 80 85

tcc cca gcc aat gtc atc gtg gtg cat gat gaa ttg gag ctt gat ttc 403
 Ser Pro Ala Asn Val Ile Val Val His Asp Glu Leu Glu Leu Asp Phe
 90 95 100

ggc tca gtg aag cta cgt cag ggt ggc ggg gat cat ggg cac aat ggt 451
 Gly Ser Val Lys Leu Arg Gln Gly Gly Gly Asp His Gly His Asn Gly
 105 110 115

ctg aaa tcc acg tcc aaa tct ttg gga act aag gac tat tgg aag ctc 499
 Leu Lys Ser Thr Ser Lys Ser Leu Gly Thr Lys Asp Tyr Trp Lys Leu
 120 125 130

agc atg ggt atc ggt agg cca ccg ggt cgg atg gat ccg gca agt ttt 547

Ser Met Gly Ile Gly Arg Pro Pro Gly Arg Met Asp Pro Ala Ser Phe
 135 140 145
 gtg ttg aag cct ttt ggc aag caa gaa ctg gcg gat att ccc atc atg 595
 Val Leu Lys Pro Phe Gly Lys Gln Glu Leu Ala Asp Ile Pro Ile Met
 150 155 160 165
 gcg gct gac gct gca gat ctc gtc gaa aag cat ttg cag cag ggc 640
 Ala Ala Asp Ala Ala Asp Leu Val Glu Lys His Leu Gln Gln Gly
 170 175 180
 tagctacttg cgccgcgcct ctt 663

<210> 190
 <211> 180
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 190
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 1 5 10 15
 Pro Gly Pro Lys Tyr Val Gly Thr Arg His Asn Ile Gly Phe Glu Val
 20 25 30
 Ala Glu Glu Leu Val Ser Arg Ser Phe Gly Ser Phe Ser Val His Lys
 35 40 45
 Arg Ser Asn Thr Asp Ile Ala Gln Leu Pro Gly Leu Ile Val Ala Lys
 50 55 60
 Pro Arg Ser Phe Met Asn Leu Ser Gly Thr Pro Ile Arg Ala Leu Cys
 65 70 75 80
 Asp Phe Phe Lys Ile Ser Pro Ala Asn Val Ile Val Val His Asp Glu
 85 90 95
 Leu Glu Leu Asp Phe Gly Ser Val Lys Leu Arg Gln Gly Gly Gly Asp
 100 105 110
 His Gly His Asn Gly Leu Lys Ser Thr Ser Lys Ser Leu Gly Thr Lys
 115 120 125
 Asp Tyr Trp Lys Leu Ser Met Gly Ile Gly Arg Pro Pro Gly Arg Met
 130 135 140
 Asp Pro Ala Ser Phe Val Leu Lys Pro Phe Gly Lys Gln Glu Leu Ala
 145 150 155 160
 Asp Ile Pro Ile Met Ala Ala Asp Ala Ala Asp Leu Val Glu Lys His
 165 170 175
 Leu Gln Gln Gly
 180

<210> 191
 <211> 784
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(784)

<223> RXN01963

<400> 191

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cagattttct ctgtgtgagc tgggggttttc tgcatttccc acttgttttt ctccaacact 60

ccacacacac accttcaaag aagaaagtgc gaaagattct atg aaa aac cgt aaa 115
                                   Met Lys Asn Arg Lys
                                   1 5

aaa atc atg tct acc ctc acc act gtc tgc gcc gta ctg ggt ata gtt 163
Lys Ile Met Ser Thr Leu Thr Thr Val Cys Ala Val Leu Gly Ile Val
                                   10 15 20

gca gct cat cca ttc cac gcc tct gct gtc atc ggc ggc tct gtc cca 211
Ala Ala His Pro Phe His Ala Ser Ala Val Ile Gly Gly Ser Val Pro
                                   25 30 35

tca act gat tcc gtt gcc aac gct gtc gca aaa atc gga cca ggc gca 259
Ser Thr Asp Ser Val Ala Asn Ala Val Ala Lys Ile Gly Pro Gly Ala
                                   40 45 50

ttg aac tgc agc ggt gtc atg atc tca cca tcg tgg gca ctc acc gca 307
Leu Asn Cys Ser Gly Val Met Ile Ser Pro Ser Trp Ala Leu Thr Ala
                                   55 60 65

cgc cac tgt gtc gat gac atc aac ata ctc ggc gac atc gac acc atc 355
Arg His Cys Val Asp Asp Ile Asn Ile Leu Gly Asp Ile Asp Thr Ile
                                   70 75 80 85

acg cct att act cca ggt att cat cgc aat gaa ggt aac tat atg ggt 403
Thr Pro Ile Thr Pro Gly Ile His Arg Asn Glu Gly Asn Tyr Met Gly
                                   90 95 100

gag gtt tac cgc gca ccg tcc ggt gat cta gcg ctc att aat atc aac 451
Glu Val Tyr Arg Ala Pro Ser Gly Asp Leu Ala Leu Ile Asn Ile Asn
                                   105 110 115

ggc gtg cac aag ggc acc att gcg cag ctc ccc aca caa gaa tat cca 499
Gly Val His Lys Gly Thr Ile Ala Gln Leu Pro Thr Gln Glu Tyr Pro
                                   120 125 130

ctg gga acc gct gca cag tca gtc ggt ttt ggt ggc ggt ggt gtc aat 547
Leu Gly Thr Ala Ala Gln Ser Val Gly Phe Gly Gly Gly Gly Val Asn
                                   135 140 145

atc cgc acc gct gaa tcg gtc aac atg att ctc acc gac ata tat agc 595
Ile Arg Thr Ala Glu Ser Val Asn Met Ile Leu Thr Asp Ile Tyr Ser
                                   150 155 160 165

gtg agg tca ggg aaa ttc cat cac ggt gtc ggt cga tca cac tat ctc 643
Val Arg Ser Gly Lys Phe His His Gly Val Gly Arg Ser His Tyr Leu
                                   170 175 180

ctc ttt gat tat gac agt gct gaa act ggt cga atc cac aaa ggt gat 691
Leu Phe Asp Tyr Asp Ser Ala Glu Thr Gly Arg Ile His Lys Gly Asp
                                   185 190 195

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tct ggc ggc ccc atc ttc att ggt gac gag gtt gtg ggc att atg tct 739
 Ser Gly Gly Pro Ile Phe Ile Gly Asp Glu Val Val Gly Ile Met Ser
 200 205 210

cac ggc aca ata aat aag aac gac ggg tct ttt gat gac gaa tcc 784
 His Gly Thr Ile Asn Lys Asn Asp Gly Ser Phe Asp Asp Glu Ser
 215 220 225

<210> 192

<211> 228

<212> PRT

<213> Corynebacterium glutamicum

<400> 192

Met Lys Asn Arg Lys Lys Ile Met Ser Thr Leu Thr Thr Val Cys Ala
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Val Leu Gly Ile Val Ala Ala His Pro Phe His Ala Ser Ala Val Ile
 20 25 30

Gly Gly Ser Val Pro Ser Thr Asp Ser Val Ala Asn Ala Val Ala Lys
 35 40 45

Ile Gly Pro Gly Ala Leu Asn Cys Ser Gly Val Met Ile Ser Pro Ser
 50 55 60

Trp Ala Leu Thr Ala Arg His Cys Val Asp Asp Ile Asn Ile Leu Gly
 65 70 75 80

Asp Ile Asp Thr Ile Thr Pro Ile Thr Pro Gly Ile His Arg Asn Glu
 85 90 95

Gly Asn Tyr Met Gly Glu Val Tyr Arg Ala Pro Ser Gly Asp Leu Ala
 100 105 110

Leu Ile Asn Ile Asn Gly Val His Lys Gly Thr Ile Ala Gln Leu Pro
 115 120 125

Thr Gln Glu Tyr Pro Leu Gly Thr Ala Ala Gln Ser Val Gly Phe Gly
 130 135 140

Gly Gly Gly Val Asn Ile Arg Thr Ala Glu Ser Val Asn Met Ile Leu
 145 150 155 160

Thr Asp Ile Tyr Ser Val Arg Ser Gly Lys Phe His His Gly Val Gly
 165 170 175

Arg Ser His Tyr Leu Leu Phe Asp Tyr Asp Ser Ala Glu Thr Gly Arg
 180 185 190

Ile His Lys Gly Asp Ser Gly Gly Pro Ile Phe Ile Gly Asp Glu Val
 195 200 205

Val Gly Ile Met Ser His Gly Thr Ile Asn Lys Asn Asp Gly Ser Phe
 210 215 220

Asp Asp Glu Ser
 225

gaa gag cgc ttt acg ttg cgc atc aag gat cta gaa act ggc gag ctg 643
Glu Glu Arg Phe Thr Leu Arg Ile Lys Asp Leu Glu Thr Gly Glu Leu
170 175 180

ctt cct gat acc ctg act ggc att ttc tac ggt gct act tgg gtg ggg 691
 Leu Pro Asp Thr Leu Thr Gly Ile Phe Tyr Gly Ala Thr Trp Val Gly
 185 190 195
 gag gag tac ctc ttt tac cag cgc gtt gat gat gcg tgg cgt cca gat 739
 Glu Glu Tyr Leu Phe Tyr Gln Arg Val Asp Asp Ala Trp Arg Pro Asp
 200 205 210
 act gtg tgg cgc cac aag gtg ggt acc ccg gtt gaa gaa gac gtg ttg 787
 Thr Val Trp Arg His Lys Val Gly Thr Pro Val Glu Glu Asp Val Leu
 215 220 225
 gtg tac cac gag cct gat gaa cgt tat tcc acc tgg gtg ggc acc act 835
 Val Tyr His Glu Pro Asp Glu Arg Tyr Ser Thr Trp Val Gly Thr Thr
 230 235 240 245
 cgt tca gaa aaa gtt cat cct ttt tgg ttg cgc ctc caa gat cac ctc 883
 Arg Ser Glu Lys Val His Pro Phe Trp Leu Arg Leu Gln Asp His Leu
 250 255 260
 tgaagtacgc gtgcttcctt tcg 906

<210> 194
 <211> 261
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 194
 Met Ser Glu Arg Leu Asn Ala Pro Gln Ala Pro Ile His Pro Ile Thr
 1 5 10 15
 Arg Thr His His Gly Ile Asp Phe Val Asp Asn Tyr Glu Trp Leu Arg
 20 25 30
 Asp Lys Glu Ser Gln Glu Thr Leu Asp Tyr Leu Glu Ala Glu Asn Ala
 35 40 45
 Phe Thr Lys Gln Glu Thr Glu Gln Leu Ala Thr Leu Arg Asp Asn Ile
 50 55 60
 Tyr Glu Glu Ile Lys Ser Arg Val Lys Glu Thr Asp Met Ser Ile Pro
 65 70 75 80
 Val Arg Ala Gly Lys His Trp Tyr Tyr Ser Arg Thr Glu Glu Gly Lys
 85 90 95
 Ser Tyr Gly Tyr Ser Cys Arg Ile Pro Val Thr Glu Gly Ser Asp Ala
 100 105 110
 Trp Thr Pro Pro Val Ile Pro Glu Gly Glu Pro Ala Gln Gly Glu Thr
 115 120 125
 Ile Ile Met Asp Ala Asn Glu Leu Ala Glu Gly His Glu Phe Phe Ser
 130 135 140

Met Gly Ala Ser Ser Val Thr Thr Ser Gly Arg Tyr Leu Ala Tyr Ser
 145 150 155 160
 Thr Asp Val Thr Gly Glu Glu Arg Phe Thr Leu Arg Ile Lys Asp Leu
 165 170 175

Glu Thr Gly Glu Leu Leu Pro Asp Thr Leu Thr Gly Ile Phe Tyr Gly
 180 185 190
 Ala Thr Trp Val Gly Glu Glu Tyr Leu Phe Tyr Gln Arg Val Asp Asp
 195 200 205
 Ala Trp Arg Pro Asp Thr Val Trp Arg His Lys Val Gly Thr Pro Val
 210 215 220
 Glu Glu Asp Val Leu Val Tyr His Glu Pro Asp Glu Arg Tyr Ser Thr
 225 230 235 240
 Trp Val Gly Thr Thr Arg Ser Glu Lys Val His Pro Phe Trp Leu Arg
 245 250 255
 Leu Gln Asp His Leu
 260

<210> 195
 <211> 906
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(883)
 <223> FRXA00621

<400> 195
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 Met Ser Glu Arg Leu
 1 5
 aac gct ccg caa gca cca atc cat ccc atc acc cga acc cac cac ggt 163
 Asn Ala Pro Gln Ala Pro Ile His Pro Ile Thr Arg Thr His His Gly
 10 15 20
 att gat ttc gta gac aac tat gaa tgg ctg agg gat aaa gaa tcc caa 211
 Ile Asp Phe Val Asp Asn Tyr Glu Trp Leu Arg Asp Lys Glu Ser Gln
 25 30 35
 gaa acc ttg gac tac ctg gag gcg gag aat gcg ttc acc aag cag gag 259
 Glu Thr Leu Asp Tyr Leu Glu Ala Glu Asn Ala Phe Thr Lys Gln Glu
 40 45 50
 act gaa cag cta gcc aca ctg cgg gac aac atc tat gaa gag att aag 307
 Thr Glu Gln Leu Ala Thr Leu Arg Asp Asn Ile Tyr Glu Glu Ile Lys
 55 60 65
 tca cgc gtt aaa gaa acc gac atg tcc atc cca gtg cgt gcc gga aag 355
 Ser Arg Val Lys Glu Thr Asp Met Ser Ile Pro Val Arg Ala Gly Lys
 70 75 80 85
 cac tgg tat tac tct cgc act gaa gaa ggc aag agc tac ggc tat tcc 403
 His Trp Tyr Tyr Ser Arg Thr Glu Glu Gly Lys Ser Tyr Gly Tyr Ser
 90 95 100

tgc cgc att cca gtg act gaa ggg tcg gat gca tgg acc cct cct gtt 451
 Cys Arg Ile Pro Val Thr Glu Gly Ser Asp Ala Trp Thr Pro Pro Val
 105 110 115

 atc cct gag ggt gag cca gcg cag ggt gaa acc atc atc atg gat gcc 499
 Ile Pro Glu Gly Glu Pro Ala Gln Gly Glu Thr Ile Ile Met Asp Ala
 120 125 130

 aac gag ttg gca gaa ggc cac gaa ttc ttc tcc atg ggt gca tca tct 547
 Asn Glu Leu Ala Glu Gly His Glu Phe Phe Ser Met Gly Ala Ser Ser
 135 140 145

 gtc acc acc tct ggc cgc tac ctt gcg tat tcc acc gat gtc acg ggc 595
 Val Thr Thr Ser Gly Arg Tyr Leu Ala Tyr Ser Thr Asp Val Thr Gly
 150 155 160 165

 gaa gag cgc ttt acg ttg cgc atc aag gat cta gaa act ggc gag ctg 643
 Glu Glu Arg Phe Thr Leu Arg Ile Lys Asp Leu Glu Thr Gly Glu Leu
 170 175 180

 ctt cct gat acc ctg act ggc att ttc tac ggt gct act tgg gtg ggg 691
 Leu Pro Asp Thr Leu Thr Gly Ile Phe Tyr Gly Ala Thr Trp Val Gly
 185 190 195

 gag gag tac ctc ttt tac cag cgc gtt gat gat gcg tgg cgt cca gat 739
 Glu Glu Tyr Leu Phe Tyr Gln Arg Val Asp Asp Ala Trp Arg Pro Asp
 200 205 210

 act gtg tgg cgc cac aag gtg ggt acc ccg gtt gaa gaa gac gtg ttg 787
 Thr Val Trp Arg His Lys Val Gly Thr Pro Val Glu Glu Asp Val Leu
 215 220 225

 gtg tac cac gag cct gat gaa cgt tat tcc acc tgg gtg ggc acc act 835
 Val Tyr His Glu Pro Asp Glu Arg Tyr Ser Thr Trp Val Gly Thr Thr
 230 235 240 245

 cgt tca gaa aaa gtt cat cct ttt tgg ttg cgc ctc caa gat cac ctc 883
 Arg Ser Glu Lys Val His Pro Phe Trp Leu Arg Leu Gln Asp His Leu
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 tgaagtacgc gtgcttcctt tcg 906

<210> 196

<211> 261

<212> PRT

<213> Corynebacterium glutamicum

<400> 196

Met Ser Glu Arg Leu Asn Ala Pro Gln Ala Pro Ile His Pro Ile Thr
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Arg Thr His His Gly Ile Asp Phe Val Asp Asn Tyr Glu Trp Leu Arg
 20 25 30

Asp Lys Glu Ser Gln Glu Thr Leu Asp Tyr Leu Glu Ala Glu Asn Ala
 35 40 45

Phe Thr Lys Gln Glu Thr Glu Gln Leu Ala Thr Leu Arg Asp Asn Ile
 50 55 60

Tyr Glu Glu Ile Lys Ser Arg Val Lys Glu Thr Asp Met Ser Ile Pro
 65 70 75 80
 Val Arg Ala Gly Lys His Trp Tyr Tyr Ser Arg Thr Glu Glu Gly Lys
 85 90 95
 Ser Tyr Gly Tyr Ser Cys Arg Ile Pro Val Thr Glu Gly Ser Asp Ala
 100 105 110
 Trp Thr Pro Pro Val Ile Pro Glu Gly Glu Pro Ala Gln Gly Glu Thr
 115 120 125
 Ile Ile Met Asp Ala Asn Glu Leu Ala Glu Gly His Glu Phe Phe Ser
 130 135 140
 Met Gly Ala Ser Ser Val Thr Thr Ser Gly Arg Tyr Leu Ala Tyr Ser
 145 150 155 160
 Thr Asp Val Thr Gly Glu Glu Arg Phe Thr Leu Arg Ile Lys Asp Leu
 165 170 175
 Glu Thr Gly Glu Leu Leu Pro Asp Thr Leu Thr Gly Ile Phe Tyr Gly
 180 185 190
 Ala Thr Trp Val Gly Glu Glu Tyr Leu Phe Tyr Gln Arg Val Asp Asp
 195 200 205
 Ala Trp Arg Pro Asp Thr Val Trp Arg His Lys Val Gly Thr Pro Val
 210 215 220
 Glu Glu Asp Val Leu Val Tyr His Glu Pro Asp Glu Arg Tyr Ser Thr
 225 230 235 240
 Trp Val Gly Thr Thr Arg Ser Glu Lys Val His Pro Phe Trp Leu Arg
 245 250 255
 Leu Gln Asp His Leu
 260

<210> 197
 <211> 1539
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1516)
 <223> RXN00622

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 Met Asn Val Ile Pro
 1 5

cct ggg tgg gca cca ctc gtt cag aaa aag ttc atc ctt ttt ggt tgc 163
 Pro Gly Trp Ala Pro Leu Val Gln Lys Lys Phe Ile Leu Phe Gly Cys
 10 15 20

gcc tcc aag atc acc tct gaa gta cgc gtg ctt cct ttc gac cag cca	211
Ala Ser Lys Ile Thr Ser Glu Val Arg Val Leu Pro Phe Asp Gln Pro	
25 30 35	
gag ggc acc cct gag gtg ctg att ccg cgc gcg gag ggt gtg gaa tac	259
Glu Gly Thr Pro Glu Val Leu Ile Pro Arg Ala Glu Gly Val Glu Tyr	
40 45 50	
gac gtc gat cat gca gtc gta gac ggc tcc gat att tgg ttg gtc aca	307
Asp Val Asp His Ala Val Val Asp Gly Ser Asp Ile Trp Leu Val Thr	
55 60 65	
cac aac gcc gag ggc ccg aac ttt tcg gtg ggg tgg gct ggc gtc gac	355
His Asn Ala Glu Gly Pro Asn Phe Ser Val Gly Trp Ala Gly Val Asp	
70 75 80 85	
aag ctc aat tct ttg gac gcg ctg gcg cca ctc gtc gcg cac aag gat	403
Lys Leu Asn Ser Leu Asp Ala Leu Ala Pro Leu Val Ala His Lys Asp	
90 95 100	
gac gtg cgc att gag ggt gtc gat acc tac cgc gat ttc atc atc ctg	451
Asp Val Arg Ile Glu Gly Val Asp Thr Tyr Arg Asp Phe Ile Ile Leu	
105 110 115	
ggc tac agg tcc ggc gcg atc ggc cag gtc gcg atc atg aag ctt atc	499
Gly Tyr Arg Ser Gly Ala Ile Gly Gln Val Ala Ile Met Lys Leu Ile	
120 125 130	
gac gga acc ttc ggc gat ttc caa cag ctg gaa ttt gac gag gaa atc	547
Asp Gly Thr Phe Gly Asp Phe Gln Gln Leu Glu Phe Asp Glu Glu Ile	
135 140 145	
tac acc gtc gca tcg ggc gga aac cca gaa tgg gac gcc ccc gtc att	595
Tyr Thr Val Ala Ser Gly Gly Asn Pro Glu Trp Asp Ala Pro Val Ile	
150 155 160 165	
cgc ctt tct tac gga tca ttc acc acc ccg gcg cag ctg ttt aac tac	643
Arg Leu Ser Tyr Gly Ser Phe Thr Thr Pro Ala Gln Leu Phe Asn Tyr	
170 175 180	
tgg att gaa tcc ggc gaa cgc acg ctg ctg aag cag cag gaa gtg ctc	691
Trp Ile Glu Ser Gly Glu Arg Thr Leu Leu Lys Gln Gln Glu Val Leu	
185 190 195	
ggc gga tac aag ccg tca gac tat gtg gcc tcc cga ttg tgg gtc act	739
Gly Gly Tyr Lys Pro Ser Asp Tyr Val Ala Ser Arg Leu Trp Val Thr	
200 205 210	
gcg aaa gat ggc gcg cag att cca gtg tcc ttg gtg cac cgc acc gac	787
Ala Lys Asp Gly Ala Gln Ile Pro Val Ser Leu Val His Arg Thr Asp	
215 220 225	
ctg gat gta tcc aag ccc aac ccc acg ttg ctc tac ggc tat ggt tcc	835
Leu Asp Val Ser Lys Pro Asn Pro Thr Leu Leu Tyr Gly Tyr Gly Ser	
230 235 240 245	
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Tyr Glu Ser Ser Ile Asp Pro Gly Phe Ser Ile Ala Arg Leu Ser Leu	
250 255 260	
atg gat cgt ggc atg att ttt gcg att gcc cac gtt cgt ggc ggt ggc	931

Met	Asp	Arg	Gly	Met	Ile	Phe	Ala	Ile	Ala	His	Val	Arg	Gly	Gly	Gly		
			265					270					275				
979																	
gaa	atg	ggt	cgt	ggc	tgg	tac	gac	aac	ggc	aaa	acc	acc	acg	aag	aaa		
Glu	Met	Gly	Arg	Gly	Trp	Tyr	Asp	Asn	Gly	Lys	Thr	Thr	Thr	Lys	Lys		
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aac	acc	ttc	acc	gac	ttc	att	gat	gtt	gcc	gac	gcc	ctc	atc	gag	cag		
Asn	Thr	Phe	Thr	Asp	Phe	Ile	Asp	Val	Ala	Asp	Ala	Leu	Ile	Glu	Gln		
	295					300				305							
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Lys	Ile	Ser	Ala	Pro	Glu	Met	Leu	Val	Ala	Glu	Gly	Gly	Ser	Ala	Gly		
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1123																	
ggc	atg	ctc	atg	ggc	gcc	att	gcc	aac	atg	gcc	ggc	gac	cgc	ttc	aag		
Gly	Met	Leu	Met	Gly	Ala	Ile	Ala	Asn	Met	Ala	Gly	Asp	Arg	Phe	Lys		
			330					335						340			
1171																	
gcg	atc	gaa	gcc	aac	gtg	cca	ttc	gtc	gat	ccg	ctg	acc	tct	atg	ctc		
Ala	Ile	Glu	Ala	Asn	Val	Pro	Phe	Val	Asp	Pro	Leu	Thr	Ser	Met	Leu		
			345					350					355				
1219																	
atg	ccg	gaa	ctg	cca	ctg	acg	gtt	atc	gaa	tgg	gat	gag	tgg	ggc	gat		
Met	Pro	Glu	Leu	Pro	Leu	Thr	Val	Ile	Glu	Trp	Asp	Glu	Trp	Gly	Asp		
		360				365					370						
1267																	
cca	ctc	cac	gat	aag	gac	gtc	tat	gaa	tac	atg	gcg	tcg	tat	gcc	cca		
Pro	Leu	His	Asp	Lys	Asp	Val	Tyr	Glu	Tyr	Met	Ala	Ser	Tyr	Ala	Pro		
	375					380				385							
1315																	
tat	gaa	aac	atc	gag	gca	aag	aac	tac	ccc	aat	atc	ttg	gcc	gta	aca		
Tyr	Glu	Asn	Ile	Glu	Ala	Lys	Asn	Tyr	Pro	Asn	Ile	Leu	Ala	Val	Thr		
390					395				400					405			
1363																	
tcg	ctc	aac	gac	acc	cga	gtg	ttg	tac	gtc	gaa	cca	gcc	aaa	tgg	gta		
Ser	Leu	Asn	Asp	Thr	Arg	Val	Leu	Tyr	Val	Glu	Pro	Ala	Lys	Trp	Val		
			410					415						420			
1411																	
gcg	cag	ctt	cgg	gcg	act	gca	acc	ggc	gga	gaa	ttc	ctt	ctg	aaa	act		
Ala	Gln	Leu	Arg	Ala	Thr	Ala	Thr	Gly	Gly	Glu	Phe	Leu	Leu	Lys	Thr		
			425					430					435				
1459																	
gaa	atg	gtt	gcc	gga	cac	ggc	ggc	gtg	tca	gga	cgc	tac	gaa	aag	tgg		
Glu	Met	Val	Ala	Gly	His	Gly	Gly	Val	Ser	Gly	Arg	Tyr	Glu	Lys	Trp		
		440				445						450					
1507																	
cgt	gag	act	gca	ttt	gag	tac	ggc	tgg	ttg	atc	aac	caa	gca	acc	ggc		
Arg	Glu	Thr	Ala	Phe	Glu	Tyr	Gly	Trp	Leu	Ile	Asn	Gln	Ala	Thr	Gly		
	455				460					465							
1539																	
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Val	Thr	Glu															
470																	

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<212> PRT

<213> Corynebacterium glutamicum

<400> 198

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Pro Phe Asp Gln Pro Glu Gly Thr Pro Glu Val Leu Ile Pro Arg Ala
 35 40 45

Glu Gly Val Glu Tyr Asp Val Asp His Ala Val Val Asp Gly Ser Asp
 50 55 60

Ile Trp Leu Val Thr His Asn Ala Glu Gly Pro Asn Phe Ser Val Gly
 65 70 75 80

Trp Ala Gly Val Asp Lys Leu Asn Ser Leu Asp Ala Leu Ala Pro Leu
 85 90 95

Val Ala His Lys Asp Asp Val Arg Ile Glu Gly Val Asp Thr Tyr Arg
 100 105 110

Asp Phe Ile Ile Leu Gly Tyr Arg Ser Gly Ala Ile Gly Gln Val Ala
 115 120 125

Ile Met Lys Leu Ile Asp Gly Thr Phe Gly Asp Phe Gln Gln Leu Glu
 130 135 140

Phe Asp Glu Glu Ile Tyr Thr Val Ala Ser Gly Gly Asn Pro Glu Trp
 145 150 155 160

Asp Ala Pro Val Ile Arg Leu Ser Tyr Gly Ser Phe Thr Thr Pro Ala
 165 170 175

Gln Leu Phe Asn Tyr Trp Ile Glu Ser Gly Glu Arg Thr Leu Leu Lys
 180 185 190

Gln Gln Glu Val Leu Gly Gly Tyr Lys Pro Ser Asp Tyr Val Ala Ser
 195 200 205

Arg Leu Trp Val Thr Ala Lys Asp Gly Ala Gln Ile Pro Val Ser Leu
 210 215 220

Val His Arg Thr Asp Leu Asp Val Ser Lys Pro Asn Pro Thr Leu Leu
 225 230 235 240

Tyr Gly Tyr Gly Ser Tyr Glu Ser Ser Ile Asp Pro Gly Phe Ser Ile
 245 250 255

Ala Arg Leu Ser Leu Met Asp Arg Gly Met Ile Phe Ala Ile Ala His
 260 265 270

Val Arg Gly Gly Gly Glu Met Gly Arg Gly Trp Tyr Asp Asn Gly Lys
 275 280 285

Thr Thr Thr Lys Lys Asn Thr Phe Thr Asp Phe Ile Asp Val Ala Asp
 290 295 300

Ala Leu Ile Glu Gln Lys Ile Ser Ala Pro Glu Met Leu Val Ala Glu
 305 310 315 320

Gly Gly Ser Ala Gly Gly Met Leu Met Gly Ala Ile Ala Asn Met Ala
 325 330 335
 Gly Asp Arg Phe Lys Ala Ile Glu Ala Asn Val Pro Phe Val Asp Pro
 340 345 350
 Leu Thr Ser Met Leu Met Pro Glu Leu Pro Leu Thr Val Ile Glu Trp
 355 360 365
 Asp Glu Trp Gly Asp Pro Leu His Asp Lys Asp Val Tyr Glu Tyr Met
 370 375 380
 Ala Ser Tyr Ala Pro Tyr Glu Asn Ile Glu Ala Lys Asn Tyr Pro Asn
 385 390 395 400
 Ile Leu Ala Val Thr Ser Leu Asn Asp Thr Arg Val Leu Tyr Val Glu
 405 410 415
 Pro Ala Lys Trp Val Ala Gln Leu Arg Ala Thr Ala Thr Gly Gly Glu
 420 425 430
 Phe Leu Leu Lys Thr Glu Met Val Ala Gly His Gly Gly Val Ser Gly
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 Arg Tyr Glu Lys Trp Arg Glu Thr Ala Phe Glu Tyr Gly Trp Leu Ile
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 <222> (101)..(1516)
 <223> FRXA00622

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 Met Asn Val Ile Pro
 1 5
 cct ggg tgg gca cca ctc gtt cag aaa aag ttc atc ctt ttt ggt tgc 163
 Pro Gly Trp Ala Pro Leu Val Gln Lys Lys Phe Ile Leu Phe Gly Cys
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 Ala Ser Lys Ile Thr Ser Glu Val Arg Val Leu Pro Phe Asp Gln Pro
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 gag ggc acc cct gag gtg ctg att ccg cgc gcg gag ggt gtg gaa tac 259
 Glu Gly Thr Pro Glu Val Leu Ile Pro Arg Ala Glu Gly Val Glu Tyr
 40 45 50
 gac gtc gat cat gca gtc gta gac ggc tcc gat att tgg ttg gtc aca 307

Asp	Val	Asp	His	Ala	Val	Val	Asp	Gly	Ser	Asp	Ile	Trp	Leu	Val	Thr		
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His	Asn	Ala	Glu	Gly	Pro	Asn	Phe	Ser	Val	Gly	Trp	Ala	Gly	Val	Asp	85	
70					75					80							
aag	ctc	aat	tct	ttg	gac	gcg	ctg	gcg	cca	ctc	gtc	gcg	cac	aag	gat	403	
Lys	Leu	Asn	Ser	Leu	Asp	Ala	Leu	Ala	Pro	Leu	Val	Ala	His	Lys	Asp	100	
				90					95								
gac	gtg	cg	att	gag	gg	gtc	gat	acc	tac	cg	gat	ttc	atc	atc	ctg	451	
Asp	Val	Arg	Ile	Glu	Gly	Val	Asp	Thr	Tyr	Arg	Asp	Phe	Ile	Ile	Leu		
			105					110					115				
ggc	tac	agg	tcc	ggc	g	atc	ggc	cag	gtc	g	atc	atg	aag	ctt	atc	499	
Gly	Tyr	Arg	Ser	Gly	Ala	Ile	Gly	Gln	Val	Ala	Ile	Met	Lys	Leu	Ile		
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Asp	Gly	Thr	Phe	Gly	Asp	Phe	Gln	Gln	Leu	Glu	Phe	Asp	Glu	Glu	Ile		
	135					140					145						
tac	acc	gtc	gca	tcg	ggc	gga	aac	cca	gaa	tgg	gac	gcc	ccc	gtc	att	595	
Tyr	Thr	Val	Ala	Ser	Gly	Gly	Asn	Pro	Glu	Trp	Asp	Ala	Pro	Val	Ile		
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cg	ctt	tct	tac	gga	tca	ttc	acc	acc	ccg	g	cag	ctg	ttt	aac	tac	643	
Arg	Leu	Ser	Tyr	Gly	Ser	Phe	Thr	Thr	Pro	Ala	Gln	Leu	Phe	Asn	Tyr		
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tgg	att	gaa	tcc	ggc	gaa	cg	acg	ctg	ctg	aag	cag	cag	gaa	gtg	ctc	691	
Trp	Ile	Glu	Ser	Gly	Glu	Arg	Thr	Leu	Leu	Lys	Gln	Gln	Glu	Val	Leu		
			185					190					195				
ggc	gga	tac	aag	ccg	tca	gac	tat	gtg	gcc	tcc	cga	ttg	tgg	gtc	act	739	
Gly	Gly	Tyr	Lys	Pro	Ser	Asp	Tyr	Val	Ala	Ser	Arg	Leu	Trp	Val	Thr		
		200					205					210					
gcg	aaa	gat	ggc	g	cag	att	cca	gtg	tcc	ttg	gtg	cac	cg	acc	gac	787	
Ala	Lys	Asp	Gly	Ala	Gln	Ile	Pro	Val	Ser	Leu	Val	His	Arg	Thr	Asp		
	215					220					225						
ctg	gat	gta	tcc	aag	ccc	aac	ccc	acg	ttg	ctc	tac	ggc	tat	gg	tcc	835	
Leu	Asp	Val	Ser	Lys	Pro	Asn	Pro	Thr	Leu	Leu	Tyr	Gly	Tyr	Gly	Ser		
230					235				240						245		
tac	gaa	tca	tcc	att	gat	cca	ggc	ttc	tct	atc	gcg	cgt	ttg	tca	ctg	883	
Tyr	Glu	Ser	Ser	Ile	Asp	Pro	Gly	Phe	Ser	Ile	Ala	Arg	Leu	Ser	Leu		
				250					255					260			
atg	gat	cgt	ggc	atg	att	ttt	gcg	att	gcc	cac	gtt	cgt	ggc	gg	ggc	931	
Met	Asp	Arg	Gly	Met	Ile	Phe	Ala	Ile	Ala	His	Val	Arg	Gly	Gly	Gly		
			265				270						275				
gaa	atg	ggt	cgt	ggc	tgg	tac	gac	aac	ggc	aaa	acc	acc	acg	aag	aaa	979	
Glu	Met	Gly	Arg	Gly	Trp	Tyr	Asp	Asn	Gly	Lys	Thr	Thr	Thr	Lys	Lys		
		280					285					290					
aac	acc	ttc	acc	gac	ttc	att	gat	g	gcc	gac	gcc	ctc	atc	gag	cag	1027	
Asn	Thr	Phe	Thr	Asp	Phe	Ile	Asp	Val	Ala	Asp	Ala	Leu	Ile	Glu	Gln		

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aag att tct gcc cct gaa atg ctg gtt gca gaa ggc ggc tca gct ggt 1075
Lys Ile Ser Ala Pro Glu Met Leu Val Ala Glu Gly Gly Ser Ala Gly
310              315              320              325

ggc atg ctc atg ggc gcc att gcc aac atg gcc ggt gac cgc ttc aag 1123
Gly Met Leu Met Gly Ala Ile Ala Asn Met Ala Gly Asp Arg Phe Lys
              330              335              340

gcg atc gaa gcc aac gtg cca ttc gtc gat ccg ctg acc tct atg ctc 1171
Ala Ile Glu Ala Asn Val Pro Phe Val Asp Pro Leu Thr Ser Met Leu
              345              350              355

atg ccg gaa ctg cca ctg acg gtt atc gaa tgg gat gag tgg ggc gat 1219
Met Pro Glu Leu Pro Leu Thr Val Ile Glu Trp Asp Glu Trp Gly Asp
              360              365              370

cca ctc cac gat aag gac gtc tat gaa tac atg gcg tcg tat gcc cca 1267
Pro Leu His Asp Lys Asp Val Tyr Glu Tyr Met Ala Ser Tyr Ala Pro
              375              380              385

tat gaa aac atc gag gca aag aac tac ccc aat atc ttg gcc gta aca 1315
Tyr Glu Asn Ile Glu Ala Lys Asn Tyr Pro Asn Ile Leu Ala Val Thr
390              395              400              405

tcg ctc aac gac acc cga gtg ttg tac gtc gaa cca gcc aaa tgg gta 1363
Ser Leu Asn Asp Thr Arg Val Leu Tyr Val Glu Pro Ala Lys Trp Val
              410              415              420

gcg cag ctt cgg gcg act gca acc ggt gga gaa ttc ctt ctg aaa act 1411
Ala Gln Leu Arg Ala Thr Ala Thr Gly Gly Glu Phe Leu Leu Lys Thr
              425              430              435

gaa atg gtt gcc gga cac ggc ggt gtg tca gga cgc tac gaa aag tgg 1459
Glu Met Val Ala Gly His Gly Gly Val Ser Gly Arg Tyr Glu Lys Trp
              440              445              450

cgt gag act gca ttt gag tac ggc tgg ttg atc aac caa gca acc ggt 1507
Arg Glu Thr Ala Phe Glu Tyr Gly Trp Leu Ile Asn Gln Ala Thr Gly
              455              460              465

gtg acc gaa taaaacttgt tcgactagcg aac 1539
Val Thr Glu
470

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<210> 200

<211> 472

<212> PRT

<213> Corynebacterium glutamicum

<400> 200

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Met Asn Val Ile Pro Pro Gly Trp Ala Pro Leu Val Gln Lys Lys Phe
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Ile Leu Phe Gly Cys Ala Ser Lys Ile Thr Ser Glu Val Arg Val Leu
      20              25              30

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Pro Phe Asp Gln Pro Glu Gly Thr Pro Glu Val Leu Ile Pro Arg Ala
      35              40              45

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Glu Gly Val Glu Tyr Asp Val Asp His Ala Val Val Asp Gly Ser Asp
 50 55 60
 Ile Trp Leu Val Thr His Asn Ala Glu Gly Pro Asn Phe Ser Val Gly
 65 70 75 80
 Trp Ala Gly Val Asp Lys Leu Asn Ser Leu Asp Ala Leu Ala Pro Leu
 85 90 95
 Val Ala His Lys Asp Asp Val Arg Ile Glu Gly Val Asp Thr Tyr Arg
 100 105 110
 Asp Phe Ile Ile Leu Gly Tyr Arg Ser Gly Ala Ile Gly Gln Val Ala
 115 120 125
 Ile Met Lys Leu Ile Asp Gly Thr Phe Gly Asp Phe Gln Gln Leu Glu
 130 135 140
 Phe Asp Glu Glu Ile Tyr Thr Val Ala Ser Gly Gly Asn Pro Glu Trp
 145 150 155 160
 Asp Ala Pro Val Ile Arg Leu Ser Tyr Gly Ser Phe Thr Thr Pro Ala
 165 170 175
 Gln Leu Phe Asn Tyr Trp Ile Glu Ser Gly Glu Arg Thr Leu Leu Lys
 180 185 190
 Gln Gln Glu Val Leu Gly Gly Tyr Lys Pro Ser Asp Tyr Val Ala Ser
 195 200 205
 Arg Leu Trp Val Thr Ala Lys Asp Gly Ala Gln Ile Pro Val Ser Leu
 210 215 220
 Val His Arg Thr Asp Leu Asp Val Ser Lys Pro Asn Pro Thr Leu Leu
 225 230 235 240
 Tyr Gly Tyr Gly Ser Tyr Glu Ser Ser Ile Asp Pro Gly Phe Ser Ile
 245 250 255
 Ala Arg Leu Ser Leu Met Asp Arg Gly Met Ile Phe Ala Ile Ala His
 260 265 270
 Val Arg Gly Gly Gly Glu Met Gly Arg Gly Trp Tyr Asp Asn Gly Lys
 275 280 285
 Thr Thr Thr Lys Lys Asn Thr Phe Thr Asp Phe Ile Asp Val Ala Asp
 290 295 300
 Ala Leu Ile Glu Gln Lys Ile Ser Ala Pro Glu Met Leu Val Ala Glu
 305 310 315 320
 Gly Gly Ser Ala Gly Gly Met Leu Met Gly Ala Ile Ala Asn Met Ala
 325 330 335
~~Gly Asp Arg Phe Lys Ala Ile Glu Ala Asn Val Pro Phe Val Asp Pro~~
~~340 345 350~~
 Leu Thr Ser Met Leu Met Pro Glu Leu Pro Leu Thr Val Ile Glu Trp
 355 360 365

Asp Glu Trp Gly Asp Pro Leu His Asp Lys Asp Val Tyr Glu Tyr Met
 370 375 380
 Ala Ser Tyr Ala Pro Tyr Glu Asn Ile Glu Ala Lys Asn Tyr Pro Asn
 385 390 395 400
 Ile Leu Ala Val Thr Ser Leu Asn Asp Thr Arg Val Leu Tyr Val Glu
 405 410 415
 Pro Ala Lys Trp Val Ala Gln Leu Arg Ala Thr Ala Thr Gly Gly Glu
 420 425 430
 Phe Leu Leu Lys Thr Glu Met Val Ala Gly His Gly Gly Val Ser Gly
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 Arg Tyr Glu Lys Trp Arg Glu Thr Ala Phe Glu Tyr Gly Trp Leu Ile
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 Asn Gln Ala Thr Gly Val Thr Glu
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 <223> RXN02146

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 Val Gly Lys His Arg
 1 5
 cgc aac aat tca aac gca act cgc aag gct gta gca gca tct gca gtt 163
 Arg Asn Asn Ser Asn Ala Thr Arg Lys Ala Val Ala Ala Ser Ala Val
 10 15 20
 gcg ctt gga gca acc gca gct atc gcc tcc cca gca cag gca gct gag 211
 Ala Leu Gly Ala Thr Ala Ala Ile Ala Ser Pro Ala Gln Ala Ala Glu
 25 30 35
 gtt gtt gtt cct ggc acc gga atc agc gtt gac atc gct ggc atc gag 259
 Val Val Val Pro Gly Thr Gly Ile Ser Val Asp Ile Ala Gly Ile Glu
 40 45 50
 acc act cca ggt ctt aac aac gtt cca gga atc gat cag tgg atc cct 307
 Thr Thr Pro Gly Leu Asn Asn Val Pro Gly Ile Asp Gln Trp Ile Pro
 55 60 65
 tcc ctt agc agc cag gca gct cct act gct tac gca gcc gtc att gat 355
 Ser Leu Ser Ser Gln Ala Ala Pro Thr Ala Tyr Ala Ala Val Ile Asp
 70 75 80 85
 gca cct gca gca cag gct gca cct gca gca agc acc ggt cag gca atc 403
 Ala Pro Ala Ala Gln Ala Ala Pro Ala Ala Ser Thr Gly Gln Ala Ile

	90	95	100	
gtt gat gca gcg cgc acc aag att ggt tcc cca tac ggt tgg ggt gct				451
Val Asp Ala Ala Arg Thr Lys Ile Gly Ser Pro Tyr Gly Trp Gly Ala				
	105	110	115	
acc ggt cct aac gct ttc gac tgc tcc ggc ctt acc tca tgg gca tac				499
Thr Gly Pro Asn Ala Phe Asp Cys Ser Gly Leu Thr Ser Trp Ala Tyr				
	120	125	130	
agc cag gtt ggc aag tcc atc cca cgt acc tcc cag gct cag gct gca				547
Ser Gln Val Gly Lys Ser Ile Pro Arg Thr Ser Gln Ala Gln Ala Ala				
	135	140	145	
cag ggc acc cct gtt gct tac tct gac ctt cag gct ggc gac atc gtt				595
Gln Gly Thr Pro Val Ala Tyr Ser Asp Leu Gln Ala Gly Asp Ile Val				
	150	155	160	165
gcg ttc tac tcc ggc gct acc cac gtt ggt atc tac tcc ggc cac ggc				643
Ala Phe Tyr Ser Gly Ala Thr His Val Gly Ile Tyr Ser Gly His Gly				
	170	175	180	
acc gtt atc cac gca ctg aac agc agc acc cct ctg tct gag cac tcc				691
Thr Val Ile His Ala Leu Asn Ser Ser Thr Pro Leu Ser Glu His Ser				
	185	190	195	
ttg gat tac atg cca ttc cac tct gca gtt cgt ttc taatctgcat				737
Leu Asp Tyr Met Pro Phe His Ser Ala Val Arg Phe				
	200	205		

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<211> 209

<212> PRT

<213> Corynebacterium glutamicum

<400> 202

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Ala Gln Ala Ala Glu Val Val Val Pro Gly Thr Gly Ile Ser Val Asp				
35	40	45		

Ile Ala Gly Ile Glu Thr Thr Pro Gly Leu Asn Asn Val Pro Gly Ile				
50	55	60		

Asp Gln Trp Ile Pro Ser Leu Ser Ser Gln Ala Ala Pro Thr Ala Tyr				
65	70	75	80	

Ala Ala Val Ile Asp Ala Pro Ala Ala Gln Ala Ala Pro Ala Ala Ser				
85	90	95		

Thr Gly Gln Ala Ile Val Asp Ala Ala Arg Thr Lys Ile Gly Ser Pro				
100	105	110		

Tyr Gly Trp Gly Ala Thr Gly Pro Asn Ala Phe Asp Cys Ser Gly Leu

115	120	125
Thr Ser Trp Ala Tyr Ser Gln Val Gly Lys Ser Ile Pro Arg Thr Ser		
130	135	140
Gln Ala Gln Ala Ala Gln Gly Thr Pro Val Ala Tyr Ser Asp Leu Gln		
145	150	155
Ala Gly Asp Ile Val Ala Phe Tyr Ser Gly Ala Thr His Val Gly Ile		
	165	170
		175
Tyr Ser Gly His Gly Thr Val Ile His Ala Leu Asn Ser Ser Thr Pro		
	180	185
		190
Leu Ser Glu His Ser Leu Asp Tyr Met Pro Phe His Ser Ala Val Arg		
	195	200
		205

Phe

<210> 203
 <211> 807
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(784)
 <223> RXN03133

<400> 203
 ggcgtcaagc acgcactcca ccacatcgat cttcgccccg ccctcgaatg ggacatcatg 60

ggattttcccg aatccccga cacgctgccc attttgc tca gtg acc tgc gcg acc 115
 Val Thr Cys Ala Thr
 1 5

ccc ctt acg cca cca ctg ctg tgc cac ctc aat cca cgc cac gct ccg 163
 Pro Leu Thr Pro Pro Leu Leu Cys His Leu Asn Pro Arg His Ala Pro
 10 15 20

ctc acc gat cca cac att gac gct tcc agg cgc cac cgc ggt ccc ttc 211
 Leu Thr Asp Pro His Ile Asp Ala Ser Arg Arg His Arg Gly Pro Phe
 25 30 35

cac gcc act ccc agc tac gca ggc ttt cac ccc tca ttt acc gac gac 259
 His Ala Thr Pro Ser Tyr Ala Gly Phe His Pro Ser Phe Thr Asp Asp
 40 45 50

acc gcc cgc atg ctg ggc aac cta gcc aaa att ggc gcg gtt gcc acc 307
 Thr Ala Arg Met Leu Gly Asn Leu Ala Lys Ile Gly Ala Val Ala Thr
 55 60 65

tgg gaa aag acg ctt gtc gac gcc gca agc tgg gcc gaa ctc ccc cac 355
 Trp Glu Lys Thr Leu Val Asp Ala Ala Ser Trp Ala Glu Leu Pro His
 70 75 80 85

cca cca gtc atc gtc ggg gat acc ccg ccc tcg act gtc acg ccg gac 403
 Pro Pro Val Ile Val Gly Asp Thr Pro Pro Ser Thr Val Thr Pro Asp
 90 95 100

aac gcc tgg tac cag ttt cgc gtc ggc aag cat ctt ggt cgc gat gcg 451
 Asn Ala Trp Tyr Gln Phe Arg Val Gly Lys His Leu Gly Arg Asp Ala
 105 110 115
 ttc gcg gaa atc gtc atg tgc ctt ggc cac gtg ttt tgc cat cat gtc 499
 Phe Ala Glu Ile Val Met Cys Leu Gly His Val Phe Cys His His Val
 120 125 130
 ccc cag gta tgg tcg aca acc tgc gca tct cag gac gct gat tcc acc 547
 Pro Gln Val Trp Ser Thr Thr Cys Ala Ser Gln Asp Ala Asp Ser Thr
 135 140 145
 acg atg ctc att gaa gcc gag acc gcg ggg gca ttg gcc atc gct cgc 595
 Thr Met Leu Ile Glu Ala Glu Thr Ala Gly Ala Leu Ala Ile Ala Arg
 150 155 160 165
 gtc ggc ggc ccg acc cgt cga ggt ggt tcc ttc ttc ggc gat gcc ctt 643
 Val Gly Gly Pro Thr Arg Arg Gly Gly Ser Phe Phe Gly Asp Ala Leu
 170 175 180
 ctc aaa gag ggg acg cca ctt cct gct ggt ttc cga cta gat gtt gtt 691
 Leu Lys Glu Gly Thr Pro Leu Pro Ala Gly Phe Arg Leu Asp Val Val
 185 190 195
 cta cac gcc gcc tca gaa att gag gat ctg ctg cgc ggt gac acc aca 739
 Leu His Ala Ala Ser Glu Ile Glu Asp Leu Leu Arg Gly Asp Thr Thr
 200 205 210
 gcc gtt gtc agc ggc gct tgg tct gtg gag gat cgc cga ggt tac 784
 Ala Val Val Ser Gly Ala Trp Ser Val Glu Asp Arg Arg Gly Tyr
 215 220 225
 taacaaatag gcccaacaaa gag 807

<210> 204
 <211> 228
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 204
 Val Thr Cys Ala Thr Pro Leu Thr Pro Pro Leu Leu Cys His Leu Asn
 1 5 10 15
 Pro Arg His Ala Pro Leu Thr Asp Pro His Ile Asp Ala Ser Arg Arg
 20 25 30
 His Arg Gly Pro Phe His Ala Thr Pro Ser Tyr Ala Gly Phe His Pro
 35 40 45
 Ser Phe Thr Asp Asp Thr Ala Arg Met Leu Gly Asn Leu Ala Lys Ile
 50 55 60
 Gly Ala Val Ala Thr Trp Glu Lys Thr Leu Val Asp Ala Ala Ser Trp
 65 70 75 80

Ala Glu Leu Pro His Pro Pro Val Ile Val Gly Asp Thr Pro Pro Ser
 85 90 95
 Thr Val Thr Pro Asp Asn Ala Trp Tyr Gln Phe Arg Val Gly Lys His

100	105	110
Leu Gly Arg Asp Ala Phe Ala Glu Ile Val Met Cys Leu Gly His Val 115 120 125		
Phe Cys His His Val Pro Gln Val Trp Ser Thr Thr Cys Ala Ser Gln 130 135 140		
Asp Ala Asp Ser Thr Thr Met Leu Ile Glu Ala Glu Thr Ala Gly Ala 145 150 155 160		
Leu Ala Ile Ala Arg Val Gly Gly Pro Thr Arg Arg Gly Gly Ser Phe 165 170 175		
Phe Gly Asp Ala Leu Leu Lys Glu Gly Thr Pro Leu Pro Ala Gly Phe 180 185 190		
Arg Leu Asp Val Val Leu His Ala Ala Ser Glu Ile Glu Asp Leu Leu 195 200 205		
Arg Gly Asp Thr Thr Ala Val Val Ser Gly Ala Trp Ser Val Glu Asp 210 215 220		
Arg Arg Gly Tyr 225		

<210> 205
 <211> 1411
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1411)
 <223> RXN02820

<400> 205
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 aatatctccc cacataaaag ttccttgata ggctcgagag atg aaa gtg acc caa 115
 Met Lys Val Thr Gln
 1 5
 agc aca ttc ctt aaa tcg gta gct gcg ttc act gtc gca gcc tta acc 163
 Ser Thr Phe Leu Lys Ser Val Ala Ala Phe Thr Val Ala Ala Leu Thr
 10 15 20
 ctg acc atc tct tcg tgt tcc agc ggt gaa gac acc tcc gca agc tcc 211
 Leu Thr Ile Ser Ser Cys Ser Ser Gly Glu Asp Thr Ser Ala Ser Ser
 25 30 35
 acg gat act gaa aac tcc tca acc caa gca gca gcg tct ccc cca ctt 259
 Thr Asp Thr Glu Asn Ser Ser Thr Gln Ala Ala Ala Ser Pro Pro Leu
 40 45 50

gcg cct tgt gaa ctt ccc gcc gac gct tct gct gaa gag gaa gta gaa 307
 Ala Pro Cys Glu Leu Pro Ala Asp Ala Ser Ala Glu Glu Glu Val Glu
 55 60 65
 ggc act cac aca ggt gaa gat att tct gtt gcc ccg gaa atc ggt acc 355

Gly 70	Thr	His	Thr	Gly	Glu 75	Asp	Ile	Ser	Val	Ala 80	Pro	Glu	Ile	Gly	Thr 85	
ggc	tac	cgc	gag	ggc	atg	acc	cct	gtt	caa	acc	caa	ggg	tat	gcg	gtg	403
Gly	Tyr	Arg	Glu	Gly	Met	Thr	Pro	Val	Gln	Thr	Gln	Gly	Tyr	Ala	Val	
				90					95					100		
gca	act	gca	aac	ccc	atc	gct	tct	gaa	gca	gcc	tgc	gcg	gtg	tta	aga	451
Ala	Thr	Ala	Asn	Pro	Ile	Ala	Ser	Glu	Ala	Ala	Cys	Ala	Val	Leu	Arg	
			105					110					115			
gaa	ggc	ggc	act	gca	gct	gat	gct	ctt	gtc	acc	gcg	cag	ttt	gtt	ttg	499
Glu	Gly	Gly	Thr	Ala	Ala	Asp	Ala	Leu	Val	Thr	Ala	Gln	Phe	Val	Leu	
		120					125					130				
gga	ctg	acg	gaa	ccg	cag	tcg	tct	ggc	ctt	ggg	ggg	ggc	gga	tac	att	547
Gly	Leu	Thr	Glu	Pro	Gln	Ser	Ser	Gly	Leu	Gly	Gly	Gly	Gly	Tyr	Ile	
	135					140					145					
ctg	tac	tac	gac	gcc	gaa	gcc	aat	gcg	gtg	aca	gcc	att	gat	ggc	cgt	595
Leu	Tyr	Tyr	Asp	Ala	Glu	Ala	Asn	Ala	Val	Thr	Ala	Ile	Asp	Gly	Arg	
150					155				160						165	
gaa	aca	gcg	cca	gtt	gct	gct	gat	gaa	aac	tat	ctc	att	cat	gtt	tct	643
Glu	Thr	Ala	Pro	Val	Ala	Ala	Asp	Glu	Asn	Tyr	Leu	Ile	His	Val	Ser	
				170					175					180		
gca	gag	gat	caa	acg	gca	cct	gtt	cct	gat	gcc	cga	cgt	tcc	ggc	agg	691
Ala	Glu	Asp	Gln	Thr	Ala	Pro	Val	Pro	Asp	Ala	Arg	Arg	Ser	Gly	Arg	
			185					190					195			
tca	att	ggg	gtg	cca	gga	atc	gtg	gca	gcc	ctt	gga	cag	ctg	cat	gat	739
Ser	Ile	Gly	Val	Pro	Gly	Ile	Val	Ala	Ala	Leu	Gly	Gln	Leu	His	Asp	
		200					205					210				
tca	ttc	gga	aag	acc	tcc	tgg	cag	gac	gtg	ctg	aca	act	ccg	cag	cag	787
Ser	Phe	Gly	Lys	Thr	Ser	Trp	Gln	Asp	Val	Leu	Thr	Thr	Pro	Gln	Gln	
	215					220					225					
ctc	gca	act	gat	ggg	ttt	tcc	atc	agc	cct	cgc	atg	tca	gca	tca	att	835
Leu	Ala	Thr	Asp	Gly	Phe	Ser	Ile	Ser	Pro	Arg	Met	Ser	Ala	Ser	Ile	
230					235					240					245	
gct	aac	tcc	gct	gag	gat	ctc	tcc	cac	gat	ccg	gaa	gct	gcc	gca	tat	883
Ala	Asn	Ser	Ala	Glu	Asp	Leu	Ser	His	Asp	Pro	Glu	Ala	Ala	Ala	Tyr	
				250					255					260		
ttc	ctt	gat	gaa	aac	ggg	gat	gcg	aag	gca	ccc	ggc	aca	ctt	tta	caa	931
Phe	Leu	Asp	Glu	Asn	Gly	Asp	Ala	Lys	Ala	Pro	Gly	Thr	Leu	Leu	Gln	
			265					270					275			
aac	cct	gac	tat	gca	gaa	acg	att	cgt	ctc	atc	tct	gaa	ggg	ggc	ccc	979
Asn	Pro	Asp	Tyr	Ala	Glu	Thr	Ile	Arg	Leu	Ile	Ser	Glu	Gly	Gly	Pro	
		280					285					290				
gat	gcg	ttc	tac	acg	ggg	gag	att	gca	gca	gac	atc	gtg	gaa	cgc	gcc	1027
Asp	Ala	Phe	Tyr	Thr	Gly	Glu	Ile	Ala	Ala	Asp	Ile	Val	Glu	Arg	Ala	
	295					300					305					
acc	cgt	gag	gtt	gac	ggg	ttc	aca	cca	tca	ctg	atg	agc	acg	gca	gat	1075
Thr	Arg	Glu	Val	Asp	Gly	Phe	Thr	Pro	Ser	Leu	Met	Ser	Thr	Ala	Asp	

310	315	320	325	
ttg gct gcc tac act ccg gaa act cgt gaa gct ttg tgt gct ccc tac				1123
Leu Ala Ala Tyr Thr Pro Glu Thr Arg Glu Ala Leu Cys Ala Pro Tyr				
	330	335	340	
cgc gac aag att gtt tgt ggc atg cca ccg tca tca tcg ggt ggc gtc				1171
Arg Asp Lys Ile Val Cys Gly Met Pro Pro Ser Ser Ser Gly Gly Val				
	345	350	355	
aca gtg atg gaa acc ctg ggt atc ttg aac aac ttt gat ctg gcc caa				1219
Thr Val Met Glu Thr Leu Gly Ile Leu Asn Asn Phe Asp Leu Ala Gln				
	360	365	370	
tac cca ccc act gag gtt ggt ttg gat ggc gga ttg cca aat gcg gaa				1267
Tyr Pro Pro Thr Glu Val Gly Leu Asp Gly Gly Leu Pro Asn Ala Glu				
	375	380	385	
gct gtt cac ctg att tca gag gct gag cgc ctg gct tat gct gat cgc				1315
Ala Val His Leu Ile Ser Glu Ala Glu Arg Leu Ala Tyr Ala Asp Arg				
	390	395	400	405
gat gct tac atc ggt gat cct gct ttc gtg gaa gtt cca gca ggt ggt				1363
Asp Ala Tyr Ile Gly Asp Pro Ala Phe Val Glu Val Pro Ala Gly Gly				
	410	415	420	
gtc caa cag tgg atc aac cat gtc cac acg ggc gaa cac tcc aaa ctt				1411
Val Gln Gln Trp Ile Asn His Val His Thr Gly Glu His Ser Lys Leu				
	425	430	435	

<210> 206

<211> 437

<212> PRT

<213> Corynebacterium glutamicum

<400> 206

Met Lys Val Thr Gln Ser Thr Phe Leu Lys Ser Val Ala Ala Phe Thr				
1	5	10	15	
Val Ala Ala Leu Thr Leu Thr Ile Ser Ser Cys Ser Ser Gly Glu Asp				
	20	25	30	
Thr Ser Ala Ser Ser Thr Asp Thr Glu Asn Ser Ser Thr Gln Ala Ala				
	35	40	45	
Ala Ser Pro Pro Leu Ala Pro Cys Glu Leu Pro Ala Asp Ala Ser Ala				
	50	55	60	
Glu Glu Glu Val Glu Gly Thr His Thr Gly Glu Asp Ile Ser Val Ala				
	65	70	75	80
Pro Glu Ile Gly Thr Gly Tyr Arg Glu Gly Met Thr Pro Val Gln Thr				
	85	90	95	
Gln Gly Tyr Ala Val Ala Thr Ala Asn Pro Ile Ala Ser Glu Ala Ala				
	100	105	110	
Cys Ala Val Leu Arg Glu Gly Gly Thr Ala Ala Asp Ala Leu Val Thr				
	115	120	125	

Ala Gln Phe Val Leu Gly Leu Thr Glu Pro Gln Ser Ser Gly Leu Gly
 130 135 140
 Gly Gly Gly Tyr Ile Leu Tyr Tyr Asp Ala Glu Ala Asn Ala Val Thr
 145 150 155 160
 Ala Ile Asp Gly Arg Glu Thr Ala Pro Val Ala Ala Asp Glu Asn Tyr
 165 170 175
 Leu Ile His Val Ser Ala Glu Asp Gln Thr Ala Pro Val Pro Asp Ala
 180 185 190
 Arg Arg Ser Gly Arg Ser Ile Gly Val Pro Gly Ile Val Ala Ala Leu
 195 200 205
 Gly Gln Leu His Asp Ser Phe Gly Lys Thr Ser Trp Gln Asp Val Leu
 210 215 220
 Thr Thr Pro Gln Gln Leu Ala Thr Asp Gly Phe Ser Ile Ser Pro Arg
 225 230 235 240
 Met Ser Ala Ser Ile Ala Asn Ser Ala Glu Asp Leu Ser His Asp Pro
 245 250 255
 Glu Ala Ala Ala Tyr Phe Leu Asp Glu Asn Gly Asp Ala Lys Ala Pro
 260 265 270
 Gly Thr Leu Leu Gln Asn Pro Asp Tyr Ala Glu Thr Ile Arg Leu Ile
 275 280 285
 Ser Glu Gly Gly Pro Asp Ala Phe Tyr Thr Gly Glu Ile Ala Ala Asp
 290 295 300
 Ile Val Glu Arg Ala Thr Arg Glu Val Asp Gly Phe Thr Pro Ser Leu
 305 310 315 320
 Met Ser Thr Ala Asp Leu Ala Ala Tyr Thr Pro Glu Thr Arg Glu Ala
 325 330 335
 Leu Cys Ala Pro Tyr Arg Asp Lys Ile Val Cys Gly Met Pro Pro Ser
 340 345 350
 Ser Ser Gly Gly Val Thr Val Met Glu Thr Leu Gly Ile Leu Asn Asn
 355 360 365
 Phe Asp Leu Ala Gln Tyr Pro Pro Thr Glu Val Gly Leu Asp Gly Gly
 370 375 380
 Leu Pro Asn Ala Glu Ala Val His Leu Ile Ser Glu Ala Glu Arg Leu
 385 390 395 400
 Ala Tyr Ala Asp Arg Asp Ala Tyr Ile Gly Asp Pro Ala Phe Val Glu
 405 410 415
 Val Pro Ala Gly Gly Val Gln Gln Trp Ile Asn His Val His Thr Gly
 420 425 430
 Glu His Ser Lys Leu
 435

<210> 207
 <211> 507
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(507)
 <223> FRXA02820

<400> 207
 gct aac tcc gct gag gat ctc tcc cac gat ccg gaa gct gcc gca tat 48
 Ala Asn Ser Ala Glu Asp Leu Ser His Asp Pro Glu Ala Ala Ala Tyr
 1 5 10 15
 ttc ctt gat gaa aac ggt gat gcg aag gca ccc ggc aca ctt tta caa 96
 Phe Leu Asp Glu Asn Gly Asp Ala Lys Ala Pro Gly Thr Leu Leu Gln
 20 25 30
 aac cct gac tat gca gaa acg att cgt ctc atc tct gaa ggt ggc ccc 144
 Asn Pro Asp Tyr Ala Glu Thr Ile Arg Leu Ile Ser Glu Gly Gly Pro
 35 40 45
 gat gcg ttc tac acg ggt gag att gca gca gac atc gtg gaa cgc gcc 192
 Asp Ala Phe Tyr Thr Gly Glu Ile Ala Ala Asp Ile Val Glu Arg Ala
 50 55 60
 acc cgt gag gtt gac ggt ttc aca cca tca ctg atg agc acg gca gat 240
 Thr Arg Glu Val Asp Gly Phe Thr Pro Ser Leu Met Ser Thr Ala Asp
 65 70 75 80
 ttg gct gcc tac act ccg gaa act cgt gaa gct ttg tgt gct ccc tac 288
 Leu Ala Ala Tyr Thr Pro Glu Thr Arg Glu Ala Leu Cys Ala Pro Tyr
 85 90 95
 cgc gac aag att gtt tgt ggc atg cca ccg tca tca tcg ggt ggc gtc 336
 Arg Asp Lys Ile Val Cys Gly Met Pro Pro Ser Ser Ser Gly Gly Val
 100 105 110
 aca gtg atg gaa acc ctg ggt atc ttg aac aac ttt gat ctc gcc caa 384
 Thr Val Met Glu Thr Leu Gly Ile Leu Asn Asn Phe Asp Leu Ala Gln
 115 120 125
 tac cca ccc act gag gtt ggt ttg gat ggc gga ttg cca aat gcg gaa 432
 Tyr Pro Pro Thr Glu Val Gly Leu Asp Gly Gly Leu Pro Asn Ala Glu
 130 135 140
 gct gtt cac ctg att tca gag gct gag cgc ctg gct tat gct gat cgc 480
 Ala Val His Leu Ile Ser Glu Ala Glu Arg Leu Ala Tyr Ala Asp Arg
 145 150 155 160
 gat gct tac atc ggt gat cct gct ttc 507
 Asp Ala Tyr Ile Gly Asp Pro Ala Phe
 165

<210> 208
 <211> 169
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 208

Ala Asn Ser Ala Glu Asp Leu Ser His Asp Pro Glu Ala Ala Ala Tyr
 1 5 10 15

Phe Leu Asp Glu Asn Gly Asp Ala Lys Ala Pro Gly Thr Leu Leu Gln
 20 25 30

Asn Pro Asp Tyr Ala Glu Thr Ile Arg Leu Ile Ser Glu Gly Gly Pro
 35 40 45

Asp Ala Phe Tyr Thr Gly Glu Ile Ala Ala Asp Ile Val Glu Arg Ala
 50 55 60

Thr Arg Glu Val Asp Gly Phe Thr Pro Ser Leu Met Ser Thr Ala Asp
 65 70 75 80

Leu Ala Ala Tyr Thr Pro Glu Thr Arg Glu Ala Leu Cys Ala Pro Tyr
 85 90 95

Arg Asp Lys Ile Val Cys Gly Met Pro Pro Ser Ser Ser Gly Gly Val
 100 105 110

Thr Val Met Glu Thr Leu Gly Ile Leu Asn Asn Phe Asp Leu Ala Gln
 115 120 125

Tyr Pro Pro Thr Glu Val Gly Leu Asp Gly Gly Leu Pro Asn Ala Glu
 130 135 140

Ala Val His Leu Ile Ser Glu Ala Glu Arg Leu Ala Tyr Ala Asp Arg
 145 150 155 160

Asp Ala Tyr Ile Gly Asp Pro Ala Phe
 165

<210> 209

<211> 604

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(604)

<223> FRXA02000

<400> 209

caacgaaaca aatgcaagcc cccaatcatg gggtttctacc aattaaattt tcttttcagaa 60

aatatctccc cacataaaag ttccttgata ggctcgagag atg aaa gtg acc caa 115
 Met Lys Val Thr Gln
 1 5

agc aca ttc ctt aaa tcg gta gct gcg ttc act gtc gca gcc tta acc 163
 Ser Thr Phe Leu Lys Ser Val Ala Ala Phe Thr Val Ala Ala Leu Thr
 10 15 20

ctg acc atc tct tcg tgt tcc agc ggt gaa gac acc tcc gca agc tcc 211
 Leu Thr Ile Ser Ser Cys Ser Ser Gly Glu Asp Thr Ser Ala Ser Ser
 25 30 35

acg gat act gaa aac tcc tca acc caa gca gca gcg tct ccc cca ctt 259

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<210> 210
<211> 168
<212> PRT
<213> Corynebacterium glutamicum
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<400> 210
Met Lys Val Thr Gln Ser Thr Phe Leu Lys Ser Val Ala Ala Phe Thr
  1             5             10             15

Val Ala Ala Leu Thr Leu Thr Ile Ser Ser Cys Ser Ser Gly Glu Asp
      20             25             30

Thr Ser Ala Ser Ser Thr Asp Thr Glu Asn Ser Ser Thr Gln Ala Ala
      35             40             45

Ala Ser Pro Pro Leu Ala Pro Cys Glu Leu Pro Ala Asp Ala Ser Ala
      50             55             60

Glu Glu Glu Val Glu Gly Thr His Thr Gly Glu Asp Ile Ser Val Ala
  65             70             75             80
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Pro Glu Ile Gly Thr Gly Tyr Arg Glu Gly Met Thr Pro Val Gln Thr
      85             90             95

Gln Gly Tyr Ala Val Ala Thr Ala Asn Pro Ile Ala Ser Glu Ala Ala

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100	105	110
Cys Ala Val Leu Arg Glu Gly Gly Thr Ala Ala Asp Ala Leu Val Thr		
115	120	125
Ala Gln Phe Val Leu Gly Leu Thr Glu Pro Gln Ser Ser Gly Leu Gly		
130	135	140
Gly Gly Gly Tyr Ile Leu Tyr Tyr Asp Ala Glu Ala Asn Ala Val Thr		
145	150	155
Ala Ile Asp Gly Arg Glu Thr Ala		
165		

<210> 211
 <211> 753
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (53)..(730)
 <223> RXN02944

<400> 211
 ggggaggtcc caacaggtgg tggcgaagag gtgaccagcg aggtcaacag gg gtg aac 58
 Val Asn
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gct cag aat ctt att gat cca gag cat tca atg ggt cag gca act gct 106
 Ala Gln Asn Leu Ile Asp Pro Glu His Ser Met Gly Gln Ala Thr Ala
 5 10 15

ggt gtg agc cag aac cca gtc atg gct gcc ctg ccg gaa agt ggc acc 154
 Gly Val Ser Gln Asn Pro Val Met Ala Ala Leu Pro Glu Ser Gly Thr
 20 25 30

agc cat att tcc atc atc gat tcc tat ggc aac gca gca tcg ttg acc 202
 Ser His Ile Ser Ile Ile Asp Ser Tyr Gly Asn Ala Ala Ser Leu Thr
 35 40 45 50

acc agt gtg gaa gct gct ttc ggt tcc ttc cac ttc acc cgt ggt ttc 250
 Thr Ser Val Glu Ala Ala Phe Gly Ser Phe His Phe Thr Arg Gly Phe
 55 60 65

att ttg aat aat cag ctg aca gat ttc tcc gct gaa cca ctt gat gag 298
 Ile Leu Asn Asn Gln Leu Thr Asp Phe Ser Ala Glu Pro Leu Asp Glu
 70 75 80

gac ggc gag ccc gtg gcc aat cgt gtc gag tca gca aag cgc cca cgg 346
 Asp Gly Glu Pro Val Ala Asn Arg Val Glu Ser Ala Lys Arg Pro Arg
 85 90 95

tct tcc atg tcg cca atg cta gtg ttc aac gcc agt ggc gat ggt gaa 394
 Ser Ser Met Ser Pro Met Leu Val Phe Asn Ala Ser Gly Asp Gly Glu
 100 105 110

atc gcg gat ctg aat atg gtg ctg ggc tcc cct ggc gga tcc ttg att 442
 Ile Ala Asp Leu Asn Met Val Leu Gly Ser Pro Gly Gly Ser Leu Ile
 115 120 125 130

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att cag tac gtg gtg aaa acc ctg gtc aac atc atc gac tgg gat atg 490
Ile Gln Tyr Val Val Lys Thr Leu Val Asn Ile Ile Asp Trp Asp Met
135 140 145

gat cca cag cag gca gtg tct gcg ccc aac ttt ggt gcg atg aac cag 538
Asp Pro Gln Gln Ala Val Ser Ala Pro Asn Phe Gly Ala Met Asn Gln
150 155 160

cct aag act gga ctg gga agc gag cat ccg ctg atc gcc aat gat tca 586
Pro Lys Thr Gly Leu Gly Ser Glu His Pro Leu Ile Ala Asn Asp Ser
165 170 175

gca gag ctt gta tct gaa ctg gaa agc aaa ggc cac gaa gtt aat gtg 634
Ala Glu Leu Val Ser Glu Leu Glu Ser Lys Gly His Glu Val Asn Val
180 185 190

ggc gag caa tcc agt ggc cta tcg gcg ttg gtg aaa aac ggc gac acc 682
Gly Glu Gln Ser Ser Gly Leu Ser Ala Leu Val Lys Asn Gly Asp Thr
195 200 205 210

att gtc ggt ggc gcc gat cca cgt aga gaa ggc gtg gtc ttg ggt ggc 730
Ile Val Gly Gly Ala Asp Pro Arg Arg Glu Gly Val Val Leu Gly Gly
215 220 225

taattagcgc gcagaccacg cag 753

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<210> 212

<211> 226

<212> PRT

<213> Corynebacterium glutamicum

<400> 212

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Val Asn Ala Gln Asn Leu Ile Asp Pro Glu His Ser Met Gly Gln Ala
1 5 10 15

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Thr Ala Gly Val Ser Gln Asn Pro Val Met Ala Ala Leu Pro Glu Ser
20 25 30

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```

Gly Thr Ser His Ile Ser Ile Ile Asp Ser Tyr Gly Asn Ala Ala Ser
35 40 45

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```

Leu Thr Thr Ser Val Glu Ala Ala Phe Gly Ser Phe His Phe Thr Arg
50 55 60

```

```

Gly Phe Ile Leu Asn Asn Gln Leu Thr Asp Phe Ser Ala Glu Pro Leu
65 70 75 80

```

```

Asp Glu Asp Gly Glu Pro Val Ala Asn Arg Val Glu Ser Ala Lys Arg
85 90 95

```

```

Pro Arg Ser Ser Met Ser Pro Met Leu Val Phe Asn Ala Ser Gly Asp
100 105 110

```

```

Gly Glu Ile Ala Asp Leu Asn Met Val Leu Gly Ser Pro Gly Gly Ser
115 120 125

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```

Leu Ile Ile Gln Tyr Val Val Lys Thr Leu Val Asn Ile Ile Asp Trp
130 135 140

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Asp Met Asp Pro Gln Gln Ala Val Ser Ala Pro Asn Phe Gly Ala Met
145 150 155 160

Asn Gln Pro Lys Thr Gly Leu Gly Ser Glu His Pro Leu Ile Ala Asn
165 170 175

Asp Ser Ala Glu Leu Val Ser Glu Leu Glu Ser Lys Gly His Glu Val
180 185 190

Asn Val Gly Glu Gln Ser Ser Gly Leu Ser Ala Leu Val Lys Asn Gly
195 200 205

Asp Thr Ile Val Gly Gly Ala Asp Pro Arg Arg Glu Gly Val Val Leu
210 215 220

Gly Gly
225

<210> 213

<211> 1335

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1312)

<223> RXS00197

<400> 213

gtc gat gata ttttggcaac cgaatctgag gcacgcgcgc gtgcgaatgc tttgatcaac 60

cggttggcaa ccaacttgta agctaaggag cttccgcctc gtg gca gcc tat ctt 115
Val Ala Ala Tyr Leu
1 5

ctt ggt gtc gta tta ttt ttc ctc ggc atc gca gta acc atc gcg ctt 163
Leu Gly Val Val Leu Phe Phe Leu Gly Ile Ala Val Thr Ile Ala Leu
10 15 20

cac gag tgg ggg cac ttc atc aca gcg cgc att ttc gga atg aaa gtg 211
His Glu Trp Gly His Phe Ile Thr Ala Arg Ile Phe Gly Met Lys Val
25 30 35

cgg cgt ttc ttc atc ggt ttc ggc ccg acg gtg ttt gcc aaa aga cgc 259
Arg Arg Phe Phe Ile Gly Phe Gly Pro Thr Val Phe Ala Lys Arg Arg
40 45 50

ggc gaa acc gtg tac ggc ctt aaa gcg att ccg gtc ggc ggt ttt tgt 307
Gly Glu Thr Val Tyr Gly Leu Lys Ala Ile Pro Val Gly Gly Phe Cys
55 60 65

gac atc gcg ggg atg act gcc caa gat gaa ctt gat ccg gaa gac ctg 355
Asp Ile Ala Gly Met Thr Ala Gln Asp Glu Leu Asp Pro Glu Asp Leu
70 75 80 85

ccg cgc gcc atg tat cta aag ccc tgg tgg cag cgc ata att gtg ctt 403
Pro Arg Ala Met Tyr Leu Lys Pro Trp Trp Gln Arg Ile Ile Val Leu
90 95 100

tcc ggc ggc gtg atc atg aat ctg atc gtc ggc ttt ttg gtg ctt tac 451

Ser	Gly	Gly	Val	Ile	Met	Asn	Leu	Ile	Val	Gly	Phe	Leu	Val	Leu	Tyr		
			105					110					115				
ggc	gtg	gcg	gtg	agc	tcc	gga	atc	ccg	aat	ccg	gat	gtg	gat	acc	acc	499	
Gly	Val	Ala	Val	Ser	Ser	Gly	Ile	Pro	Asn	Pro	Asp	Val	Asp	Thr	Thr		
		120					125					130					
gcg	aca	gtc	gac	acc	gtt	cag	tgc	gtg	ccg	gaa	acc	caa	att	tcc	gca	547	
Ala	Thr	Val	Asp	Thr	Val	Gln	Cys	Val	Pro	Glu	Thr	Gln	Ile	Ser	Ala		
	135					140					145						
act	gaa	ctg	tcc	tcc	tgc	gta	ggc	tca	ggc	cca	gag	ggc	gac	gcc	ggc	595	
Thr	Glu	Leu	Ser	Ser	Cys	Val	Gly	Ser	Gly	Pro	Ala	Gly	Asp	Ala	Gly		
150					155					160					165		
att	gag	cac	ggc	gat	aag	att	ttg	gcc	gtc	aac	ggc	caa	gag	atg	gca	643	
Ile	Glu	His	Gly	Asp	Lys	Ile	Leu	Ala	Val	Asn	Gly	Gln	Glu	Met	Ala		
			170					175						180			
agc	ttc	acc	gcc	atc	cgc	gat	gag	atc	ctc	gag	ctc	cca	ggc	gaa	acg	691	
Ser	Phe	Thr	Ala	Ile	Arg	Asp	Ala	Ile	Leu	Glu	Leu	Pro	Gly	Glu	Thr		
			185					190					195				
gca	acg	ctg	acg	att	gaa	cgg	gag	gga	acg	ctt	ttc	gac	gtc	gac	ctc	739	
Ala	Thr	Leu	Thr	Ile	Glu	Arg	Glu	Gly	Thr	Leu	Phe	Asp	Val	Asp	Leu		
		200					205					210					
cag	gtt	gcc	tct	gtc	acc	cgt	ctc	gcc	tct	gac	ggc	tca	gaa	att	acc	787	
Gln	Val	Ala	Ser	Val	Thr	Arg	Leu	Ala	Ser	Asp	Gly	Ser	Glu	Ile	Thr		
	215					220					225						
gtc	ggc	gag	gtg	ggc	atg	tcg	agc	ctt	cca	ccg	acc	gat	gtg	tac	aaa	835	
Val	Gly	Ala	Val	Gly	Met	Ser	Ser	Leu	Pro	Pro	Thr	Asp	Val	Tyr	Lys		
230					235				240						245		
aaa	tac	ggc	cca	atc	gag	ggc	gtg	gga	gca	act	gca	cgt	ttc	acc	ggc	883	
Lys	Tyr	Gly	Pro	Ile	Glu	Gly	Val	Gly	Ala	Thr	Ala	Arg	Phe	Thr	Gly		
			250					255						260			
gac	atg	atc	agc	gcc	acg	tgg	gat	ggc	ctc	aaa	gcc	ttc	ccg	gag	aaa	931	
Asp	Met	Ile	Ser	Ala	Thr	Trp	Asp	Gly	Leu	Lys	Ala	Phe	Pro	Ala	Lys		
			265					270					275				
atc	cca	ggg	gtc	gtc	gca	tcc	atc	ttc	ggc	gca	gaa	cga	gat	gta	gaa	979	
Ile	Pro	Gly	Val	Val	Ala	Ser	Ile	Phe	Gly	Ala	Glu	Arg	Asp	Val	Glu		
		280					285					290					
agc	ccc	atg	agt	gtg	gtg	ggc	gcc	gta	cgc	atc	ggc	ggc	gaa	ttt	gtc	1027	
Ser	Pro	Met	Ser	Val	Val	Gly	Ala	Val	Arg	Ile	Gly	Gly	Glu	Phe	Val		
		295				300					305						
gaa	cgt	tcc	atg	tgg	gac	atg	ttc	atg	atg	atg	ctg	gcc	agc	ctg	aac	1075	
Glu	Arg	Ser	Met	Trp	Asp	Met	Phe	Met	Met	Met	Leu	Ala	Ser	Leu	Asn		
310					315					320					325		
ttc	ttc	ctc	gag	ctg	ttt	aac	ctc	gtg	ccg	ctg	cca	cca	ctt	gat	ggc	1123	
Phe	Phe	Leu	Ala	Leu	Phe	Asn	Leu	Val	Pro	Leu	Pro	Pro	Leu	Asp	Gly		
			330					335						340			
gga	cac	att	gcc	gtg	gtg	atc	tat	gaa	aaa	atc	cgc	gac	ttc	ttc	cgc	1171	
Gly	His	Ile	Ala	Val	Val	Ile	Tyr	Glu	Lys	Ile	Arg	Asp	Phe	Phe	Arg		

345 350 355
 aaa ctg cgc gga aaa cca gcg ggc ggc cca gcg gat tac acc aaa cta 1219
 Lys Leu Arg Gly Lys Pro Ala Gly Gly Pro Ala Asp Tyr Thr Lys Leu
 360 365 370
 atg ccc gtc acc gta gct gtc gca gcc ttg ctg atg aca gtg gga ggc 1267
 Met Pro Val Thr Val Ala Val Ala Ala Leu Leu Met Thr Val Gly Gly
 375 380 385
 ctg gtc att gtc gcc gat gtg gtc aat ccc atc cga ctc ttt ggc 1312
 Leu Val Ile Val Ala Asp Val Val Asn Pro Ile Arg Leu Phe Gly
 390 395 400
 taacgatacg gaattgaact gcc 1335

<210> 214

<211> 404

<212> PRT

<213> Corynebacterium glutamicum

<400> 214

Val Ala Ala Tyr Leu Leu Gly Val Val Leu Phe Phe Leu Gly Ile Ala
 1 5 10 15
 Val Thr Ile Ala Leu His Glu Trp Gly His Phe Ile Thr Ala Arg Ile
 20 25 30
 Phe Gly Met Lys Val Arg Arg Phe Phe Ile Gly Phe Gly Pro Thr Val
 35 40 45
 Phe Ala Lys Arg Arg Gly Glu Thr Val Tyr Gly Leu Lys Ala Ile Pro
 50 55 60
 Val Gly Gly Phe Cys Asp Ile Ala Gly Met Thr Ala Gln Asp Glu Leu
 65 70 75 80
 Asp Pro Glu Asp Leu Pro Arg Ala Met Tyr Leu Lys Pro Trp Trp Gln
 85 90 95
 Arg Ile Ile Val Leu Ser Gly Gly Val Ile Met Asn Leu Ile Val Gly
 100 105 110
 Phe Leu Val Leu Tyr Gly Val Ala Val Ser Ser Gly Ile Pro Asn Pro
 115 120 125
 Asp Val Asp Thr Thr Ala Thr Val Asp Thr Val Gln Cys Val Pro Glu
 130 135 140
 Thr Gln Ile Ser Ala Thr Glu Leu Ser Ser Cys Val Gly Ser Gly Pro
 145 150 155 160
 Ala Gly Asp Ala Gly Ile Glu His Gly Asp Lys Ile Leu Ala Val Asn
 165 170 175
 Gly Gln Glu Met Ala Ser Phe Thr Ala Ile Arg Asp Ala Ile Leu Glu
 180 185 190
 Leu Pro Gly Glu Thr Ala Thr Leu Thr Ile Glu Arg Glu Gly Thr Leu
 195 200 205

Phe Asp Val Asp Leu Gln Val Ala Ser Val Thr Arg Leu Ala Ser Asp
 210 215 220
 Gly Ser Glu Ile Thr Val Gly Ala Val Gly Met Ser Ser Leu Pro Pro
 225 230 235 240
 Thr Asp Val Tyr Lys Lys Tyr Gly Pro Ile Glu Gly Val Gly Ala Thr
 245 250 255
 Ala Arg Phe Thr Gly Asp Met Ile Ser Ala Thr Trp Asp Gly Leu Lys
 260 265 270
 Ala Phe Pro Ala Lys Ile Pro Gly Val Val Ala Ser Ile Phe Gly Ala
 275 280 285
 Glu Arg Asp Val Glu Ser Pro Met Ser Val Val Gly Ala Val Arg Ile
 290 295 300
 Gly Gly Glu Phe Val Glu Arg Ser Met Trp Asp Met Phe Met Met Met
 305 310 315 320
 Leu Ala Ser Leu Asn Phe Phe Leu Ala Leu Phe Asn Leu Val Pro Leu
 325 330 335
 Pro Pro Leu Asp Gly Gly His Ile Ala Val Val Ile Tyr Glu Lys Ile
 340 345 350
 Arg Asp Phe Phe Arg Lys Leu Arg Gly Lys Pro Ala Gly Gly Pro Ala
 355 360 365
 Asp Tyr Thr Lys Leu Met Pro Val Thr Val Ala Val Ala Ala Leu Leu
 370 375 380
 Met Thr Val Gly Gly Leu Val Ile Val Ala Asp Val Val Asn Pro Ile
 385 390 395 400
 Arg Leu Phe Gly

<210> 215
 <211> 735
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(712)
 <223> RXS01223

<400> 215
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 aggatgctca tggcaccatc ctaggcgcgcc ctgccatagg atg act tcc gtg agt 115
 Met Thr Ser Val Ser

1

5

ttt ttg tct aaa atc caa gca ctg ttt gcc ccc aag cct gaa ctt ccc 163
 Phe Leu Ser Lys Ile Gln Ala Leu Phe Ala Pro Lys Pro Glu Leu Pro
 10 15 20

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gcc gcc aaa tgg ctg gtc gtg ggc ctg ggc aac ccc ggc gcc aag tac 211
Ala Ala Lys Trp Leu Val Val Gly Leu Gly Asn Pro Gly Ala Lys Tyr
      25                      30                      35

gaa tcc acc cga cac aac gtc ggt tac atg tgc caa gac atg ctt atc 259
Glu Ser Thr Arg His Asn Val Gly Tyr Met Cys Gln Asp Met Leu Ile
      40                      45                      50

gac gcc cac cag cag cag ccc ctc acc ccc gcc acg ggc tac aag gcc 307
Asp Ala His Gln Gln Gln Pro Leu Thr Pro Ala Thr Gly Tyr Lys Ala
      55                      60                      65

ctc aca acg cag ctc gca cca ggg gtg ctc gcc gtt cga tcc acc act 355
Leu Thr Thr Gln Leu Ala Pro Gly Val Leu Ala Val Arg Ser Thr Thr
      70                      75                      80                      85

ttt atg aac cac tcc ggc caa ggt gtc gca ccg atc gcc gca gcg ttg 403
Phe Met Asn His Ser Gly Gln Gly Val Ala Pro Ile Ala Ala Ala Leu
      90                      95                      100

ggt atc cca gca gag cgc atc atc gtg atc cac gac gag ctc gat ctg 451
Gly Ile Pro Ala Glu Arg Ile Ile Val Ile His Asp Glu Leu Asp Leu
      105                      110                      115

ccc gct gga aaa gta cgc ctg aaa aag ggc gga aac gaa aac ggt cac 499
Pro Ala Gly Lys Val Arg Leu Lys Lys Gly Gly Asn Glu Asn Gly His
      120                      125                      130

aac ggc ctg aaa tcc ctc acg gaa gag ctc ggc acc aga gac tac ctg 547
Asn Gly Leu Lys Ser Leu Thr Glu Glu Leu Gly Thr Arg Asp Tyr Leu
      135                      140                      145

cgc gtc cgc atc ggc att tca cga cca cca gca gga atg gcc gtg ccc 595
Arg Val Arg Ile Gly Ile Ser Arg Pro Pro Ala Gly Met Ala Val Pro
      150                      155                      160                      165

gac tac gtt ttg gaa cca gtc gat cac gac caa cca ggc att gaa ctt 643
Asp Tyr Val Leu Glu Pro Val Asp His Asp Gln Pro Gly Ile Glu Leu
      170                      175                      180

gcc gcc gag gca gtg gat ttg ctg ctg gcc cag gga tta tct gct gcg 691
Ala Ala Glu Ala Val Asp Leu Leu Leu Ala Gln Gly Leu Ser Ala Ala
      185                      190                      195

caa aac gct atc cac agc cgc tagattgcta gagattcccg cac 735
Gln Asn Ala Ile His Ser Arg
      200

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<210> 216

<211> 204

<212> PRT

<213> Corynebacterium glutamicum

<400> 216

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Met Thr Ser Val Ser Phe Leu Ser Lys Ile Gln Ala Leu Phe Ala Pro
  1              5              10              15

Lys Pro Glu Leu Pro Ala Ala Lys Trp Leu Val Val Gly Leu Gly Asn
      20              25              30

```

Pro Gly Ala Lys Tyr Glu Ser Thr Arg His Asn Val Gly Tyr Met Cys
35 40 45

Gln Asp Met Leu Ile Asp Ala His Gln Gln Gln Pro Leu Thr Pro Ala
50 55 60

Thr Gly Tyr Lys Ala Leu Thr Thr Gln Leu Ala Pro Gly Val Leu Ala
65 70 75 80

Val Arg Ser Thr Thr Phe Met Asn His Ser Gly Gln Gly Val Ala Pro
85 90 95

Ile Ala Ala Ala Leu Gly Ile Pro Ala Glu Arg Ile Ile Val Ile His
100 105 110

Asp Glu Leu Asp Leu Pro Ala Gly Lys Val Arg Leu Lys Lys Gly Gly
115 120 125

Asn Glu Asn Gly His Asn Gly Leu Lys Ser Leu Thr Glu Glu Leu Gly
130 135 140

Thr Arg Asp Tyr Leu Arg Val Arg Ile Gly Ile Ser Arg Pro Pro Ala
145 150 155 160

Gly Met Ala Val Pro Asp Tyr Val Leu Glu Pro Val Asp His Asp Gln
165 170 175

Pro Gly Ile Glu Leu Ala Ala Glu Ala Val Asp Leu Leu Leu Ala Gln
180 185 190

Gly Leu Ser Ala Ala Gln Asn Ala Ile His Ser Arg
195 200

<210> 217

<211> 1365

<212> DNA

<213> Corynebacterium glutamicum

 $\langle 220 \rangle$

<221> CDS

 $\langle 222 \rangle \quad (101) \dots (1342)$

<223> RXS01642

<400> 217

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ggaatgctgc gcggtcttga tattggattc ggtggataag atg cgc aga ctc atc 115
Met Arg Arg Leu Ile
1 5

gcg gtt agc ttg gcc gct ctg ttt atg ttg gct tcc act cca gcg acg 163
Ala Val Ser Leu Ala Ala Leu Phe Met Leu Ala Ser Thr Pro Ala Thr
10 15 20

agg gca cag gaa gta gaa gct ctc gct tgc ccc gag gta gcg atc gcc 211
Arg Ala Gln Glu Val Glu Ala Leu Ala Cys Pro Glu Val Ala Ile Ala
25 30 35

gat cct tcc tcc gca gtt tta gat gaa cac ctt tcg caq tca tta tcc 259

Asp	Pro	Ser	Ser	Ala	Val	Leu	Asp	Glu	His	Leu	Ser	Gln	Ser	Leu	Ser		
		40					45					50					
caa	gct	cac	caa	cta	gca	act	ggc	gcc	ggt	gtg	atg	gtg	gca	gtc	atc	307	
Gln	Ala	His	Gln	Leu	Ala	Thr	Gly	Ala	Gly	Val	Met	Val	Ala	Val	Ile		
	55					60					65						
gac	acc	gga	gta	tcc	ctg	cat	cca	cgt	ctg	ccc	cac	tta	att	ccc	ggc	355	
Asp	Thr	Gly	Val	Ser	Leu	His	Pro	Arg	Leu	Pro	His	Leu	Ile	Pro	Gly		
	70				75				80					85			
ggt	gat	ttc	gtg	ggc	gcc	cac	caa	agc	ccc	gat	gtg	cca	ggt	gaa	ctt	403	
Gly	Asp	Phe	Val	Gly	Ala	His	Gln	Ser	Pro	Asp	Val	Pro	Gly	Glu	Leu		
			90						95					100			
atc	gat	tgc	gac	ggc	cac	ggc	acc	atc	gtc	gcc	gga	atc	atc	gcc	tcc	451	
Ile	Asp	Cys	Asp	Gly	His	Gly	Thr	Ile	Val	Ala	Gly	Ile	Ile	Ala	Ser		
			105					110						115			
caa	gga	aac	ccc	ggc	acc	ggc	tgg	cca	tat	gac	ggc	agc	tcc	gat	cct	499	
Gln	Gly	Asn	Pro	Gly	Thr	Gly	Trp	Pro	Tyr	Asp	Gly	Ser	Ser	Asp	Pro		
		120					125					130					
tat	atc	ggt	gtc	gcc	cca	gat	tcc	gga	atc	atc	tcc	att	aaa	caa	acc	547	
Tyr	Ile	Gly	Val	Ala	Pro	Asp	Ser	Gly	Ile	Ile	Ser	Ile	Lys	Gln	Thr		
	135					140					145						
agc	tca	tat	gtg	cgt	act	cgt	gaa	gat	tcc	aac	gtc	gga	acg	ctg	agc	595	
Ser	Ser	Tyr	Val	Arg	Thr	Arg	Glu	Asp	Ser	Asn	Val	Gly	Thr	Leu	Ser		
	150				155				160					165			
acc	ctg	gcg	gaa	tcc	atc	cac	cga	gct	ctc	gat	tcc	ggt	gcc	cac	gtg	643	
Thr	Leu	Ala	Glu	Ser	Ile	His	Arg	Ala	Leu	Asp	Ser	Gly	Ala	His	Val		
				170					175					180			
atc	aat	att	tcc	gtg	gtg	tcc	tgt	ttg	ccc	caa	tca	ccc	gac	gag	gcc	691	
Ile	Asn	Ile	Ser	Val	Val	Ser	Cys	Leu	Pro	Gln	Ser	Pro	Asp	Glu	Ala		
			185					190						195			
gca	tcg	ttc	cag	cct	ctg	acg	gat	gct	ctt	aac	aga	gca	gaa	ctt	caa	739	
Ala	Ser	Phe	Gln	Pro	Leu	Thr	Asp	Ala	Leu	Asn	Arg	Ala	Glu	Leu	Gln		
		200					205					210					
ggg	gtg	ata	gtg	gtg	gca	gca	gca	gga	aac	ctc	ggg	cag	gat	tgt	cca	787	
Gly	Val	Ile	Val	Val	Ala	Ala	Ala	Gly	Asn	Leu	Gly	Gln	Asp	Cys	Pro		
	215					220					225						
gtt	gga	tct	acc	gtt	tat	cct	gca	cat	tca	gac	act	gtg	ctc	tct	gtg	835	
Val	Gly	Ser	Thr	Val	Tyr	Pro	Ala	His	Ser	Asp	Thr	Val	Leu	Ser	Val		
	230				235					240				245			
tcg	gca	cgt	ttt	gat	tct	cac	acg	ctt	gca	gaa	tat	tcc	atg	cct	ggc	883	
Ser	Ala	Arg	Phe	Asp	Ser	His	Thr	Leu	Ala	Glu	Tyr	Ser	Met	Pro	Gly		
			250					255						260			
aac	caa	caa	atc	ctc	tct	gca	cca	agc	cac	att	cag	gct	ggt	cta	tca	931	
Asn	Gln	Gln	Ile	Leu	Ser	Ala	Pro	Ser	His	Ile	Gln	Ala	Gly	Leu	Ser		
			265					270					275				
ccg	cgt	ggc	gac	ggc	ttc	gcc	agc	cac	atg	atc	acc	acc	gct	ggc	gaa	979	
Pro	Arg	Gly	Asp	Gly	Phe	Ala	Ser	His	Met	Ile	Thr	Thr	Ala	Gly	Glu		

280	285	290	
agc ccc ttc gag ggc acc	agt ttt gcc gct cca gtt gtc agc gcc aca		1027
Ser Pro Phe Glu Gly Thr	Ser Phe Ala Ala Pro Val Val Ser Ala Thr		
295	300	305	
gct gca ctg ctt cgc cag cat ttt ccc ttt gcc aca ccc tat gaa att			1075
Ala Ala Leu Leu Arg Gln His Phe Pro Phe Ala Thr Pro Tyr Glu Ile			
310	315	320	325
cgt gca cga atc ttc aac agc atc gac cct gca aga ggc gct att gat			1123
Arg Ala Arg Ile Phe Asn Ser Ile Asp Pro Ala Arg Gly Ala Ile Asp			
330	335	340	
ccc tac ctg gca ctt act caa gaa atc tat ccc acc act ccc ctg gtt			1171
Pro Tyr Leu Ala Leu Thr Gln Glu Ile Tyr Pro Thr Thr Pro Leu Val			
345	350	355	
cat gag atc gca cta agt gtt ccc acg ccg ccg gat gat tct cca cgg			1219
His Glu Ile Ala Leu Ser Val Pro Thr Pro Pro Asp Asp Ser Pro Arg			
360	365	370	
gag cgg ggc atc cta gtt acc gca atc att gtt ggg ttg ctc gca gtg			1267
Glu Arg Gly Ile Leu Val Thr Ala Ile Ile Val Gly Leu Leu Ala Val			
375	380	385	
tta gct gtg ctg atg gga cta cgc cga att cat cat cac tcg gcc ttt			1315
Leu Ala Val Leu Met Gly Leu Arg Arg Ile His His His Ser Ala Phe			
390	395	400	405
caa aaa gct agc tca agt gtt atc act taatctatga ggcaccgttc aga			1365
Gln Lys Ala Ser Ser Ser Val Ile Thr			
410			

<210> 218

<211> 414

<212> PRT

<213> Corynebacterium glutamicum

<400> 218

Met Arg Arg Leu Ile Ala Val Ser Leu Ala Ala Leu Phe Met Leu Ala
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Ser Thr Pro Ala Thr Arg Ala Gln Glu Val Glu Ala Leu Ala Cys Pro
20 25 30

Glu Val Ala Ile Ala Asp Pro Ser Ser Ala Val Leu Asp Glu His Leu
35 40 45

Ser Gln Ser Leu Ser Gln Ala His Gln Leu Ala Thr Gly Ala Gly Val
50 55 60

Met Val Ala Val Ile Asp Thr Gly Val Ser Leu His Pro Arg Leu Pro
65 70 75 80

His Leu Ile Pro Gly Gly Asp Phe Val Gly Ala His Gln Ser Pro Asp
85 90 95

Val Pro Gly Glu Leu Ile Asp Cys Asp Gly His Gly Thr Ile Val Ala
100 105 110

Gly Ile Ile Ala Ser Gln Gly Asn Pro Gly Thr Gly Trp Pro Tyr Asp
 115 120 125
 Gly Ser Ser Asp Pro Tyr Ile Gly Val Ala Pro Asp Ser Gly Ile Ile
 130 135 140
 Ser Ile Lys Gln Thr Ser Ser Tyr Val Arg Thr Arg Glu Asp Ser Asn
 145 150 155 160
 Val Gly Thr Leu Ser Thr Leu Ala Glu Ser Ile His Arg Ala Leu Asp
 165 170 175
 Ser Gly Ala His Val Ile Asn Ile Ser Val Val Ser Cys Leu Pro Gln
 180 185 190
 Ser Pro Asp Glu Ala Ala Ser Phe Gln Pro Leu Thr Asp Ala Leu Asn
 195 200 205
 Arg Ala Glu Leu Gln Gly Val Ile Val Val Ala Ala Ala Gly Asn Leu
 210 215 220
 Gly Gln Asp Cys Pro Val Gly Ser Thr Val Tyr Pro Ala His Ser Asp
 225 230 235 240
 Thr Val Leu Ser Val Ser Ala Arg Phe Asp Ser His Thr Leu Ala Glu
 245 250 255
 Tyr Ser Met Pro Gly Asn Gln Gln Ile Leu Ser Ala Pro Ser His Ile
 260 265 270
 Gln Ala Gly Leu Ser Pro Arg Gly Asp Gly Phe Ala Ser His Met Ile
 275 280 285
 Thr Thr Ala Gly Glu Ser Pro Phe Glu Gly Thr Ser Phe Ala Ala Pro
 290 295 300
 Val Val Ser Ala Thr Ala Ala Leu Leu Arg Gln His Phe Pro Phe Ala
 305 310 315 320
 Thr Pro Tyr Glu Ile Arg Ala Arg Ile Phe Asn Ser Ile Asp Pro Ala
 325 330 335
 Arg Gly Ala Ile Asp Pro Tyr Leu Ala Leu Thr Gln Glu Ile Tyr Pro
 340 345 350
 Thr Thr Pro Leu Val His Glu Ile Ala Leu Ser Val Pro Thr Pro Pro
 355 360 365
 Asp Asp Ser Pro Arg Glu Arg Gly Ile Leu Val Thr Ala Ile Ile Val
 370 375 380
 Gly Leu Leu Ala Val Leu Ala Val Leu Met Gly Leu Arg Arg Ile His
 385 390 395 400
 His His Ser Ala Phe Gln Lys Ala Ser Ser Ser Val Ile Thr
 405 410

<210> 219

<211> 1098

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1075)

<223> RXA01728

<400> 219

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ggaaagtgat tttggcacct gccgcagtt gaaggaagct atg gca gat gcc gtt 115
 Met Ala Asp Ala Val
 1 5

gag cgc gag gtc ttc gga tac cca cca gat gct act ggg ttg aat gat 163
 Glu Arg Glu Val Phe Gly Tyr Pro Pro Asp Ala Thr Gly Leu Asn Asp
 10 15 20

gcg ttg act gga ttc tac gag cgt cgc tat ggg ttt ggc cca aat ccg 211
 Ala Leu Thr Gly Phe Tyr Glu Arg Arg Tyr Gly Phe Gly Pro Asn Pro
 25 30 35

gaa agt gtt ttc gcc att ccg gat gtg gtt cgt ggc ctg aag ctt gcc 259
 Glu Ser Val Phe Ala Ile Pro Asp Val Val Arg Gly Leu Lys Leu Ala
 40 45 50

att gag cat ttc act aag cct ggt tgc gcg atc att gtg ccg ttg cct 307
 Ile Glu His Phe Thr Lys Pro Gly Ser Ala Ile Ile Val Pro Leu Pro
 55 60 65

gca tac cct cct ttc att gag ttg cct aag gtg act ggt cgt cag gcg 355
 Ala Tyr Pro Pro Phe Ile Glu Leu Pro Lys Val Thr Gly Arg Gln Ala
 70 75 80 85

atc tac att gat gcg cat gag tac gat ttg aag gaa att gag aag gcc 403
 Ile Tyr Ile Asp Ala His Glu Tyr Asp Leu Lys Glu Ile Glu Lys Ala
 90 95 100

ttc gct gac ggt gcg gga tca ctg ttg ttc tgc aat cca cac aac cca 451
 Phe Ala Asp Gly Ala Gly Ser Leu Leu Phe Cys Asn Pro His Asn Pro
 105 110 115

ctg ggc acg gtc ttt tct gaa gag tac atc cgc gag ctc acc gat att 499
 Leu Gly Thr Val Phe Ser Glu Glu Tyr Ile Arg Glu Leu Thr Asp Ile
 120 125 130

gcg gcg aag tac gat gcc cgc atc atc gtc gat gag atc cac gcg cca 547
 Ala Ala Lys Tyr Asp Ala Arg Ile Ile Val Asp Glu Ile His Ala Pro
 135 140 145

ctg gtt tat gaa ggc acc cat gtg gtt gct gct ggt gtt tct gag aac 595
 Leu Val Tyr Glu Gly Thr His Val Val Ala Ala Gly Val Ser Glu Asn
 150 155 160 165

gct gca aac act tgc atc acc atc acc gca act tct aag gcg tgg aac 643
 Ala Ala Asn Thr Cys Ile Thr Ile Thr Ala Thr Ser Lys Ala Trp Asn
 170 175 180

act gct ggt ttg aag tgt gct cag atc ttc ttc agt aat gaa gcc gat 691
 Thr Ala Gly Leu Lys Cys Ala Gln Ile Phe Phe Ser Asn Glu Ala Asp

185										190										195																			
gtg	aag	gcc	tgg	aag	aat	ttg	tcg	gat	att	acc	cgt	gac	ggg	gtg	tcc	739																							
Val	Lys	Ala	Trp	Lys	Asn	Leu	Ser	Asp	Ile	Thr	Arg	Asp	Gly	Val	Ser																								
200										205										210																			
atc	ctt	gga	ttg	atc	gct	gcg	gag	aca	gtg	tac	aac	gag	ggc	gaa	gaa	787																							
Ile	Leu	Gly	Leu	Ile	Ala	Ala	Glu	Thr	Val	Tyr	Asn	Glu	Gly	Glu	Glu																								
215										220										225																			
ttc	ctt	gat	gag	tca	att	cag	att	ctc	aag	gac	aac	cgt	gac	ttt	gcg	835																							
Phe	Leu	Asp	Glu	Ser	Ile	Gln	Ile	Leu	Lys	Asp	Asn	Arg	Asp	Phe	Ala																								
230										235										240										245									
gct	gct	gaa	ctg	gaa	aag	ctt	ggc	gtg	aag	gtc	tac	gca	ccg	gac	tcc	883																							
Ala	Ala	Glu	Leu	Glu	Lys	Leu	Gly	Val	Lys	Val	Tyr	Ala	Pro	Asp	Ser																								
250										255										260																			
act	tat	ttg	atg	tgg	ttg	gac	ttc	gct	ggc	acc	aag	atc	gaa	gag	gcg	931																							
Thr	Tyr	Leu	Met	Trp	Leu	Asp	Phe	Ala	Gly	Thr	Lys	Ile	Glu	Glu	Ala																								
265										270										275																			
cct	tct	aaa	att	ctt	cgt	gag	gag	ggg	aag	gtc	atg	ctg	aat	gat	ggc	979																							
Pro	Ser	Lys	Ile	Leu	Arg	Glu	Glu	Gly	Lys	Val	Met	Leu	Asn	Asp	Gly																								
280										285										290																			
gca	gct	ttt	ggg	ggg	ttc	acc	acc	tgc	gct	cgt	ctt	aat	ttt	gcg	tgt	1027																							
Ala	Ala	Phe	Gly	Gly	Phe	Thr	Thr	Cys	Ala	Arg	Leu	Asn	Phe	Ala	Cys																								
295										300										305																			
tcc	aga	gag	acc	ctt	gag	gag	ggg	ctg	cgc	cgt	atc	gcc	agc	gtg	ttg	1075																							
Ser	Arg	Glu	Thr	Leu	Glu	Glu	Gly	Leu	Arg	Arg	Ile	Ala	Ser	Val	Leu																								
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<210> 220

<211> 325

<212> PRT

<213> Corynebacterium glutamicum

<400> 220

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Thr	Gly	Leu	Asn	Asp	Ala	Leu	Thr	Gly	Phe	Tyr	Glu	Arg	Arg	Tyr	Gly
		20						25					30		

Phe	Gly	Pro	Asn	Pro	Glu	Ser	Val	Phe	Ala	Ile	Pro	Asp	Val	Val	Arg
		35					40					45			

Gly	Leu	Lys	Leu	Ala	Ile	Glu	His	Phe	Thr	Lys	Pro	Gly	Ser	Ala	Ile
	50					55					60				

Ile	Val	Pro	Leu	Pro	Ala	Tyr	Pro	Pro	Phe	Ile	Glu	Leu	Pro	Lys	Val
65					70					75				80	

Thr	Gly	Arg	Gln	Ala	Ile	Tyr	Ile	Asp	Ala	His	Glu	Tyr	Asp	Leu	Lys
				85					90					95	

Glu Ile Glu Lys Ala Phe Ala Asp Gly Ala Gly Ser Leu Leu Phe Cys
 100 105 110
 Asn Pro His Asn Pro Leu Gly Thr Val Phe Ser Glu Glu Tyr Ile Arg
 115 120 125
 Glu Leu Thr Asp Ile Ala Ala Lys Tyr Asp Ala Arg Ile Ile Val Asp
 130 135 140
 Glu Ile His Ala Pro Leu Val Tyr Glu Gly Thr His Val Val Ala Ala
 145 150 155 160
 Gly Val Ser Glu Asn Ala Ala Asn Thr Cys Ile Thr Ile Thr Ala Thr
 165 170 175
 Ser Lys Ala Trp Asn Thr Ala Gly Leu Lys Cys Ala Gln Ile Phe Phe
 180 185 190
 Ser Asn Glu Ala Asp Val Lys Ala Trp Lys Asn Leu Ser Asp Ile Thr
 195 200 205
 Arg Asp Gly Val Ser Ile Leu Gly Leu Ile Ala Ala Glu Thr Val Tyr
 210 215 220
 Asn Glu Gly Glu Glu Phe Leu Asp Glu Ser Ile Gln Ile Leu Lys Asp
 225 230 235 240
 Asn Arg Asp Phe Ala Ala Ala Glu Leu Glu Lys Leu Gly Val Lys Val
 245 250 255
 Tyr Ala Pro Asp Ser Thr Tyr Leu Met Trp Leu Asp Phe Ala Gly Thr
 260 265 270
 Lys Ile Glu Glu Ala Pro Ser Lys Ile Leu Arg Glu Glu Gly Lys Val
 275 280 285
 Met Leu Asn Asp Gly Ala Ala Phe Gly Gly Phe Thr Thr Cys Ala Arg
 290 295 300
 Leu Asn Phe Ala Cys Ser Arg Glu Thr Leu Glu Glu Gly Leu Arg Arg
 305 310 315 320
 Ile Ala Ser Val Leu
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<210> 221

<211> 732

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(709)

<223> RXA02214

<400> 221

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 Met Ser Pro Thr Val

	1	5	
ttg cct gct aca caa gct gac ttc cct aag atc gtc gat gtt ctg gtt			163
Leu Pro Ala Thr Gln Ala Asp Phe Pro Lys Ile Val Asp Val Leu Val			
	10	20	
gaa gca ttc gcc aac gat cca gca ttt tta cga tgg atc ccg cag ccg			211
Glu Ala Phe Ala Asn Asp Pro Ala Phe Leu Arg Trp Ile Pro Gln Pro			
	25	35	
gac ccc ggt tca gca aag ctt cga gca ctt ttc gaa ctg cag att gag			259
Asp Pro Gly Ser Ala Lys Leu Arg Ala Leu Phe Glu Leu Gln Ile Glu			
	40	50	
aag cag tat gca gtg gcg gga aat att gat gtc gcg cgt gat tct gag			307
Lys Gln Tyr Ala Val Ala Gly Asn Ile Asp Val Ala Arg Asp Ser Glu			
	55	65	
gga gaa atc gtc ggc gtc gcg tta tgg gat cgg cca gat ggt aat cac			355
Gly Glu Ile Val Gly Val Ala Leu Trp Asp Arg Pro Asp Gly Asn His			
	70	80	85
agt gcc aaa gat caa gca gcg atg ctc ccc cgg ctc gtc tcc att ttc			403
Ser Ala Lys Asp Gln Ala Ala Met Leu Pro Arg Leu Val Ser Ile Phe			
	90	95	100
ggg atc aag gct gca cac gtg gcg tgg acg gat ttg agt tcg gct cgt			451
Gly Ile Lys Ala Ala His Val Ala Trp Thr Asp Leu Ser Ser Ala Arg			
	105	110	115
ttc cac ccc aaa ttc ccc cat tgg tac ctc tac acc gtg gca aca tct			499
Phe His Pro Lys Phe Pro His Trp Tyr Leu Tyr Thr Val Ala Thr Ser			
	120	125	130
agc tct gcc cgt gga acg gat gtt ggc agt gcg ctt ctt aat cac gga			547
Ser Ser Ala Arg Gly Thr Asp Val Gly Ser Ala Leu Leu Asn His Gly			
	135	140	145
atc gct cgc gcg gct gat gaa gct atc tat ttg gag gcg acg ccg act			595
Ile Ala Arg Ala Ala Asp Glu Ala Ile Tyr Leu Glu Ala Thr Pro Thr			
	150	155	160
cgt gcg gct caa cta tat aac cgt ctg gga ttc gtg ccc ttg ggt tat			643
Arg Ala Ala Gln Leu Tyr Asn Arg Leu Gly Phe Val Pro Leu Gly Tyr			
	170	175	180
atc ccc tca gat gat gat ggc act cct gaa ctg gcg atg tgg aaa ccg			691
Ile Pro Ser Asp Asp Asp Gly Thr Pro Glu Leu Ala Met Trp Lys Pro			
	185	190	195
cca gcg atg cca act gtt taaccctgaa ggcgatttaa ggg			732
Pro Ala Met Pro Thr Val			
	200		

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<211> 203

<212> PRT

<213> Corynebacterium glutamicum

<400> 222

Met Ser Pro Thr Val Leu Pro Ala Thr Gln Ala Asp Phe Pro Lys Ile
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 Val Asp Val Leu Val Glu Ala Phe Ala Asn Asp Pro Ala Phe Leu Arg
 20 25 30
 Trp Ile Pro Gln Pro Asp Pro Gly Ser Ala Lys Leu Arg Ala Leu Phe
 35 40 45
 Glu Leu Gln Ile Glu Lys Gln Tyr Ala Val Ala Gly Asn Ile Asp Val
 50 55 60
 Ala Arg Asp Ser Glu Gly Glu Ile Val Gly Val Ala Leu Trp Asp Arg
 65 70 75 80
 Pro Asp Gly Asn His Ser Ala Lys Asp Gln Ala Ala Met Leu Pro Arg
 85 90 95
 Leu Val Ser Ile Phe Gly Ile Lys Ala Ala His Val Ala Trp Thr Asp
 100 105 110
 Leu Ser Ser Ala Arg Phe His Pro Lys Phe Pro His Trp Tyr Leu Tyr
 115 120 125
 Thr Val Ala Thr Ser Ser Ser Ala Arg Gly Thr Asp Val Gly Ser Ala
 130 135 140
 Leu Leu Asn His Gly Ile Ala Arg Ala Ala Asp Glu Ala Ile Tyr Leu
 145 150 155 160
 Glu Ala Thr Pro Thr Arg Ala Ala Gln Leu Tyr Asn Arg Leu Gly Phe
 165 170 175
 Val Pro Leu Gly Tyr Ile Pro Ser Asp Asp Asp Gly Thr Pro Glu Leu
 180 185 190
 Ala Met Trp Lys Pro Pro Ala Met Pro Thr Val
 195 200

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 <211> 684
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(661)
 <223> RXA02716

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 Val Ser Pro Ile Ile
 1 5

cgt aaa ttg agt atc ccc gag ttc acc acc aac acc cca gtg ttg gtg 163
 Arg Lys Leu Ser Ile Pro Glu Phe Thr Thr Asn Thr Pro Val Leu Val
 10 15 20

gat atc tac atc gca gcg atg aac tat gac aaa gca atc agg gat acc 211
Asp Ile Tyr Ile Ala Ala Met Asn Tyr Asp Lys Ala Ile Arg Asp Thr
25 30 35

cgg atc gaa gtc tgg cgg aga aac tcc cag aac ccc gga ttc aca gca 259
Arg Ile Glu Val Trp Arg Arg Asn Ser Gln Asn Pro Gly Phe Thr Ala
40 45 50

gtg gca gcg ctg atg gat gat cag gtc gtg ggc gtg gcc tat ggc ttc 307
Val Ala Ala Leu Met Asp Asp Gln Val Val Gly Val Ala Tyr Gly Phe
55 60 65

aat ggc agc cca gat cat tgg tgg caa cac caa tta cgc cgg gga ctc 355
Asn Gly Ser Pro Asp His Trp Trp Gln His Gln Leu Arg Arg Gly Leu
70 75 80 85

cga caa caa gga ggc ccg acg gaa gag gaa atc cat atc atc cac aac 403
Arg Gln Gln Gly Gly Pro Thr Glu Glu Glu Ile His Ile Ile His Asn
90 95 100

tac ttt gag gtt gcg gaa gtt cat gtt cag cct ggc ttc caa ggt cac 451
Tyr Phe Glu Val Ala Glu Val His Val Gln Pro Gly Phe Gln Gly His
105 110 115

ggc att ggc cga aag ctg atg cat gaa ctg tta aaa gac aaa caa aac 499
Gly Ile Gly Arg Lys Leu Met His Glu Leu Leu Lys Asp Lys Gln Asn
120 125 130

act ttt gcc att ttg tct aca ccc gag gtc gac gat gag gcg aac cat 547
Thr Phe Ala Ile Leu Ser Thr Pro Glu Val Asp Asp Glu Ala Asn His
135 140 145

gcg ttt agc ctg tat cgc tct ctc ggc ttc act gac ttg ctc agg cag 595
Ala Phe Ser Leu Tyr Arg Ser Leu Gly Phe Thr Asp Leu Leu Arg Gln
150 155 160 165

ttt agg ttt gac ggg gat caa cgg ccg ttt gcc gta ttg atc acc gcc 643
Phe Arg Phe Asp Gly Asp Gln Arg Pro Phe Ala Val Leu Ile Thr Ala
170 175 180

ctc ccc ctt cat gat tcc taagagggct taacgcaccg cgt 684
Leu Pro Leu His Asp Ser
185

<210> 224

<211> 187

<212> PRT

<213> Corynebacterium glutamicum

<400> 224

Val Ser Pro Ile Ile Arg Lys Leu Ser Ile Pro Glu Phe Thr Thr Asn
1 5 10 15

Thr Pro Val Leu Val Asp Ile Tyr Ile Ala Ala Met Asn Tyr Asp Lys
20 25 30

Ala Ile Arg Asp Thr Arg Ile Glu Val Trp Arg Arg Asn Ser Gln Asn
35 40 45

Pro Gly Phe Thr Ala Val Ala Ala Leu Met Asp Asp Gln Val Val Gly

50	55	60
Val Ala Tyr Gly Phe Asn Gly Ser Pro Asp His Trp Trp Gln His Gln 65 70 75 80		
Leu Arg Arg Gly Leu Arg Gln Gln Gly Gly Pro Thr Glu Glu Glu Ile 85 90 95		
His Ile Ile His Asn Tyr Phe Glu Val Ala Glu Val His Val Gln Pro 100 105 110		
Gly Phe Gln Gly His Gly Ile Gly Arg Lys Leu Met His Glu Leu Leu 115 120 125		
Lys Asp Lys Gln Asn Thr Phe Ala Ile Leu Ser Thr Pro Glu Val Asp 130 135 140		
Asp Glu Ala Asn His Ala Phe Ser Leu Tyr Arg Ser Leu Gly Phe Thr 145 150 155 160		
Asp Leu Leu Arg Gln Phe Arg Phe Asp Gly Asp Gln Arg Pro Phe Ala 165 170 175		
Val Leu Ile Thr Ala Leu Pro Leu His Asp Ser 180 185		

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 <212> DNA
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 <222> (101)..(3922)
 <223> RXN01499

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 Leu Trp Asp Val Leu
 1 5
 gaa tcc gtc gcc tct act tat cct gag gca gca gct att gac gat ggc 163
 Glu Ser Val Ala Ser Thr Tyr Pro Glu Ala Ala Ala Ile Asp Asp Gly
 10 15 20
 cag gtg ttg acc tac gca gag ttg atg gaa gaa gtc acc gcg ttg gct 211
 Gln Val Leu Thr Tyr Ala Glu Leu Met Glu Glu Val Thr Ala Leu Ala
 25 30 35
 gat tcc att cat gca cag ggc att cgc cgt ggt gat cgc atc ggt att 259
 Asp Ser Ile His Ala Gln Gly Ile Arg Arg Gly Asp Arg Ile Gly Ile
 40 45 50
 cgc atg ccg tct ggt acg cgt gac ctt tac atc gct att ttg gcc act 307
 Arg Met Pro Ser Gly Thr Arg Asp Leu Tyr Ile Ala Ile Leu Ala Thr
 55 60 65
 ctc gct gct ggt gct gct tac gtg cca gtt gat gca gat gat cct gaa 355

Leu	Ala	Ala	Gly	Ala	Ala	Tyr	Val	Pro	Val	Asp	Ala	Asp	Asp	Pro	Glu	
70					75					80					85	
gag	cgc	gcc	gag	atg	gtg	ttt	ggt	gaa	gca	aat	att	aat	gcg	ctt	ttc	403
Glu	Arg	Ala	Glu	Met	Val	Phe	Gly	Glu	Ala	Asn	Ile	Asn	Ala	Leu	Phe	
				90					95					100		
gac	gcc	acc	ggc	ttc	cat	atg	ctt	cgc	ccg	acc	gcg	ggc	ggc	gat	acc	451
Asp	Ala	Thr	Gly	Phe	His	Met	Leu	Arg	Pro	Thr	Ala	Gly	Gly	Asp	Thr	
			105					110					115			
cgt	aga	cca	cgc	ttg	gat	gat	acg	gcg	tgg	att	atc	ttt	act	tcc	ggt	499
Arg	Arg	Pro	Arg	Leu	Asp	Asp	Thr	Ala	Trp	Ile	Ile	Phe	Thr	Ser	Gly	
		120					125					130				
tcc	acc	ggc	aag	cct	aag	ggt	gtg	gct	gtg	tcc	cac	cgt	tca	gct	gcg	547
Ser	Thr	Gly	Lys	Pro	Lys	Gly	Val	Ala	Val	Ser	His	Arg	Ser	Ala	Ala	
	135					140					145					
gct	ttc	gtg	gat	gcc	gaa	gca	caa	atg	ttc	ctt	gtc	gat	cac	cct	tcc	595
Ala	Phe	Val	Asp	Ala	Glu	Ala	Gln	Met	Phe	Leu	Val	Asp	His	Pro	Ser	
150					155					160					165	
ggc	ccc	ctt	ggc	cca	gaa	gac	cga	gtc	ctt	gcg	gga	ttg	tct	gta	gcc	643
Gly	Pro	Leu	Gly	Pro	Glu	Asp	Arg	Val	Leu	Ala	Gly	Leu	Ser	Val	Ala	
				170					175					180		
ttt	gac	gca	tct	tgt	gag	gaa	atg	tgg	ttg	gcc	tgg	ggc	cac	ggc	gcc	691
Phe	Asp	Ala	Ser	Cys	Glu	Glu	Met	Trp	Leu	Ala	Trp	Gly	His	Gly	Ala	
			185					190					195			
tgc	ttg	gtg	cca	gca	cca	cgc	tcc	cta	gtc	cgt	tcc	ggt	atg	gac	ttg	739
Cys	Leu	Val	Pro	Ala	Pro	Arg	Ser	Leu	Val	Arg	Ser	Gly	Met	Asp	Leu	
		200					205					210				
ggc	cca	tgg	ctg	att	cgc	cgc	gac	atc	agt	gtc	gtc	tcc	acc	gtc	cca	787
Gly	Pro	Trp	Leu	Ile	Arg	Arg	Asp	Ile	Ser	Val	Val	Ser	Thr	Val	Pro	
	215					220					225					
act	ctg	gct	ggt	ctg	tgg	cca	gca	gaa	gca	ttg	tca	cag	gtc	cgc	ttg	835
Thr	Leu	Ala	Gly	Leu	Trp	Pro	Ala	Glu	Ala	Leu	Ser	Gln	Val	Arg	Leu	
230					235					240					245	
ctc	atc	gtc	ggc	ggc	gag	gct	tgc	tcg	cag	gag	ctc	gtt	gaa	cgc	tta	883
Leu	Ile	Val	Gly	Gly	Glu	Ala	Cys	Ser	Gln	Glu	Leu	Val	Glu	Arg	Leu	
				250					255					260		
tcg	acg	cct	gac	cgc	gag	gtg	tgg	aac	act	tac	ggc	ccc	acc	gaa	gca	931
Ser	Thr	Pro	Asp	Arg	Glu	Val	Trp	Asn	Thr	Tyr	Gly	Pro	Thr	Glu	Ala	
			265					270					275			
acg	gtg	gtt	gcc	tgt	ggc	act	caa	ctc	tat	gct	ggt	cag	cca	gtg	ggc	979
Thr	Val	Val	Ala	Cys	Gly	Thr	Gln	Leu	Tyr	Ala	Gly	Gln	Pro	Val	Gly	
		280					285					290				
att	ggt	ttg	cca	ctt	gct	ggt	tgg	gat	ctt	ggt	ggt	gtc	gac	gat	gcc	1027
Ile	Gly	Leu	Pro	Leu	Ala	Gly	Trp	Asp	Leu	Val	Val	Val	Asp	Asp	Ala	
	295					300					305					
ggc	gaa	cct	gtc	gga	atc	ggc	gag	gtc	ggc	gaa	ttg	gtc	atc	ggt	ggt	1075
Gly	Glu	Pro	Val	Gly	Ile	Gly	Glu	Val	Gly	Glu	Leu	Val	Ile	Gly	Gly	

310	315	320	325	
gtg ggt ctt gca cgc tac ctt gat cca gaa aaa gac cgc gag aag tat				1123
Val Gly Leu Ala Arg Tyr Leu Asp Pro Glu Lys Asp Arg Glu Lys Tyr	330	335	340	
gcg cca ctg aag tct gtt ggt tgg acc cgc gct tat cgt tcc ggt gac				1171
Ala Pro Leu Lys Ser Val Gly Trp Thr Arg Ala Tyr Arg Ser Gly Asp	345	350	355	
cac gtt cgt ctg gaa gaa gat ggc ctc tac ttt gtg ggc cgc gtt gat				1219
His Val Arg Leu Glu Glu Asp Gly Leu Tyr Phe Val Gly Arg Val Asp	360	365	370	
gat cag gtg aaa atc ggc ggt cga cgc atc gag ctc ggt gaa gtt gat				1267
Asp Gln Val Lys Ile Gly Gly Arg Arg Ile Glu Leu Gly Glu Val Asp	375	380	385	
gcc aat gtg gca gcg ctt tcc aac gtt cgt tcc tcc gca gtg gtt gtt				1315
Ala Asn Val Ala Ala Leu Ser Asn Val Arg Ser Ser Ala Val Val Val	390	395	400	405
cag acc act ggt gcg gat caa aaa gtt ctg gtt gca tac gtt tct ttg				1363
Gln Thr Thr Gly Ala Asp Gln Lys Val Leu Val Ala Tyr Val Ser Leu	410	415	420	
gaa gat gct gca gct gga ttt gat cac aac gtc gcg act gcc cga ctc				1411
Glu Asp Ala Ala Ala Gly Phe Asp His Asn Val Ala Thr Ala Arg Leu	425	430	435	
acc gaa acc atg cct gct gct ttg gtt ccg cgc att cac gtg atg gat				1459
Thr Glu Thr Met Pro Ala Ala Leu Val Pro Arg Ile His Val Met Asp	440	445	450	
gat ctg cct gtc acc acc tcc ggc aag gtt gat aag aag tct ttg ccg				1507
Asp Leu Pro Val Thr Thr Ser Gly Lys Val Asp Lys Lys Ser Leu Pro	455	460	465	
tgg cct ctt cct ggc acc gtg gtg gaa gct aat gac ctc agc gca acg				1555
Trp Pro Leu Pro Gly Thr Val Val Glu Ala Asn Asp Leu Ser Ala Thr	470	475	480	485
gaa gcg tgg att gct cag gaa tgg gtc gat atc ctc ggc act tct gtg				1603
Glu Ala Trp Ile Ala Gln Glu Trp Val Asp Ile Leu Gly Thr Ser Val	490	495	500	
agc agc aaa gac gcc gac ttc ttc tcc ctt ggc ggt acc tct ctc gcg				1651
Ser Ser Lys Asp Ala Asp Phe Phe Ser Leu Gly Gly Thr Ser Leu Ala	505	510	515	
gct gcg act ttg gtt ggc cgg gta cgc gca aag gtt ccc acc gct gcg				1699
Ala Ala Thr Leu Val Gly Arg Val Arg Ala Lys Val Pro Thr Ala Ala	520	525	530	
gtg cgt gat ctt tac gat cac cct cgc ttg gag aaa ttc gcc gag cgt				1747
Val Arg Asp Leu Tyr Asp His Pro Arg Leu Glu Lys Phe Ala Glu Arg	535	540	545	
gtc gag gct atc gcc gcc gac act ggc att tct ttg gag gcg cca aac				1795
Val Glu Ala Ile Ala Ala Asp Thr Gly Ile Ser Leu Glu Ala Pro Asn	550	555	560	565

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Gln	Val	Glu	Glu	Arg	Val	Val	Lys	Pro	Val	Ser	Phe	Gly	Thr	Arg	Val	
				570					575					580		
atg	cag	acc	ctc	atc	cag	att	ccg	atc	atg	acg	ctg	caa	gca	gca	cag	1891
Met	Gln	Thr	Leu	Ile	Gln	Ile	Pro	Ile	Met	Thr	Leu	Gln	Ala	Ala	Gln	
			585					590					595			
tgg	att	gca	tgg	ttg	ctg	ttg	ggc	aac	aac	atc	atg	gca	gcg	ctt	gat	1939
Trp	Ile	Ala	Trp	Leu	Leu	Leu	Gly	Asn	Asn	Ile	Met	Ala	Ala	Leu	Asp	
		600					605					610				
ttc	gat	tgg	gct	gtt	cat	gtc	tcc	tgg	tgg	ctt	gtc	atc	ggc	atg	att	1987
Phe	Asp	Trp	Ala	Val	His	Val	Ser	Trp	Trp	Leu	Val	Ile	Gly	Met	Ile	
	615					620					625					
ttg	gtg	ttc	gct	acc	ccg	att	ggg	cgc	ttg	ccg	atc	ggc	ggg	tgg	ggc	2035
Leu	Val	Phe	Ala	Thr	Pro	Ile	Gly	Arg	Leu	Pro	Ile	Gly	Gly	Trp	Gly	
630					635					640					645	
gcc	cgc	atc	atc	acc	cgt	ggc	ata	act	cct	ggc	tcc	tac	cct	cgt	ggc	2083
Ala	Arg	Ile	Ile	Thr	Arg	Gly	Ile	Thr	Pro	Gly	Ser	Tyr	Pro	Arg	Gly	
				650					655					660		
ggt	tcc	act	cac	ctg	cgc	att	tgg	tcc	gcc	gag	cgc	ctt	gct	gat	gcc	2131
Gly	Ser	Thr	His	Leu	Arg	Ile	Trp	Ser	Ala	Glu	Arg	Leu	Ala	Asp	Ala	
			665					670					675			
tct	ggc	tct	cgc	aat	att	tct	ggc	gca	acc	tgg	gtg	aac	tac	ttc	gcg	2179
Ser	Gly	Ser	Arg	Asn	Ile	Ser	Gly	Ala	Thr	Trp	Val	Asn	Tyr	Phe	Ala	
		680					685					690				
cgt	tcc	ctg	ggg	gtg	aag	atg	ggc	aag	ggc	gtg	gat	ctt	cac	tcc	ctg	2227
Arg	Ser	Leu	Gly	Val	Lys	Met	Gly	Lys	Gly	Val	Asp	Leu	His	Ser	Leu	
	695					700					705					
cca	cca	atc	act	ggc	ctt	ttg	acc	ttg	ggc	aac	aat	gtt	tcc	atc	gag	2275
Pro	Pro	Ile	Thr	Gly	Leu	Leu	Thr	Leu	Gly	Asn	Asn	Val	Ser	Ile	Glu	
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caa	gaa	gtt	gac	ctt	cgt	ggc	tac	tgg	ctc	gac	ggc	gat	atc	ctg	cgt	2323
Gln	Glu	Val	Asp	Leu	Arg	Gly	Tyr	Trp	Leu	Asp	Gly	Asp	Ile	Leu	Arg	
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gta	ggc	acc	att	gag	gtc	cat	gac	aac	gct	cgc	atc	ggc	gct	cgt	tcc	2371
Val	Gly	Thr	Ile	Glu	Val	His	Asp	Asn	Ala	Arg	Ile	Gly	Ala	Arg	Ser	
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Thr	Leu	Leu	Pro	Gly	Thr	Val	Val	Gly	Thr	Gly	Ala	His	Leu	Leu	Pro	
		760					765					770				
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Gly	Ser	Thr	Val	Thr	Gly	Asp	Lys	Thr	Ile	Lys	Pro	Gly	Ser	Arg	Trp	
	775					780					785					
gct	ggc	tcc	cct	gca	caa	aag	gtg	ggg	cgt	gca	aag	cac	cgg	ttc	cca	2515
Ala	Gly	Ser	Pro	Ala	Gln	Lys	Val	Gly	Arg	Ala	Lys	His	Arg	Phe	Pro	
790					795					800					805	

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Thr Ser His Pro Pro Arg Arg Ser Arg Trp Val Pro Val Phe Gly Ala	
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Thr Ser Ile Val Leu Ser Leu Leu Pro Leu Gln Ala Leu Ala Ile Gly	
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Ala Ala Ile Thr Leu Trp Leu Ala Thr Ile Ser Pro Leu Pro Leu Ile	
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Trp Gly Val Leu Val Phe Ala Thr Val Gly Ala Leu Ala Ala Phe Phe	
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Ala Tyr Thr Val Thr Ile Trp Val Leu Val Arg Leu Ile Gln Ile Gly	
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Ile Lys Gly Gly Thr Ala Pro Val Arg Ser Arg Leu Gly Trp Gln Val	
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Lys Ile Gly Lys Asp Val Glu Ile Ser Thr Ala Val Met Val Pro Lys	
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Arg Lys Leu Ala Lys Asn Ser Leu Val Ala Val Leu Ser Ser Thr Pro	
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Lys Lys Ala Lys Ala Asn Ser Asn Trp Trp Gly Ser Pro Pro Glu Arg	
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Met Arg Arg Val Thr Val Glu Val Asp Glu Gly Glu Ala Lys Thr Tyr	
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Ser Pro Gly Phe Gly Val Lys Phe Ala Arg Gly Ala Val Glu Thr Ala
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ctg ctc atg cag tac ctg ctc act gag ttc aac atg tgg atc acc tgg 3379
Leu Leu Met Gln Tyr Leu Leu Thr Glu Phe Asn Met Trp Ile Thr Trp
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Leu Leu Gly Gly Leu Ile Leu Met Thr Val Gly Val Leu Ala Met Gly
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Glu His Pro Leu Phe Ser Arg Phe Val Trp Leu Asn Glu Leu Gln Asp
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gcg ttc gtg gaa tcc gtg gct ggc cca tgg ttc ctc gtg ccc aac ctg 3571
Ala Phe Val Glu Ser Val Ala Gly Pro Trp Phe Leu Val Pro Asn Leu
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ggc acc ggc gcg ctg aac gcc ggc atg agc gcg ctt ggc gca cac atc 3619
Gly Thr Gly Ala Leu Asn Ala Gly Met Ser Ala Leu Gly Ala His Ile
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Gly Arg Gly Ala Trp Ile Glu Ser Tyr Trp Leu Pro Glu Thr Asp Leu
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Cys Tyr Ile Gly Lys Gly Ala Thr Val Gly Pro Gly Val Val Val Gln
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acc cac ctc ttc cag gac cgc gtg atg agc cta gat acg gtg acc gtc 3763
Thr His Leu Phe Gln Asp Arg Val Met Ser Leu Asp Thr Val Thr Val
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Ala Asp Gly Ala Thr Leu Ala Asp His Ser Val Ala Leu Pro Ala Ser
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Leu Ile Asp Ala Ser Ala Thr Ile Gly Pro Gly Ser Leu Val Met Arg
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Gly Asp Lys Val Pro Ala His Thr Arg Trp Gln Gly Asn Pro Ile Glu
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Val Thr Ala Leu Ala Asp Ser Ile His Ala Gln Gly Ile Arg Arg Gly
      35          40          45

Asp Arg Ile Gly Ile Arg Met Pro Ser Gly Thr Arg Asp Leu Tyr Ile
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Ala Ile Leu Ala Thr Leu Ala Ala Gly Ala Ala Tyr Val Pro Val Asp
      65          70          75          80

Ala Asp Asp Pro Glu Glu Arg Ala Glu Met Val Phe Gly Glu Ala Asn
          85          90          95

Ile Asn Ala Leu Phe Asp Ala Thr Gly Phe His Met Leu Arg Pro Thr
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Ala Gly Gly Asp Thr Arg Arg Pro Arg Leu Asp Asp Thr Ala Trp Ile
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Ile Phe Thr Ser Gly Ser Thr Gly Lys Pro Lys Gly Val Ala Val Ser
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His Arg Ser Ala Ala Ala Phe Val Asp Ala Glu Ala Gln Met Phe Leu
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Val Asp His Pro Ser Gly Pro Leu Gly Pro Glu Asp Arg Val Leu Ala
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Gly Leu Ser Val Ala Phe Asp Ala Ser Cys Glu Glu Met Trp Leu Ala
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Trp Gly His Gly Ala Cys Leu Val Pro Ala Pro Arg Ser Leu Val Arg
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Ser Gly Met Asp Leu Gly Pro Trp Leu Ile Arg Arg Asp Ile Ser Val
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Val Ser Thr Val Pro Thr Leu Ala Gly Leu Trp Pro Ala Glu Ala Leu
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Ser Gln Val Arg Leu Leu Ile Val Gly Gly Glu Ala Cys Ser Gln Glu
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Gly Pro Thr Glu Ala Thr Val Val Ala Cys Gly Thr Gln Leu Tyr Ala
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Gly Gln Pro Val Gly Ile Gly Leu Pro Leu Ala Gly Trp Asp Leu Val
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Val	Val	Asp	Asp	Ala	Gly	Glu	Pro	Val	Gly	Ile	Gly	Glu	Val	Gly	Glu		305	310	315	320
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Asp	Arg	Glu	Lys	Tyr	Ala	Pro	Leu	Lys	Ser	Val	Gly	Trp	Thr	Arg	Ala		340		345	350
Tyr	Arg	Ser	Gly	Asp	His	Val	Arg	Leu	Glu	Glu	Asp	Gly	Leu	Tyr	Phe		355	360	365	
Val	Gly	Arg	Val	Asp	Asp	Gln	Val	Lys	Ile	Gly	Gly	Arg	Arg	Ile	Glu		370	375	380	
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Ser	Ala	Val	Val	Val	Gln	Thr	Thr	Gly	Ala	Asp	Gln	Lys	Val	Leu	Val			405	410	415
Ala	Tyr	Val	Ser	Leu	Glu	Asp	Ala	Ala	Ala	Gly	Phe	Asp	His	Asn	Val			420	425	430
Ala	Thr	Ala	Arg	Leu	Thr	Glu	Thr	Met	Pro	Ala	Ala	Leu	Val	Pro	Arg		435	440	445	
Ile	His	Val	Met	Asp	Asp	Leu	Pro	Val	Thr	Thr	Ser	Gly	Lys	Val	Asp		450	455	460	
Lys	Lys	Ser	Leu	Pro	Trp	Pro	Leu	Pro	Gly	Thr	Val	Val	Glu	Ala	Asn		465	470	475	480
Asp	Leu	Ser	Ala	Thr	Glu	Ala	Trp	Ile	Ala	Gln	Glu	Trp	Val	Asp	Ile			485	490	495
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Gly	Thr	Ser	Leu	Ala	Ala	Ala	Thr	Leu	Val	Gly	Arg	Val	Arg	Ala	Lys		515	520	525	
Val	Pro	Thr	Ala	Ala	Val	Arg	Asp	Leu	Tyr	Asp	His	Pro	Arg	Leu	Glu		530	535	540	
Lys	Phe	Ala	Glu	Arg	Val	Glu	Ala	Ile	Ala	Ala	Asp	Thr	Gly	Ile	Ser		545	550	555	560
Leu	Glu	Ala	Pro	Asn	Gln	Val	Glu	Glu	Arg	Val	Val	Lys	Pro	Val	Ser			565	570	575
Phe	Gly	Thr	Arg	Val	Met	Gln	Thr	Leu	Ile	Gln	Ile	Pro	Ile	Met	Thr		580	585	590	
Leu	Gln	Ala	Ala	Gln	Trp	Ile	Ala	Trp	Leu	Leu	Leu	Gly	Asn	Asn	Ile		595	600	605	
Met	Ala	Ala	Leu	Asp	Phe	Asp	Trp	Ala	Val	His	Val	Ser	Trp	Trp	Leu		610	615	620	

Val Ile Gly Met Ile Leu Val Phe Ala Thr Pro Ile Gly Arg Leu Pro
 625 630 635 640
 Ile Gly Gly Trp Gly Ala Arg Ile Ile Thr Arg Gly Ile Thr Pro Gly
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 Ser Tyr Pro Arg Gly Gly Ser Thr His Leu Arg Ile Trp Ser Ala Glu
 660 665 670
 Arg Leu Ala Asp Ala Ser Gly Ser Arg Asn Ile Ser Gly Ala Thr Trp
 675 680 685
 Val Asn Tyr Phe Ala Arg Ser Leu Gly Val Lys Met Gly Lys Gly Val
 690 695 700
 Asp Leu His Ser Leu Pro Pro Ile Thr Gly Leu Leu Thr Leu Gly Asn
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 Asn Val Ser Ile Glu Gln Glu Val Asp Leu Arg Gly Tyr Trp Leu Asp
 725 730 735
 Gly Asp Ile Leu Arg Val Gly Thr Ile Glu Val His Asp Asn Ala Arg
 740 745 750
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 755 760 765
 Ala His Leu Leu Pro Gly Ser Thr Val Thr Gly Asp Lys Thr Ile Lys
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 Pro Gly Ser Arg Trp Ala Gly Ser Pro Ala Gln Lys Val Gly Arg Ala
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 Lys His Arg Phe Pro Thr Ser His Pro Pro Arg Arg Ser Arg Trp Val
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 Pro Val Phe Gly Ala Thr Ser Ile Val Leu Ser Leu Leu Pro Leu Gln
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 Pro Leu Pro Leu Ile Trp Gly Val Leu Val Phe Ala Thr Val Gly Ala
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 865 870 875 880
 Leu Ile Gln Ile Gly Ile Lys Gly Gly Thr Ala Pro Val Arg Ser Arg
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 Thr Tyr Leu Phe Pro Leu Tyr Ala Ser Gln Leu Thr Pro Leu Trp Phe
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 Arg Ser Leu Gly Ala Lys Ile Gly Lys Asp Val Glu Ile Ser Thr Ala
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 Val Met Val Pro Lys Leu Ala Asp Ile Arg Glu Gly Ala Phe Leu Ala

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Ser Gly Glu Thr Arg Val Gly Lys Arg Ser Phe Ile Gly Asn Ser Gly	980	985	990
Ile Ala Gly Pro Glu Arg Lys Leu Ala Lys Asn Ser Leu Val Ala Val	995	1000	1005
Leu Ser Ser Thr Pro Lys Lys Ala Lys Ala Asn Ser Asn Trp Trp Gly	1010	1015	1020
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Ala Ala Leu Ser Leu Leu Leu Met Gln Tyr Leu Leu Thr Glu Phe Asn	1075	1080	1085
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Val Leu Ala Met Gly Ile Thr Val Val Met Lys Trp Val Cys Val Gly	1105	1110	1115
Lys His Lys Pro Ser Glu His Pro Leu Phe Ser Arg Phe Val Trp Leu	1125	1130	1135
Asn Glu Leu Gln Asp Ala Phe Val Glu Ser Val Ala Gly Pro Trp Phe	1140	1145	1150
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Leu Gly Ala His Ile Gly Arg Gly Ala Trp Ile Glu Ser Tyr Trp Leu	1170	1175	1180
Pro Glu Thr Asp Leu Cys Tyr Ile Gly Lys Gly Ala Thr Val Gly Pro	1185	1190	1195
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Ala Leu Pro Ala Ser Leu Ile Asp Ala Ser Ala Thr Ile Gly Pro Gly	1235	1240	1245
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Glu Ala Trp Ile Ala Gln Glu Trp Val Asp Ile Leu Gly Thr Ser Val	
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Ser Ser Lys Asp Ala Asp Phe Phe Ser Leu Gly Gly Thr Ser Leu Ala	
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Ala Ala Thr Leu Val Gly Arg Val Arg Ala Lys Val Pro Thr Ala Ala	
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Val Glu Ala Ile Ala Ala Asp Thr Gly Ile Ser Leu Glu Ala Pro Asn	
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Gln Val Glu Glu Arg Val Val Lys Pro Val Ser Phe Gly Thr Arg Val	
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Met Gln Thr Leu Ile Gln Ile Pro Ile Met Thr Leu Gln Ala Ala Gln	
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Trp Ile Ala Trp Leu Leu Leu Gly Asn Asn Ile Met Ala Ala Leu Asp	
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Phe Asp Trp Ala Val His Val Ser Trp Trp Leu Val Ile Gly Met Ile	
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Ala Arg Ile Ile Thr Arg Gly Ile Thr Pro Gly Ser Tyr Pro Arg Gly	
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Gly Ser Thr His Leu Arg Ile Trp Ser Ala Glu Arg Leu Ala Asp Ala	
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Ser Gly Ser Arg Asn Ile Ser Gly Ala Thr Trp Val Asn Tyr Phe Ala	
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Arg Ser Leu Gly Val Lys Met Gly Lys Gly Val Asp Leu His Ser Leu	
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Pro Pro Ile Thr Gly Leu Leu Thr Leu Gly Asn Asn Val Ser Ile Glu	
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Gln Glu Val Asp Leu Arg Gly Tyr Trp Leu Asp Gly Asp Ile Leu Arg	
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Val Gly Thr Ile Glu Val His Asp Asn Ala Arg Ile Gly Ala Arg Ser	
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Ile Lys Gly Gly Thr Ala Pro Val Arg Ser Arg Leu Gly Trp Gln Val	
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cgc	aag	ctc	gct	aag	aac	tcc	ctg	gtt	gca	gtg	ctc	tcc	tcc	acc	ccg	3139	
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Lys	Lys	Ala	Lys	Ala	Asn	Ser	Asn	Trp	Trp	Gly	Ser	Pro	Pro	Glu	Arg		
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gcg	ttc	gtg	gaa	tcc	gtg	gct	ggc	cca	tgg	ttc	ctc	gtg	ccc	aac	ctg	3571	
Ala	Phe	Val	Glu	Ser	Val	Ala	Gly	Pro	Trp	Phe	Leu	Val	Pro	Asn	Leu		

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Gly Thr Gly Ala Leu Asn Ala Gly Met Ser Ala Leu Gly Ala His Ile			
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Cys Tyr Ile Gly Lys Gly Ala Thr Val Gly Pro Gly Val Val Val Gln			
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Thr His Leu Phe Gln Asp Arg Val Met Ser Leu Asp Thr Val Thr Val			
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Ala Asp Gly Ala Thr Leu Ala Asp His Ser Val Ala Leu Pro Ala Ser			
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Leu Ile Asp Ala Ser Ala Thr Ile Gly Pro Gly Ser Leu Val Met Arg			
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Gly Asp Lys Val Pro Ala His Thr Arg Trp Gln Gly Asn Pro Ile Glu			
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Val Thr Ala Leu Ala Asp Ser Ile His Ala Gln Gly Ile Arg Arg Gly			
35	40	45	
Asp Arg Ile Gly Ile Arg Met Pro Ser Gly Thr Arg Asp Leu Tyr Ile			
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Ala Ile Leu Ala Thr Leu Ala Ala Gly Ala Ala Tyr Val Pro Val Asp			
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Ala Asp Asp Pro Glu Glu Arg Ala Glu Met Val Phe Gly Glu Ala Asn			
85	90	95	
Ile Asn Ala Leu Phe Asp Ala Thr Gly Phe His Met Leu Arg Pro Thr			
100	105	110	

Ala	Gly	Gly	Asp	Thr	Arg	Arg	Pro	Arg	Leu	Asp	Asp	Thr	Ala	Trp	Ile	115	120	125
Ile	Phe	Thr	Ser	Gly	Ser	Thr	Gly	Lys	Pro	Lys	Gly	Val	Ala	Val	Ser	130	135	140
His	Arg	Ser	Ala	Ala	Ala	Phe	Val	Asp	Ala	Glu	Ala	Gln	Met	Phe	Leu	145	150	155
Val	Asp	His	Pro	Ser	Gly	Pro	Leu	Gly	Pro	Glu	Asp	Arg	Val	Leu	Ala	165	170	175
Gly	Leu	Ser	Val	Ala	Phe	Asp	Ala	Ser	Cys	Glu	Glu	Met	Trp	Leu	Ala	180	185	190
Trp	Gly	His	Gly	Ala	Cys	Leu	Val	Pro	Ala	Pro	Arg	Ser	Leu	Val	Arg	195	200	205
Ser	Gly	Met	Asp	Leu	Gly	Pro	Trp	Leu	Ile	Arg	Arg	Asp	Ile	Ser	Val	210	215	220
Val	Ser	Thr	Val	Pro	Thr	Leu	Ala	Gly	Leu	Trp	Pro	Ala	Glu	Ala	Leu	225	230	235
Ser	Gln	Val	Arg	Leu	Leu	Ile	Val	Gly	Gly	Glu	Ala	Cys	Ser	Gln	Glu	245	250	255
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Asp	Arg	Glu	Lys	Tyr	Ala	Pro	Leu	Lys	Ser	Val	Gly	Trp	Thr	Arg	Ala	340	345	350
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Val	Gly	Arg	Val	Asp	Asp	Gln	Val	Lys	Ile	Gly	Gly	Arg	Arg	Ile	Glu	370	375	380
Leu	Gly	Glu	Val	Asp	Ala	Asn	Val	Ala	Ala	Leu	Ser	Asn	Val	Arg	Ser	385	390	395
Ser	Ala	Val	Val	Val	Gln	Thr	Thr	Gly	Ala	Asp	Gln	Lys	Val	Leu	Val	405	410	415
Ala	Tyr	Val	Ser	Leu	Glu	Asp	Ala	Ala	Ala	Gly	Phe	Asp	His	Asn	Val	420	425	430

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 Ser Tyr Pro Arg Gly Gly Ser Thr His Leu Arg Ile Trp Ser Ala Glu
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 Ile Gly Ala Arg Ser Thr Leu Leu Pro Gly Thr Val Val Gly Thr Gly

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Lys	His	Arg	Phe	Pro	Thr	Ser	His	Pro	Pro	Arg	Arg	Ser	Arg	Trp	Val
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Ile	Val	Leu	Val	Ser	Asp	Gly	Ile	Ala	Asn	Cys	Thr	Pro	Pro	Asp	Val				
150				155				160				165							
tgc	gaa	gta	gcc	caa	gaa	ctg	gct	caa	agt	gga	atc	aac	ctg	gtt	atc	643			
Cys	Glu	Val	Ala	Gln	Glu	Leu	Ala	Gln	Ser	Gly	Ile	Asn	Leu	Val	Ile				
170				175				180											
aac	acc	atc	gga	cta	aat	gtt	gat	cca	gca	gcg	cgc	gaa	gaa	ctg	gag	691			
Asn	Thr	Ile	Gly	Leu	Asn	Val	Asp	Pro	Ala	Ala	Arg	Glu	Glu	Leu	Glu				
185				190				195											
tgc	atc	gct	gga	gtc	ggg	ggg	ggc	act	tac	gcg	gat	gct	tcc	gac	gcg	739			
Cys	Ile	Ala	Gly	Val	Gly	Gly	Gly	Thr	Tyr	Ala	Asp	Ala	Ser	Asp	Ala				
200				205				210											
cag	agc	ctt	acc	gat	gcg	ctg	aca	cga	gcc	gcc	agt	agg	caa	tac	aac	787			
Gln	Ser	Leu	Thr	Asp	Ala	Leu	Thr	Arg	Ala	Ala	Ser	Arg	Gln	Tyr	Asn				
215				220				225											
tct	tac	acc	tcc	gat	gtg	aca	aaa	att	gat	ggg	gca	tcg	gaa	caa	agc	835			
Ser	Tyr	Thr	Ser	Asp	Val	Thr	Lys	Ile	Asp	Gly	Ala	Ser	Glu	Gln	Ser				
230				235				240				245							
gca	gcc	gta	gaa	att	gat	gag	gat	aca	gaa	cta	ttc	ctc	acc	gac	ctg	883			
Ala	Ala	Val	Glu	Ile	Asp	Glu	Asp	Thr	Glu	Leu	Phe	Leu	Thr	Asp	Leu				
250				255				260											
cca	caa	gaa	tcc	cgc	ttt	tgg	aaa	at											

atc tca gtt tct gcc aac aca gtt acc gac cca aca gta ctc acc atg	979
Ile Ser Val Ser Ala Asn Thr Val Thr Asp Pro Thr Val Leu Thr Met	
280 285 290	
ggg caa ggc gga atc aag ctt gaa gcc caa ctc cat act gaa gag gct	1027
Gly Gln Gly Gly Ile Lys Leu Glu Ala Gln Leu His Thr Glu Glu Ala	
295 300 305	
cca caa tac ggc ctg cgt ggt cgg tgc act cgg gtc tca ttt gat aat	1075
Pro Gln Tyr Gly Leu Arg Gly Arg Cys Thr Arg Val Ser Phe Asp Asn	
310 315 320 325	
ttc aag ccc ggc ctt ggt gta cgc gga atc caa aac gcg tcc gtt gca	1123
Phe Lys Pro Gly Leu Gly Val Arg Gly Ile Gln Asn Ala Ser Val Ala	
330 335 340	
tca aaa gaa gtg ggc acc aac aac tgt gac acc gat gcc atc tac ctc	1171
Ser Lys Glu Val Gly Thr Asn Asn Cys Asp Thr Asp Ala Ile Tyr Leu	
345 350 355	
gaa att tct aga agc gga gat tac ctc aac ggg cag gac att cca acg	1219
Glu Ile Ser Arg Ser Gly Asp Tyr Leu Asn Gly Gln Asp Ile Pro Thr	
360 365 370	
gaa atc acc atc gag cgc ttc gga aaa gta gat gaa tca aca atc gga	1267
Glu Ile Thr Ile Glu Arg Phe Gly Lys Val Asp Glu Ser Thr Ile Gly	
375 380 385	
aat gtc aca gag gaa cat agc tcc gtc gat ctt acc gag gct gca gca	1315
Asn Val Thr Glu Glu His Ser Ser Val Asp Leu Thr Glu Ala Ala Ala	
390 395 400 405	
tca gag gca cac cct gtc aca cct ggc cag tgg ttc aca tcg gcc gct	1363
Ser Glu Ala His Pro Val Thr Pro Gly Gln Trp Phe Thr Ser Ala Ala	
410 415 420	
gat cta gat ccc gca ggt gag aaa gtc tcc tcc atc atc gtt cca gga	1411
Asp Leu Asp Pro Ala Gly Glu Lys Val Ser Ser Ile Ile Val Pro Gly	
425 430 435	
gaa acc cac ttc tat gcg ctg cct gtc gac tac ggc caa gaa ctg cgc	1459
Glu Thr His Phe Tyr Ala Leu Pro Val Asp Tyr Gly Gln Glu Leu Arg	
440 445 450	
gca gct gta gaa aca act ttt gac caa atc gac agt tcc gcg ctt ggc	1507
Ala Ala Val Glu Thr Thr Phe Asp Gln Ile Asp Ser Ser Ala Leu Gly	
455 460 465	
acg cat ctt tat atc caa gcg ttc agc cca aac cgg gca gag ata gag	1555
Thr His Leu Tyr Ile Gln Ala Phe Ser Pro Asn Arg Ala Glu Ile Glu	
470 475 480 485	
ctc acc aat aga gat acg tca tat gcg gac gac aac ggg ctc aaa act	1603
Leu Thr Asn Arg Asp Thr Ser Tyr Ala Asp Asp Asn Gly Leu Lys Thr	
490 495 500	
ttt gga ttc ttc acc cca gtg agt gca gca aat ttg ttc gag aaa agt	1651
Phe Gly Phe Phe Thr Pro Val Ser Ala Ala Asn Leu Phe Glu Lys Ser	
505 510 515	

tct caa ggc ata tcg cta agg agc cca tgg caa ggt ggc acc caa tac 1699
 Ser Gln Gly Ile Ser Leu Arg Ser Pro Trp Gln Gly Gly Thr Gln Tyr
 520 525 530

ctc gca gtg aca tac cta cca agt ggt caa gat gaa gat gta tcc gca 1747
 Leu Ala Val Thr Tyr Leu Pro Ser Gly Gln Asp Glu Asp Val Ser Ala
 535 540 545

act gat cag ctg ccc aca ttg gaa tat gaa ctc gtg gca gaa gcg ttt 1795
 Thr Asp Gln Leu Pro Thr Leu Glu Tyr Glu Leu Val Ala Glu Ala Phe
 550 555 560 565

gga gac cct gtt gac cca ccg gtt ttc gct tca ttg acg gga gca acc 1843
 Gly Asp Pro Val Asp Pro Pro Val Phe Ala Ser Leu Thr Gly Ala Thr
 570 575 580

cca agc acc tcc acc ccc cca tca gat gtt gcg gaa gat gaa caa atc 1891
 Pro Ser Thr Ser Thr Pro Pro Ser Asp Val Ala Glu Asp Glu Gln Ile
 585 590 595

tcc gag gca aca gaa gaa gac tca agc agt ttc ccc atc gtg tgg att 1939
 Ser Glu Ala Thr Glu Glu Asp Ser Ser Ser Phe Pro Ile Val Trp Ile
 600 605 610

ggg ctg ggt gtc att ggc tta ggc ata atc att ggt ttg atc ttt gcg 1987
 Gly Leu Gly Val Ile Gly Leu Gly Ile Ile Ile Gly Leu Ile Phe Ala
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ctg aga aga aag aat taagccctaa aagataaaga gtc 2025
 Leu Arg Arg Lys Asn
 630

<210> 230

<211> 634

<212> PRT

<213> Corynebacterium glutamicum

<400> 230

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Ser Ala Phe Ile Val Ala Leu Ala Phe Ser Leu Ser Pro Val Ala Lys
 20 25 30

Ala Gln Ala Asn Glu Thr Pro Thr Met Ile Val Leu Asp Asn Ser Gly
 35 40 45

Ser Met Thr Ala Gln Asp Ala Gly Gly Gln Thr Arg Ile Asp Ala Ala
 50 55 60

Lys Gln Ala Ser Thr Gln Leu Ile Asn Asp Ile Ser Asp Arg Thr Asp
 65 70 75 80

Val Gly Leu Thr Tyr Tyr Gly Gly Asn Thr Gly Glu Thr Glu Ala Asp
 85 90 95

Val Glu Met Gly Cys Gln Asp Val Thr Ile Leu Gly Gly Pro Ser Arg
 100 105 110

Gly Asn Ala Asp Thr Leu Ile Asp Thr Ile Asn Ser Leu Gln Pro Arg

115					120					125						
Gly	Phe	Thr	Pro	Ile	Gly	Lys	Ala	Leu	Thr	Asp	Thr	Ala	Ala	Glu	Leu	
130					135					140						
Pro	Glu	Gly	Gly	Asn	Ile	Val	Leu	Val	Ser	Asp	Gly	Ile	Ala	Asn	Cys	
145					150					155					160	
Thr	Pro	Pro	Asp	Val	Cys	Glu	Val	Ala	Gln	Glu	Leu	Ala	Gln	Ser	Gly	
165					170					175						
Ile	Asn	Leu	Val	Ile	Asn	Thr	Ile	Gly	Leu	Asn	Val	Asp	Pro	Ala	Ala	
180					185					190						
Arg	Glu	Glu	Leu	Glu	Cys	Ile	Ala	Gly	Val	Gly	Gly	Gly	Thr	Tyr	Ala	
195					200					205						
Asp	Ala	Ser	Asp	Ala	Gln	Ser	Leu	Thr	Asp	Ala	Leu	Thr	Arg	Ala	Ala	
210					215					220						
Ser	Arg	Gln	Tyr	Asn	Ser	Tyr	Thr	Ser	Asp	Val	Thr	Lys	Ile	Asp	Gly	
225					230					235					240	
Ala	Ser	Glu	Gln	Ser	Ala	Ala	Val	Glu	Ile	Asp	Glu	Asp	Thr	Glu	Leu	
245					250					255						
Phe	Leu	Thr	Asp	Leu	Pro	Gln	Glu	Ser	Arg	Phe	Trp	Lys	Ile	Pro	Val	
260					265					270						
Glu	Pro	Gly	Glu	Thr	Ile	Ser	Val	Ser	Ala	Asn	Thr	Val	Thr	Asp	Pro	
275					280					285						
Thr	Val	Leu	Thr	Met	Gly	Gln	Gly	Gly	Ile	Lys	Leu	Glu	Ala	Gln	Leu	
290					295					300						
His	Thr	Glu	Glu	Ala	Pro	Gln	Tyr	Gly	Leu	Arg	Gly	Arg	Cys	Thr	Arg	
305					310					315					320	
Val	Ser	Phe	Asp	Asn	Phe	Lys	Pro	Gly	Leu	Gly	Val	Arg	Gly	Ile	Gln	
325					330					335						
Asn	Ala	Ser	Val	Ala	Ser	Lys	Glu	Val	Gly	Thr	Asn	Asn	Cys	Asp	Thr	
340					345					350						
Asp	Ala	Ile	Tyr	Leu	Glu	Ile	Ser	Arg	Ser	Gly	Asp	Tyr	Leu	Asn	Gly	
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Gln	Asp	Ile	Pro	Thr	Glu	Ile	Thr	Ile	Glu	Arg	Phe	Gly	Lys	Val	Asp	
370					375					380						
Glu	Ser	Thr	Ile	Gly	Asn	Val	Thr	Glu	Glu	His	Ser	Ser	Val	Asp	Leu	
385					390					395					400	
Thr	Glu	Ala	Ala	Ala	Ser	Glu	Ala	His	Pro	Val	Thr	Pro	Gly	Gln	Trp	
405					410					415						
Phe	Thr	Ser	Ala	Ala	Asp	Leu	Asp	Pro	Ala	Gly	Glu	Lys	Val	Ser	Ser	
420					425					430						
Ile	Ile	Val	Pro	Gly	Glu	Thr	His	Phe	Tyr	Ala	Leu	Pro	Val	Asp	Tyr	
435					440					445						

Gly Gln Glu Leu Arg Ala Ala Val Glu Thr Thr Phe Asp Gln Ile Asp
 450 455 460
 Ser Ser Ala Leu Gly Thr His Leu Tyr Ile Gln Ala Phe Ser Pro Asn
 465 470 475 480
 Arg Ala Glu Ile Glu Leu Thr Asn Arg Asp Thr Ser Tyr Ala Asp Asp
 485 490 495
 Asn Gly Leu Lys Thr Phe Gly Phe Phe Thr Pro Val Ser Ala Ala Asn
 500 505 510
 Leu Phe Glu Lys Ser Ser Gln Gly Ile Ser Leu Arg Ser Pro Trp Gln
 515 520 525
 Gly Gly Thr Gln Tyr Leu Ala Val Thr Tyr Leu Pro Ser Gly Gln Asp
 530 535 540
 Glu Asp Val Ser Ala Thr Asp Gln Leu Pro Thr Leu Glu Tyr Glu Leu
 545 550 555 560
 Val Ala Glu Ala Phe Gly Asp Pro Val Asp Pro Pro Val Phe Ala Ser
 565 570 575
 Leu Thr Gly Ala Thr Pro Ser Thr Ser Thr Pro Pro Ser Asp Val Ala
 580 585 590
 Glu Asp Glu Gln Ile Ser Glu Ala Thr Glu Glu Asp Ser Ser Ser Phe
 595 600 605
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 Gly Leu Ile Phe Ala Leu Arg Arg Lys Asn
 625 630

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 <223> FRXA00787

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gtatttttgaa acaccttcag cccctttttt aggagccaca gtg tct cag cct ctc 115
 Val Ser Gln Pro Leu
 1 5

agc aag cgt ctc agc ata cga aaa gca ctc gcc agc gcc ttc ata gtt 163
 Ser Lys Arg Leu Ser Ile Arg Lys Ala Leu Ala Ser Ala Phe Ile Val
 10 15 20

gcg ctg gcg ttt tcg ctt tcc cca gta gcc aaa gcc caa gcc aat gaa 211
 Ala Leu Ala Phe Ser Leu Ser Pro Val Ala Lys Ala Gln Ala Asn Glu

25										30					35					
act	ccg	acg	atg	atc	gtg	ttg	gac	aat	tca	ggc	tcc	atg	aca	gct	caa	259				
Thr	Pro	Thr	Met	Ile	Val	Leu	Asp	Asn	Ser	Gly	Ser	Met	Thr	Ala	Gln					
		40					45					50								
gat	gcc	ggc	gga	cag	acc	cgt	atc	gat	gca	gca	aaa	caa	gcc	tcc	act	307				
Asp	Ala	Gly	Gly	Gln	Thr	Arg	Ile	Asp	Ala	Ala	Lys	Gln	Ala	Ser	Thr					
	55					60					65									
cag	tta	att	aat	gac	atc	tcc	gac	cgc	acc	gac	gta	ggc	ctg	acc	tac	355				
Gln	Leu	Ile	Asn	Asp	Ile	Ser	Asp	Arg	Thr	Asp	Val	Gly	Leu	Thr	Tyr					
	70				75					80					85					
tac	ggc	gga	aac	acc	ggc	gaa	aca	gaa	gca	gac	gtt	gag	atg	gga	tgc	403				
Tyr	Gly	Gly	Asn	Thr	Gly	Glu	Thr	Glu	Ala	Asp	Val	Glu	Met	Gly	Cys					
				90					95					100						
caa	gac	gtc	acc	atc	ctt	ggc	ggc	ccc	tcc	cga	gga	aat	gca	gac	acc	451				
Gln	Asp	Val	Thr	Ile	Leu	Gly	Gly	Pro	Ser	Arg	Gly	Asn	Ala	Asp	Thr					
			105					110					115							
tta	att	gac	acg	atc	aac	agc	ctg	cag	cct	cga	ggc	ttc	acc	ccc	atc	499				
Leu	Ile	Asp	Thr	Ile	Asn	Ser	Leu	Gln	Pro	Arg	Gly	Phe	Thr	Pro	Ile					
		120					125					130								
ggc	aaa	gca	ctc	acc	gat	acc	gcc	gcc	gag	ctc	ccc	gaa	ggc	gga	aac	547				
Gly	Lys	Ala	Leu	Thr	Asp	Thr	Ala	Ala	Glu	Leu	Pro	Glu	Gly	Gly	Asn					
	135					140					145									
att	gtg	ttg	gtc	tcc	gat	ggc	atc	gcc	aac	tgc	acc	cca	ccg	gat	gtc	595				
Ile	Val	Leu	Val	Ser	Asp	Gly	Ile	Ala	Asn	Cys	Thr	Pro	Pro	Asp	Val					
	150				155					160					165					
tgc	gaa	gta	gcc	caa	gaa	ctg	gct	caa	agt	gga	atc	aac	ctg	gtt	atc	643				
Cys	Glu	Val	Ala	Gln	Glu	Leu	Ala	Gln	Ser	Gly	Ile	Asn	Leu	Val	Ile					
				170				175						180						
aac	acc	atc	gga	cta	aat	gtt	gat	cca	gca	gcg	cgc	gaa	gaa	ctg	gag	691				
Asn	Thr	Ile	Gly	Leu	Asn	Val	Asp	Pro	Ala	Ala	Arg	Glu	Glu	Leu	Glu					
			185					190					195							
tgc																694				
Cys																				

<210> 232

<211> 198

<212> PRT

<213> Corynebacterium glutamicum

<400> 232

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Ser	Ala	Phe	Ile	Val	Ala	Leu	Ala	Phe	Ser	Leu	Ser	Pro	Val	Ala	Lys
			20					25					30		

Ala	Gln	Ala	Asn	Glu	Thr	Pro	Thr	Met	Ile	Val	Leu	Asp	Asn	Ser	Gly
	35						40					45			

Ser Met Thr Ala Gln Asp Ala Gly Gly Gln Thr Arg Ile Asp Ala Ala
 50 55 60
 Lys Gln Ala Ser Thr Gln Leu Ile Asn Asp Ile Ser Asp Arg Thr Asp
 65 70 75 80
 Val Gly Leu Thr Tyr Tyr Gly Gly Asn Thr Gly Glu Thr Glu Ala Asp
 85 90 95
 Val Glu Met Gly Cys Gln Asp Val Thr Ile Leu Gly Gly Pro Ser Arg
 100 105 110
 Gly Asn Ala Asp Thr Leu Ile Asp Thr Ile Asn Ser Leu Gln Pro Arg
 115 120 125
 Gly Phe Thr Pro Ile Gly Lys Ala Leu Thr Asp Thr Ala Ala Glu Leu
 130 135 140
 Pro Glu Gly Gly Asn Ile Val Leu Val Ser Asp Gly Ile Ala Asn Cys
 145 150 155 160
 Thr Pro Pro Asp Val Cys Glu Val Ala Gln Glu Leu Ala Gln Ser Gly
 165 170 175
 Ile Asn Leu Val Ile Asn Thr Ile Gly Leu Asn Val Asp Pro Ala Ala
 180 185 190
 Arg Glu Glu Leu Glu Cys
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<210> 233
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 <212> DNA
 <213> *Corynebacterium glutamicum*

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 <222> (1)..(828)
 <223> FRXA00791

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 gta gag cca ggt gaa acc atc tca gtt tct gcc aac aca gtt acc gac 96
 Val Glu Pro Gly Glu Thr Ile Ser Val Ser Ala Asn Thr Val Thr Asp
 20 25 30
 cca aca gta ctc acc atg ggg caa ggc gga atc aag ctt gaa gcc caa 144
 Pro Thr Val Leu Thr Met Gly Gln Gly Gly Ile Lys Leu Glu Ala Gln
 35 40 45
~~ctc cat act gaa gag gct cca caa tac ggc ctg cgt ggt cgg tgc act 192~~
~~Leu His Thr Glu Glu Ala Pro Gln Tyr Gly Leu Arg Gly Arg Cys Thr~~
~~50 55 60~~
 cgg gtc tca ttt gat aat ttc aag ccc ggc ctt ggt gta cgc gga atc 240
 Arg Val Ser Phe Asp Asn Phe Lys Pro Gly Leu Gly Val Arg Gly Ile

65	70	75	80	
caa aac gcg tcc gtt gca tca aaa gaa gtg ggc acc aac aac tgt gac				288
Gln Asn Ala Ser Val Ala Ser Lys Glu Val Gly Thr Asn Asn Cys Asp	85	90	95	
acc gat gcc atc tac ctc gaa att tct aga agc gga gat tac ctc aac				336
Thr Asp Ala Ile Tyr Leu Glu Ile Ser Arg Ser Gly Asp Tyr Leu Asn	100	105	110	
ggg cag gac att cca acg gaa atc acc atc gag cgc ttc gga aaa gta				384
Gly Gln Asp Ile Pro Thr Glu Ile Thr Ile Glu Arg Phe Gly Lys Val	115	120	125	
gat gaa tca aca atc gga aat gtc aca gag gaa cat agc tcc gtc gat				432
Asp Glu Ser Thr Ile Gly Asn Val Thr Glu Glu His Ser Ser Val Asp	130	135	140	
ctt acc gag gct gca gca tca gag gca cac cct gtc aca cct ggc cag				480
Leu Thr Glu Ala Ala Ala Ser Glu Ala His Pro Val Thr Pro Gly Gln	145	150	155	160
tgg ttc aca tcg gcc gct gat cta gat ccc gca ggt gag aaa gtc tcc				528
Trp Phe Thr Ser Ala Ala Asp Leu Asp Pro Ala Gly Glu Lys Val Ser	165	170	175	
tcc atc atc gtt cca gga gaa acc cac ttc tat gcg ctg cct gtc gac				576
Ser Ile Ile Val Pro Gly Glu Thr His Phe Tyr Ala Leu Pro Val Asp	180	185	190	
tac ggc caa gaa ctg cgc gca gct gta gaa aca act ttt gac caa atc				624
Tyr Gly Gln Glu Leu Arg Ala Ala Val Glu Thr Thr Phe Asp Gln Ile	195	200	205	
gac agt tcc gcg ctt ggc acg cat ctt tat atc caa gcg ttc agc cca				672
Asp Ser Ser Ala Leu Gly Thr His Leu Tyr Ile Gln Ala Phe Ser Pro	210	215	220	
aac cgg gca gag ata gag ctc acc aat aga gat acg tca tat gcg gac				720
Asn Arg Ala Glu Ile Glu Leu Thr Asn Arg Asp Thr Ser Tyr Ala Asp	225	230	235	240
gac aac ggg ctc aaa act ttt gga ttc ttc acc cca gtg agt gca gca				768
Asp Asn Gly Leu Lys Thr Phe Gly Phe Phe Thr Pro Val Ser Ala Ala	245	250	255	
aat ttg ttc gag aaa agt tct caa ggc ata tcg cta agg agc cca tgg				816
Asn Leu Phe Glu Lys Ser Ser Gln Gly Ile Ser Leu Arg Ser Pro Trp	260	265	270	
caa ggt ggc acc				828
Gln Gly Gly Thr	275			

<210> 234

<211> 276

<212> PRT

<213> Corynebacterium glutamicum

<400> 234

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 20 25 30
 Pro Thr Val Leu Thr Met Gly Gln Gly Gly Ile Lys Leu Glu Ala Gln
 35 40 45
 Leu His Thr Glu Glu Ala Pro Gln Tyr Gly Leu Arg Gly Arg Cys Thr
 50 55 60
 Arg Val Ser Phe Asp Asn Phe Lys Pro Gly Leu Gly Val Arg Gly Ile
 65 70 75 80
 Gln Asn Ala Ser Val Ala Ser Lys Glu Val Gly Thr Asn Asn Cys Asp
 85 90 95
 Thr Asp Ala Ile Tyr Leu Glu Ile Ser Arg Ser Gly Asp Tyr Leu Asn
 100 105 110
 Gly Gln Asp Ile Pro Thr Glu Ile Thr Ile Glu Arg Phe Gly Lys Val
 115 120 125
 Asp Glu Ser Thr Ile Gly Asn Val Thr Glu Glu His Ser Ser Val Asp
 130 135 140
 Leu Thr Glu Ala Ala Ala Ser Glu Ala His Pro Val Thr Pro Gly Gln
 145 150 155 160
 Trp Phe Thr Ser Ala Ala Asp Leu Asp Pro Ala Gly Glu Lys Val Ser
 165 170 175
 Ser Ile Ile Val Pro Gly Glu Thr His Phe Tyr Ala Leu Pro Val Asp
 180 185 190
 Tyr Gly Gln Glu Leu Arg Ala Ala Val Glu Thr Thr Phe Asp Gln Ile
 195 200 205
 Asp Ser Ser Ala Leu Gly Thr His Leu Tyr Ile Gln Ala Phe Ser Pro
 210 215 220
 Asn Arg Ala Glu Ile Glu Leu Thr Asn Arg Asp Thr Ser Tyr Ala Asp
 225 230 235 240
 Asp Asn Gly Leu Lys Thr Phe Gly Phe Phe Thr Pro Val Ser Ala Ala
 245 250 255
 Asn Leu Phe Glu Lys Ser Ser Gln Gly Ile Ser Leu Arg Ser Pro Trp
 260 265 270
 Gln Gly Gly Thr
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<210> 235

<211> 1626

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1603)

<223> RXA01057

<400> 235

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tacgccgatt ggtgaatccc tgcgcaaggc tgcagcagaa	ttg cct gaa ggc caa	115
	Leu Pro Glu Gly Gln	
	1 5	

tct ggc acc atc gta ttg gtc tct gat ggc att gca acg tgt acg ccc	163
Ser Gly Thr Ile Val Leu Val Ser Asp Gly Ile Ala Thr Cys Thr Pro	
10 15 20	

cct cca gtg tgt gag gtt gct gca gaa cta gcc gac cag ggt gtt gat	211
Pro Pro Val Cys Glu Val Ala Ala Glu Leu Ala Asp Gln Gly Val Asp	
25 30 35	

ctg gtg att aac act gtt gga ttc aac gtc gat gag tct gct cgc gcg	259
Leu Val Ile Asn Thr Val Gly Phe Asn Val Asp Glu Ser Ala Arg Ala	
40 45 50	

gaa ctg gag tgc att gcg cag gct gga aac ggt act tat gca gat gcg	307
Glu Leu Glu Cys Ile Ala Gln Ala Gly Asn Gly Thr Tyr Ala Asp Ala	
55 60 65	

agc gat gcg gat tcg ctt gtg gca gaa ctg aag cga gct gcc acc cgc	355
Ser Asp Ala Asp Ser Leu Val Ala Glu Leu Lys Arg Ala Ala Thr Arg	
70 75 80 85	

acg gca gtg ggc tat gaa tca gac ctg gaa caa atc gat ggc aac agc	403
Thr Ala Val Gly Tyr Glu Ser Asp Leu Glu Gln Ile Asp Gly Asn Ser	
90 95 100	

agc caa aca agc ctg acc cca att cca gat gat gtg gaa ttg ttc aaa	451
Ser Gln Thr Ser Leu Thr Pro Ile Pro Asp Asp Val Glu Leu Phe Lys	
105 110 115	

gcc gat ctt cca gca cta gat aat aaa gac ggc gaa gta act cag tac	499
Ala Asp Leu Pro Ala Leu Asp Asn Lys Asp Gly Glu Val Thr Gln Tyr	
120 125 130	

tgg tcc att ccc gtt gaa gat tat gaa cgt gtg cag gta acc acc tcg	547
Trp Ser Ile Pro Val Glu Asp Tyr Glu Arg Val Gln Val Thr Thr Ser	
135 140 145	

tat gtt gcg cca gtg act ttt gga ctc ggg aac gac tac ctg agc att	595
Tyr Val Ala Pro Val Thr Phe Gly Leu Gly Asn Asp Tyr Leu Ser Ile	
150 155 160 165	

agg aat gaa ctg ctt ttc gga gat gaa caa gat caa acc tgt cat cgt	643
Arg Asn Glu Leu Leu Phe Gly Asp Glu Gln Asp Gln Thr Cys His Arg	
170 175 180	

tcg atc agc aat gat caa att ctt gat aat tac ggt gcg cgg cct ttg	691
Ser Ile Ser Asn Asp Gln Ile Leu Asp Asn Tyr Gly Ala Arg Pro Leu	
185 190 195	

gtt gcc agt gtg gag tca gat gtg att gga gat aag tgc gat acc gat	739
Val Ala Ser Val Glu Ser Asp Val Ile Gly Asp Lys Cys Asp Thr Asp	

200						205					210						
gaa	ctg	gtt	ctc	gca	atc	acc	aga	agc	cag	cct	ttc	aat	tgg	gaa	gaa	787	
Glu	Leu	Val	Leu	Ala	Ile	Thr	Arg	Ser	Gln	Pro	Phe	Asn	Trp	Glu	Glu		
215						220					225						
gaa	tta	cct	gtt	gag	atc	gtg	gta	aag	cgc	ctt	aat	cac	gcg	gat	acg	835	
Glu	Leu	Pro	Val	Glu	Ile	Val	Val	Lys	Arg	Leu	Asn	His	Ala	Asp	Thr		
230						235					240					245	
tca	ggg	ctt	cca	ctc	ggg	gat	caa	cag	cgt	gaa	atc	cca	gat	ctc	gac	883	
Ser	Gly	Leu	Pro	Leu	Gly	Asp	Gln	Gln	Arg	Glu	Ile	Pro	Asp	Leu	Asp		
250						255					260						
gtg	gcc	gca	gta	caa	aca	tgg	gca	ccc	acc	act	ggc	gga	tct	tgg	ttt	931	
Val	Ala	Ala	Val	Gln	Thr	Trp	Ala	Pro	Thr	Thr	Gly	Gly	Ser	Trp	Phe		
265						270					275						
acc	aac	gct	acg	gag	cta	act	cca	ggg	gaa	ggg	gtt	gaa	gca	gag	atc	979	
Thr	Asn	Ala	Thr	Glu	Leu	Thr	Pro	Gly	Glu	Gly	Val	Glu	Ala	Glu	Ile		
280						285					290						
gta	cct	ggg	gaa	aat	cac	gtt	tat	cgc	ctg	cct	atg	gca	act	ggg	cag	1027	
Val	Pro	Gly	Glu	Asn	His	Val	Tyr	Arg	Leu	Pro	Met	Ala	Thr	Gly	Gln		
295						300					305						
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Gln	Leu	His	Gly	Phe	Val	Glu	Val	Val	Glu	Asn	Thr	Ala	Pro	Asp	Asp		
310						315					320					325	
cct	ggc	gtg	acg	gac	aaa	ttg	ggg	gtt	gca	gtg	tat	tcg	cca	aca	cga	1123	
Pro	Gly	Val	Thr	Asp	Lys	Leu	Gly	Val	Ala	Val	Tyr	Ser	Pro	Thr	Arg		
330						335					340						
cag	gac	gcc	gga	gtt	gat	atg	tgg	acg	gat	atc	gct	cca	cgt	gag	ggc	1171	
Gln	Asp	Ala	Gly	Val	Asp	Met	Trp	Thr	Asp	Ile	Ala	Pro	Arg	Glu	Gly		
345						350					355						
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Thr	Ser	Glu	Tyr	Phe	Ala	Ala	Pro	Val	Ala	Leu	Thr	Tyr	Leu	Asn	Met		
360						365					370						
ttc	cct	gct	gaa	ggc	gga	ttt	ggc	act	act	tct	aag	gcc	acc	agc	acg	1267	
Phe	Pro	Ala	Glu	Gly	Gly	Phe	Gly	Thr	Thr	Ser	Lys	Ala	Thr	Ser	Thr		
375						380					385						
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Phe	Thr	Phe	Glu	Gly	Asp	Tyr	Tyr	Leu	Val	Val	His	Tyr	Asp	Asp	Leu		
390						395					400					405	
agt	ggc	agt	aca	atc	aga	gat	gcc	agc	aac	cag	cag	tct	ttt	ccc	ctt	1363	
Ser	Gly	Ser	Thr	Ile	Arg	Asp	Ala	Ser	Asn	Gln	Gln	Ser	Phe	Pro	Leu		
410						415					420						
cgt	tat	cgc	tta	gca	gcg	gat	gct	ttt	ggg	gat	gca	gag	cca	ggc	cca	1411	
Arg	Tyr	Arg	Leu	Ala	Ala	Asp	Ala	Phe	Gly	Asp	Ala	Glu	Pro	Gly	Pro		
425						430					435						
gtg	ttt	gaa	aag	gtt	tct	gca	acc	acc	tca	gaa	tcc	tct	agc	cca	agc	1459	
Val	Phe	Glu	Lys	Val	Ser	Ala	Thr	Thr	Ser	Glu	Ser	Ser	Ser	Pro	Ser		
440						445					450						

act caa cca gat gag cca gct caa aat acc gca act gag gaa agc agc 1507
 Thr Gln Pro Asp Glu Pro Ala Gln Asn Thr Ala Thr Glu Glu Ser Ser
 455 460 465

act gga atc tcc ccg ctc att gtt ggc gct atc gtc gca ctc att ttg 1555
 Thr Gly Ile Ser Pro Leu Ile Val Gly Ala Ile Val Ala Leu Ile Leu
 470 475 480 485

gcg ttc gct gcg ttt gcc agc tgg cta gtt ttg aaa ggc cgc aag aaa 1603
 Ala Phe Ala Ala Phe Ala Ser Trp Leu Val Leu Lys Gly Arg Lys Lys
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<211> 501

<212> PRT

<213> Corynebacterium glutamicum

<400> 236

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 20 25 30

Asp Gln Gly Val Asp Leu Val Ile Asn Thr Val Gly Phe Asn Val Asp
 35 40 45

Glu Ser Ala Arg Ala Glu Leu Glu Cys Ile Ala Gln Ala Gly Asn Gly
 50 55 60

Thr Tyr Ala Asp Ala Ser Asp Ala Asp Ser Leu Val Ala Glu Leu Lys
 65 70 75 80

Arg Ala Ala Thr Arg Thr Ala Val Gly Tyr Glu Ser Asp Leu Glu Gln
 85 90 95

Ile Asp Gly Asn Ser Ser Gln Thr Ser Leu Thr Pro Ile Pro Asp Asp
 100 105 110

Val Glu Leu Phe Lys Ala Asp Leu Pro Ala Leu Asp Asn Lys Asp Gly
 115 120 125

Glu Val Thr Gln Tyr Trp Ser Ile Pro Val Glu Asp Tyr Glu Arg Val
 130 135 140

Gln Val Thr Thr Ser Tyr Val Ala Pro Val Thr Phe Gly Leu Gly Asn
 145 150 155 160

Asp Tyr Leu Ser Ile Arg Asn Glu Leu Leu Phe Gly Asp Glu Gln Asp
 165 170 175

Gln Thr Cys His Arg Ser Ile Ser Asn Asp Gln Ile Leu Asp Asn Tyr
 180 185 190

Gly Ala Arg Pro Leu Val Ala Ser Val Glu Ser Asp Val Ile Gly Asp
 195 200 205

Lys Cys Asp Thr Asp Glu Leu Val Leu Ala Ile Thr Arg Ser Gln Pro
 210 215 220
 Phe Asn Trp Glu Glu Glu Leu Pro Val Glu Ile Val Val Lys Arg Leu
 225 230 235 240
 Asn His Ala Asp Thr Ser Gly Leu Pro Leu Gly Asp Gln Gln Arg Glu
 245 250 255
 Ile Pro Asp Leu Asp Val Ala Ala Val Gln Thr Trp Ala Pro Thr Thr
 260 265 270
 Gly Gly Ser Trp Phe Thr Asn Ala Thr Glu Leu Thr Pro Gly Glu Gly
 275 280 285
 Val Glu Ala Glu Ile Val Pro Gly Glu Asn His Val Tyr Arg Leu Pro
 290 295 300
 Met Ala Thr Gly Gln Gln Leu His Gly Phe Val Glu Val Val Glu Asn
 305 310 315 320
 Thr Ala Pro Asp Asp Pro Gly Val Thr Asp Lys Leu Gly Val Ala Val
 325 330 335
 Tyr Ser Pro Thr Arg Gln Asp Ala Gly Val Asp Met Trp Thr Asp Ile
 340 345 350
 Ala Pro Arg Glu Gly Thr Ser Glu Tyr Phe Ala Ala Pro Val Ala Leu
 355 360 365
 Thr Tyr Leu Asn Met Phe Pro Ala Glu Gly Gly Phe Gly Thr Thr Ser
 370 375 380
 Lys Ala Thr Ser Thr Phe Thr Phe Glu Gly Asp Tyr Tyr Leu Val Val
 385 390 395 400
 His Tyr Asp Asp Leu Ser Gly Ser Thr Ile Arg Asp Ala Ser Asn Gln
 405 410 415
 Gln Ser Phe Pro Leu Arg Tyr Arg Leu Ala Ala Asp Ala Phe Gly Asp
 420 425 430
 Ala Glu Pro Gly Pro Val Phe Glu Lys Val Ser Ala Thr Thr Ser Glu
 435 440 445
 Ser Ser Ser Pro Ser Thr Gln Pro Asp Glu Pro Ala Gln Asn Thr Ala
 450 455 460
 Thr Glu Glu Ser Ser Thr Gly Ile Ser Pro Leu Ile Val Gly Ala Ile
 465 470 475 480
 Val Ala Leu Ile Leu Ala Phe Ala Ala Phe Ala Ser Trp Leu Val Leu
 485 490 495
 Lys Gly Arg Lys Lys
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<213> Corynebacterium glutamicum

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<223> RXA01055

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gaccaaggcg gagaacattt acgttgccgg tggtcacggc atg tgg ggt gtg gtg 115
                                   Met Trp Gly Val Val
                                   1 5
ctg ggc cct gcc acc ggt aag tat ttg gcg gag ctg atg gct acg ggc 163
Leu Gly Pro Ala Thr Gly Lys Tyr Leu Ala Glu Leu Met Ala Thr Gly
                                   10 15 20
aac acc aac ccg atc atc aag ccg ttc gat ccg ctg cgt taactgccca 212
Asn Thr Asn Pro Ile Ile Lys Pro Phe Asp Pro Leu Arg
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ataattgggtt gaa 225

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<210> 238

<211> 34

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<213> Corynebacterium glutamicum

<400> 238

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 20 25 30
Leu Arg

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                                   Met Ser Ser Ser Gly
                                   1 5
aaa gtc att gtt gtt gga gcc ggc ata gtg ggt ctt gcc acc gcc tgg 163
Lys Val Ile Val Val Gly Ala Gly Ile Val Gly Leu Ala Thr Ala Trp
                                   10 15 20

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cat	tta	cag	gag	cac	ggg	ttc	gag	gtg	agc	gtc	ctt	gat	cgg	gat	ggc	211
His	Leu	Gln	Glu	His	Gly	Phe	Glu	Val	Ser	Val	Leu	Asp	Arg	Asp	Gly	
		25						30					35			
gtc	gct	gca	ggc	tct	tcg	tgg	ggc	aat	gct	ggc	tgg	tta	gcg	ccg	gcg	259
Val	Ala	Ala	Gly	Ser	Ser	Trp	Gly	Asn	Ala	Gly	Trp	Leu	Ala	Pro	Ala	
		40					45					50				
aaa	act	att	ccg	ttg	tcg	gag	ccg	ggg	ctg	tgg	acg	tat	ggc	ccg	aaa	307
Lys	Thr	Ile	Pro	Leu	Ser	Glu	Pro	Gly	Leu	Trp	Thr	Tyr	Gly	Pro	Lys	
	55					60					65					
gag	ctg	ttc	aat	ccg	gtg	tcg	ccg	atg	cat	atg	cca	ctt	cgt	gtg	gat	355
Glu	Leu	Phe	Asn	Pro	Val	Ser	Pro	Met	His	Met	Pro	Leu	Arg	Val	Asp	
	70					75				80					85	
ccc	aaa	ctg	tgg	ctt	ttc	ttg	gcg	caa	ttt	atg	gcg	cag	gct	ttt	caa	403
Pro	Lys	Leu	Trp	Leu	Phe	Leu	Ala	Gln	Phe	Met	Ala	Gln	Ala	Phe	Gln	
				90					95					100		
cgc	aag	tgg	gat	tcc	acg	atg	gcg	gac	ctc	acg	gag	atc	gat	aag	gtc	451
Arg	Lys	Trp	Asp	Ser	Thr	Met	Ala	Asp	Leu	Thr	Glu	Ile	Asp	Lys	Val	
			105					110					115			
gcg	ctc	gaa	gct	ttt	gat	gaa	ctg	tcg	atc	ggc	ggc	gtg	gaa	ggc	ctc	499
Ala	Leu	Glu	Ala	Phe	Asp	Glu	Leu	Ser	Ile	Gly	Gly	Val	Glu	Gly	Leu	
		120					125					130				
acc	cat	gaa	ggc	cca	ttt	gtt	att	ggc	ttt	gag	gaa	gag	cgc	caa	tcg	547
Thr	His	Glu	Gly	Pro	Phe	Val	Ile	Gly	Phe	Glu	Glu	Glu	Arg	Gln	Ser	
	135					140					145					
gcg	ggc	ttc	cgt	aag	gaa	att	gat	ggc	gtg	agc	agg	cac	ggc	cag	aaa	595
Ala	Gly	Phe	Arg	Lys	Glu	Ile	Asp	Gly	Val	Ser	Arg	His	Gly	Gln	Lys	
	150				155					160					165	
gtg	gag	atg	tct	cga	ctg	gag	aat	cca	caa	gag	ttg	gcg	ccg	atg	ctg	643
Val	Glu	Met	Ser	Arg	Leu	Glu	Asn	Pro	Gln	Glu	Leu	Ala	Pro	Met	Leu	
				170					175					180		
aat	gag	caa	att	cag	gtg	gct	tac	cgt	ttg	gaa	ggc	cag	cgt	ttc	atc	691
Asn	Glu	Gln	Ile	Gln	Val	Ala	Tyr	Arg	Leu	Glu	Gly	Gln	Arg	Phe	Ile	
			185					190					195			
gag	ccg	ggc	cca	tac	gtg	cag	tca	ttg	gcg	gat	gct	gtg	gtg	aag	cgt	739
Glu	Pro	Gly	Pro	Tyr	Val	Gln	Ser	Leu	Ala	Asp	Ala	Val	Val	Lys	Arg	
		200					205					210				
ggc	ggc	gtg	atc	cgc	gcc	ggg	gca	gaa	gtt	gtg	cat	gtg	gcg	aag	ggc	787
Gly	Gly	Val	Ile	Arg	Ala	Gly	Ala	Glu	Val	Val	His	Val	Ala	Lys	Gly	
	215					220					225					
gat	cgt	ccc	gcg	gtc	att	ttg	gcg	gat	ggc	agc	cgt	gaa	gaa	gcg	gac	835
Asp	Arg	Pro	Ala	Val	Ile	Leu	Ala	Asp	Gly	Ser	Arg	Glu	Glu	Ala	Asp	
	230				235					240					245	
aag	gtg	gtt	gtg	gca	acg	ggc	gcc	tgg	ctg	ccg	ggc	cta	acg	cgt	gaa	883
Lys	Val	Val	Val	Ala	Thr	Gly	Ala	Trp	Leu	Pro	Gly	Leu	Thr	Arg	Glu	
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Leu	Asp	Arg 35	Asp	Gly	Val	Ala	Ala 40	Gly	Ser	Ser	Trp	Gly 45	Asn	Ala	Gly
Trp	Leu 50	Ala	Pro	Ala	Lys	Thr 55	Ile	Pro	Leu	Ser	Glu 60	Pro	Gly	Leu	Trp
Thr 65	Tyr	Gly	Pro	Lys	Glu 70	Leu	Phe	Asn	Pro	Val 75	Ser	Pro	Met	His	Met 80
Pro	Leu	Arg	Val	Asp 85	Pro	Lys	Leu	Trp	Leu 90	Phe	Leu	Ala	Gln	Phe 95	Met
Ala	Gln	Ala	Phe 100	Gln	Arg	Lys	Trp	Asp	Ser	Thr	Met	Ala	Asp 110	Leu	Thr
Glu	Ile 115	Asp	Lys	Val	Ala	Leu	Glu 120	Ala	Phe	Asp	Glu 125	Leu	Ser	Ile	Gly
Gly 130	Val	Glu	Gly	Leu	Thr	His 135	Glu	Gly	Pro	Phe	Val 140	Ile	Gly	Phe	Glu
Glu 145	Glu	Arg	Gln	Ser	Ala 150	Gly	Phe	Arg	Lys	Glu 155	Ile	Asp	Gly	Val	Ser 160
Arg	His	Gly	Gln	Lys 165	Val	Glu	Met	Ser	Arg 170	Leu	Glu	Asn	Pro	Gln 175	Glu
Leu	Ala	Pro	Met 180	Leu	Asn	Glu	Gln	Ile 185	Gln	Val	Ala	Tyr	Arg 190	Leu	Glu
Gly	Gln	Arg	Phe 195	Ile	Glu	Pro	Gly	Pro	Tyr	Val	Gln	Ser	Leu	Ala	Asp
Ala	Val 210	Val	Lys	Arg	Gly	Gly 215	Val	Ile	Arg	Ala	Gly 220	Ala	Glu	Val	Val

His Val Ala Lys Gly Asp Arg Pro Ala Val Ile Leu Ala Asp Gly Ser
 225 230 235 240

Arg Glu Glu Ala Asp Lys Val Val Val Ala Thr Gly Ala Trp Leu Pro
 245 250 255

Gly Leu Thr Arg Glu Tyr Gly Val Lys Thr Leu Val Gln Ala Gly Arg
 260 265 270

Gly Tyr Ser Phe Ser Val Ala Thr Asp Ile Pro Ala Lys His Ser Val
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Tyr Leu Pro His His Arg His Gly Leu His Ala Val
 290 295 300

<210> 241
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1048)
 <223> RXN02021

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 Met Ser Glu Asn Ile
 1 5

cgc gga gcc caa gca gtt gga atc gca aat atc gcc atg gac ggg acc 163
 Arg Gly Ala Gln Ala Val Gly Ile Ala Asn Ile Ala Met Asp Gly Thr
 10 15 20

atc ctg gac acg tgg tac cca gaa ccc caa att ttc aac ccg gat cag 211
 Ile Leu Asp Thr Trp Tyr Pro Glu Pro Gln Ile Phe Asn Pro Asp Gln
 25 30 35

tgg gct gaa cgc tac cca ttg gaa gtg ggc acc aca cgc ctc gga gca 259
 Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr Thr Arg Leu Gly Ala
 40 45 50

aac gaa ctc acc cca cgg atg ctg cag ttg gta aaa ctg gac caa gat 307
 Asn Glu Leu Thr Pro Arg Met Leu Gln Leu Val Lys Leu Asp Gln Asp
 55 60 65

cgc ctc gtc gaa cag gta gca gtc cgc acc gtt atc ccc gat ctg tct 355
 Arg Leu Val Glu Gln Val Ala Val Arg Thr Val Ile Pro Asp Leu Ser
 70 75 80 85

caa cct cca gta gac gcg cac gat gtt tac ctg cgc ctc cac ctg ctt 403
 Gln Pro Pro Val Asp Ala His Asp Val Tyr Leu Arg Leu His Leu Leu
 90 95 100

tcc cac cgg ctg gtc cgc ccc cac gaa atg cac atg caa aac acc ttg 451
 Ser His Arg Leu Val Arg Pro His Glu Met His Met Gln Asn Thr Leu
 105 110 115

gag ctg ctg tcc gac gtg gtg tgg aca aac aag ggc cct tgc ctt cct 499
 Glu Leu Leu Ser Asp Val Val Trp Thr Asn Lys Gly Pro Cys Leu Pro
 120 125 130

gaa aac ttt gag tgg gtg cgt ggt gct ctg cgg tcc cgc gga ctc atc 547
 Glu Asn Phe Glu Trp Val Arg Gly Ala Leu Arg Ser Arg Gly Leu Ile
 135 140 145

cac gtc tac tgt gtg gac cgt ctt ccc cgc atg gtc gac tat gtg gtt 595
 His Val Tyr Cys Val Asp Arg Leu Pro Arg Met Val Asp Tyr Val Val
 150 155 160 165

ccc cct gga gtc cgc atc tcc gaa gca gaa cgc gtg cgc cta ggt gca 643
 Pro Pro Gly Val Arg Ile Ser Glu Ala Glu Arg Val Arg Leu Gly Ala
 170 175 180

tac ctt gct ccg ggt acc tct gtg ctg cgt gaa ggt ttc gtg tct ttc 691
 Tyr Leu Ala Pro Gly Thr Ser Val Leu Arg Glu Gly Phe Val Ser Phe
 185 190 195

aac tcc ggc acc ttg ggt gcc gca aag gtg gaa ggc cgc ctg agt tcc 739
 Asn Ser Gly Thr Leu Gly Ala Ala Lys Val Glu Gly Arg Leu Ser Ser
 200 205 210

ggt gtg gtc atc ggt gaa ggt tcc gag att gga ctg tct tct act att 787
 Gly Val Val Ile Gly Glu Gly Ser Glu Ile Gly Leu Ser Ser Thr Ile
 215 220 225

cag tcc ccg aga gat gaa cag cgc cgc cgt ttg ccg ttg agc atc ggc 835
 Gln Ser Pro Arg Asp Glu Gln Arg Arg Arg Leu Pro Leu Ser Ile Gly
 230 235 240 245

caa aac tgc aac ttt ggt gtc agc tcc gga atc atc gga gtc agt ctg 883
 Gln Asn Cys Asn Phe Gly Val Ser Ser Gly Ile Ile Gly Val Ser Leu
 250 255 260

gga gac aat tgc gac atc gga aat aac att gtc ttg gat gga gat acc 931
 Gly Asp Asn Cys Asp Ile Gly Asn Asn Ile Val Leu Asp Gly Asp Thr
 265 270 275

ccc att tgg ttc gca gcc gat gag gag tta cgc act atc gac tcc atc 979
 Pro Ile Trp Phe Ala Ala Asp Glu Glu Leu Arg Thr Ile Asp Ser Ile
 280 285 290

gaa ggc caa gca aat tgg tca atc aag cgt gaa tcc ggc ttc cat gag 1027
 Glu Gly Gln Ala Asn Trp Ser Ile Lys Arg Glu Ser Gly Phe His Glu
 295 300 305

cca gtt gcc cgc ctc aaa gct tgacccatctt tcataaccag tgc 1071
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<213> Corynebacterium glutamicum

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Thr	Arg	Leu	Gly	Ala	Asn	Glu	Leu	Thr	Pro	Arg	Met	Leu	Gln	Leu	Val	50	55	60
Lys	Leu	Asp	Gln	Asp	Arg	Leu	Val	Glu	Gln	Val	Ala	Val	Arg	Thr	Val	65	70	75
Ile	Pro	Asp	Leu	Ser	Gln	Pro	Pro	Val	Asp	Ala	His	Asp	Val	Tyr	Leu	85	90	95
Arg	Leu	His	Leu	Leu	Ser	His	Arg	Leu	Val	Arg	Pro	His	Glu	Met	His	100	105	110
Met	Gln	Asn	Thr	Leu	Glu	Leu	Leu	Ser	Asp	Val	Val	Trp	Thr	Asn	Lys	115	120	125
Gly	Pro	Cys	Leu	Pro	Glu	Asn	Phe	Glu	Trp	Val	Arg	Gly	Ala	Leu	Arg	130	135	140
Ser	Arg	Gly	Leu	Ile	His	Val	Tyr	Cys	Val	Asp	Arg	Leu	Pro	Arg	Met	145	150	155
Val	Asp	Tyr	Val	Val	Pro	Pro	Gly	Val	Arg	Ile	Ser	Glu	Ala	Glu	Arg	165	170	175
Val	Arg	Leu	Gly	Ala	Tyr	Leu	Ala	Pro	Gly	Thr	Ser	Val	Leu	Arg	Glu	180	185	190
Gly	Phe	Val	Ser	Phe	Asn	Ser	Gly	Thr	Leu	Gly	Ala	Ala	Lys	Val	Glu	195	200	205
Gly	Arg	Leu	Ser	Ser	Gly	Val	Val	Ile	Gly	Glu	Gly	Ser	Glu	Ile	Gly	210	215	220
Leu	Ser	Ser	Thr	Ile	Gln	Ser	Pro	Arg	Asp	Glu	Gln	Arg	Arg	Arg	Leu	225	230	235
Pro	Leu	Ser	Ile	Gly	Gln	Asn	Cys	Asn	Phe	Gly	Val	Ser	Ser	Gly	Ile	245	250	255
Ile	Gly	Val	Ser	Leu	Gly	Asp	Asn	Cys	Asp	Ile	Gly	Asn	Asn	Ile	Val	260	265	270
Leu	Asp	Gly	Asp	Thr	Pro	Ile	Trp	Phe	Ala	Ala	Asp	Glu	Glu	Leu	Arg	275	280	285
Thr	Ile	Asp	Ser	Ile	Glu	Gly	Gln	Ala	Asn	Trp	Ser	Ile	Lys	Arg	Glu	290	295	300
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<211> 771

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<213> *Corynebacterium glutamicum*

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<222> (101)..(748)

<223> RXS00949

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				1				5	

atc	ggc	gct	gcg	ggt	ggc	atc	ggc	aat	cga	ctt	tcc	agc	ctg	ctt	cac	163
Ile	Gly	Ala	Ala	Gly	Gly	Ile	Gly	Asn	Arg	Leu	Ser	Ser	Leu	Leu	His	
				10				15						20		

gcc	agg	gga	gat	gca	ggt	agc	ggc	atg	cac	cgc	aat	ctt	gag	cag	gcc	211
Ala	Arg	Gly	Asp	Ala	Val	Ser	Gly	Met	His	Arg	Asn	Leu	Glu	Gln	Ala	
			25					30					35			

tca	aaa	atc	aca	gac	act	ggg	gca	act	gcc	gta	ctc	ggg	gat	ctc	atc	259
Ser	Lys	Ile	Thr	Asp	Thr	Gly	Ala	Thr	Ala	Val	Leu	Gly	Asp	Leu	Ile	
		40					45					50				

cac	aac	agc	acg	gag	gag	ctt	gcg	gag	ctt	ttc	cgc	ggt	cac	gat	gcc	307
His	Asn	Ser	Thr	Glu	Glu	Leu	Ala	Glu	Leu	Phe	Arg	Gly	His	Asp	Ala	
	55					60					65					

atc	gta	ttt	tct	gca	ggc	gcc	cac	gga	aca	ggg	caa	gaa	aat	acc	acg	355
Ile	Val	Phe	Ser	Ala	Gly	Ala	His	Gly	Thr	Gly	Gln	Glu	Asn	Thr	Thr	
70					75					80					85	

ctt	atc	gac	ggc	gcc	ggc	ctc	cgt	aaa	gcc	gcc	gac	gct	gcc	agc	gcg	403
Leu	Ile	Asp	Gly	Ala	Gly	Leu	Arg	Lys	Ala	Ala	Asp	Ala	Ala	Ser	Ala	
			90						95					100		

gcc	aac	gtt	tca	cgc	ttc	atc	ttg	gtc	tct	gcg	ttt	ccg	gaa	tcc	tcc	451
Ala	Asn	Val	Ser	Arg	Phe	Ile	Leu	Val	Ser	Ala	Phe	Pro	Glu	Ser	Ser	
			105				110						115			

cgc	ggg	gag	aac	acc	acc	gag	aac	ttt	gag	cac	tat	atg	aag	gtg	aag	499
Arg	Gly	Glu	Asn	Thr	Thr	Glu	Asn	Phe	Glu	His	Tyr	Met	Lys	Val	Lys	
	120						125					130				

aag	tcc	gcc	gat	gtc	tac	ctc	agt	cac	act	gac	cta	gac	tggt	ggt	att	547
Lys	Ser	Ala	Asp	Val	Tyr	Leu	Ser	His	Thr	Asp	Leu	Asp	Trp	Val	Ile	
	135					140					145					

gtc	cga	cca	ggc	gtg	ctt	caa	gat	gag	gca	ggg	gat	ggt	tta	gtc	act	595
Val	Arg	Pro	Gly	Val	Leu	Gln	Asp	Glu	Ala	Gly	Asp	Gly	Leu	Val	Thr	
150					155					160					165	

gct	ggc	tta	gcg	att	aat	tac	ggc	aat	gtt	gct	cgc	gat	aat	gtc	gca	643
Ala	Gly	Leu	Ala	Ile	Asn	Tyr	Gly	Asn	Val	Ala	Arg	Asp	Asn	Val	Ala	
				170				175						180		

gcg	ttc	att	gat	gaa	gct	ctg	cat	caa	ccg	cag	ttg	tca	aag	atc	att	691
Ala	Phe	Ile	Asp	Glu	Ala	Leu	His	Gln	Pro	Gln	Leu	Ser	Lys	Ile	Ile	

185 190 195
 gtt gaa ctc acc gac ggt tca act ccg gtg gcg gaa gcc gta gaa cgc 739
 Val Glu Leu Thr Asp Gly Ser Thr Pro Val Ala Glu Ala Val Glu Arg
 200 205 210

ctc atc aag taaagacgaa aagagggaga atg 771
 Leu Ile Lys
 215

<210> 244
 <211> 216
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 244
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 20 25 30

Asn Leu Glu Gln Ala Ser Lys Ile Thr Asp Thr Gly Ala Thr Ala Val
 35 40 45

Leu Gly Asp Leu Ile His Asn Ser Thr Glu Glu Leu Ala Glu Leu Phe
 50 55 60

Arg Gly His Asp Ala Ile Val Phe Ser Ala Gly Ala His Gly Thr Gly
 65 70 75 80

Gln Glu Asn Thr Thr Leu Ile Asp Gly Ala Gly Leu Arg Lys Ala Ala
 85 90 95

Asp Ala Ala Ser Ala Ala Asn Val Ser Arg Phe Ile Leu Val Ser Ala
 100 105 110

Phe Pro Glu Ser Ser Arg Gly Glu Asn Thr Thr Glu Asn Phe Glu His
 115 120 125

Tyr Met Lys Val Lys Lys Ser Ala Asp Val Tyr Leu Ser His Thr Asp
 130 135 140

Leu Asp Trp Val Ile Val Arg Pro Gly Val Leu Gln Asp Glu Ala Gly
 145 150 155 160

Asp Gly Leu Val Thr Ala Gly Leu Ala Ile Asn Tyr Gly Asn Val Ala
 165 170 175

Arg Asp Asn Val Ala Ala Phe Ile Asp Glu Ala Leu His Gln Pro Gln
 180 185 190

Leu Ser Lys Ile Ile Val Glu Leu Thr Asp Gly Ser Thr Pro Val Ala
 195 200 205

Glu Ala Val Glu Arg Leu Ile Lys
 210 215

<210> 245

<400> 245															
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Val Leu Thr Gln Leu 5															
att gaa tca tcg att ttc gac aac gtt gcg agc agg gag tcc tct gaa 163															
Ile Glu Ser Ser Ile Phe Asp Asn Val Ala Ser Arg Glu Ser Ser Glu 20															
10 15															
ttt ctc ggc cat gct gcc atc gat cta ctt gct ggc ctt gtc tat gaa 211															
Phe Leu Gly His Ala Ala Ile Asp Leu Leu Ala Gly Leu Val Tyr Glu 35															
25 30															
aaa gcc act ccc tat gct cca gat gaa gca ctt aga gtg gca gtt tat 259															
Lys Ala Thr Pro Tyr Ala Pro Asp Glu Ala Leu Arg Val Ala Val Tyr 50															
40 45															
ggc tat att cgg gag aac ctt gga tcc tca caa ctt acg gtc gca gct 307															
Gly Tyr Ile Arg Glu Asn Leu Gly Ser Ser Gln Leu Thr Val Ala Ala 65															
55 60															
gta gcc ggg gcg cat aga atc gcg gtt cgt acg ttg cat cga tta ttt 355															
Val Ala Gly Ala His Arg Ile Ala Val Arg Thr Leu His Arg Leu Phe 85															
70 75 80															
gaa ggc gaa gca tac gga gta gcg gaa tta atc cga cac ctc cga tta 403															
Glu Gly Glu Ala Tyr Gly Val Ala Glu Leu Ile Arg His Leu Arg Leu 100															
90 95															
gag gca gta tat gaa gac ctt cgg gat cct cgc ctc cag aac ctg acc 451															
Glu Ala Val Tyr Glu Asp Leu Arg Asp Pro Arg Leu Gln Asn Leu Thr 115															
105 110															
att ttg gct atc ggc atg cgc cac ggc att tcc agc caa gct cat tta 499															
Ile Leu Ala Ile Gly Met Arg His Gly Ile Ser Ser Gln Ala His Leu 130															
120 125															
aca aga ctg ttt cgc gct aaa tat ggg gta ccg ccg gca gag ttt cgc 547															
Thr Arg Leu Phe Arg Ala Lys Tyr Gly Val Pro Pro Ala Glu Phe Arg 145															
135 140 145															
cga ggg tat att aat agc gct gct tgagggcacc gcaagcgtgg cgc 594															
Arg Gly Tyr Ile Asn Ser Ala Ala 155															
150 155															

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<210> 246
<211> 157
<212> PRT
<213> Corynebacterium glutamicum
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<400> 246

Val Leu Thr Gln Leu Ile Glu Ser Ser Ile Phe Asp Asn Val Ala Ser
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Arg Glu Ser Ser Glu Phe Leu Gly His Ala Ala Ile Asp Leu Leu Ala
 20 25 30

Gly Leu Val Tyr Glu Lys Ala Thr Pro Tyr Ala Pro Asp Glu Ala Leu
 35 40 45

Arg Val Ala Val Tyr Gly Tyr Ile Arg Glu Asn Leu Gly Ser Ser Gln
 50 55 60

Leu Thr Val Ala Ala Val Ala Gly Ala His Arg Ile Ala Val Arg Thr
 65 70 75 80

Leu His Arg Leu Phe Glu Gly Glu Ala Tyr Gly Val Ala Glu Leu Ile
 85 90 95

Arg His Leu Arg Leu Glu Ala Val Tyr Glu Asp Leu Arg Asp Pro Arg
 100 105 110

Leu Gln Asn Leu Thr Ile Leu Ala Ile Gly Met Arg His Gly Ile Ser
 115 120 125

Ser Gln Ala His Leu Thr Arg Leu Phe Arg Ala Lys Tyr Gly Val Pro
 130 135 140

Pro Ala Glu Phe Arg Arg Gly Tyr Ile Asn Ser Ala Ala
 145 150 155

<210> 247

<211> 783

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(760)

<223> RXS00166

<400> 247

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gacttatcac gatgtccgac ctggatatcc ggctgaggcc gtg gag tta gcc cgt 115
 Val Glu Leu Ala Arg
 1 5

ggg ttt ggc cga gtc ctg gat gtc ggt gca ggt acc gga aaa cta acc 163
 Gly Phe Gly Arg Val Leu Asp Val Gly Ala Gly Thr Gly Lys Leu Thr
 10 15 20

agt gag cta aca gct gat cag gtc cta gcc ctt gat cca agc atg gac 211
 Ser Glu Leu Thr Ala Asp Gln Val Leu Ala Leu Asp Pro Ser Met Asp
 25 30 35

atg ttg cgg gtg ttt cgc tcc gcg ctt ccg gcg gtt ccc tgc tgg caa 259
 Met Leu Arg Val Phe Arg Ser Ala Leu Pro Ala Val Pro Cys Trp Gln
 40 45 50

gcg aca gca gaa cac aca gga ata cgt gac aac gcg gtt gat ctg att 307
 Ala Thr Ala Glu His Thr Gly Ile Arg Asp Asn Ala Val Asp Leu Ile
 55 60 65
 acg tgc gca caa acg tgg cat tgg gtt gac gtg acg gct gcc tca gcg 355
 Thr Cys Ala Gln Thr Trp His Trp Val Asp Val Thr Ala Ala Ser Ala
 70 75 80 85
 gaa ttt gat cgg gtg att gca cct gag ggt gca gtc ctg ctc gtg tgg 403
 Glu Phe Asp Arg Val Ile Ala Pro Glu Gly Ala Val Leu Leu Val Trp
 90 95 100
 aat aac ctg gac acc tcc atc gcg tgg gta cac cga ctc agt cgc att 451
 Asn Asn Leu Asp Thr Ser Ile Ala Trp Val His Arg Leu Ser Arg Ile
 105 110 115
 atg cat gcc ggc gat gta ctc aag ccg gga ttc acc cca gaa acc gca 499
 Met His Ala Gly Asp Val Leu Lys Pro Gly Phe Thr Pro Glu Thr Ala
 120 125 130
 gct ccc tgg ata att gat cga gaa att cgc acc acg tgg aat cag cac 547
 Ala Pro Trp Ile Ile Asp Arg Glu Ile Arg Thr Thr Trp Asn Gln His
 135 140 145
 ctc acc cct gaa gaa atc atc cag ctc gct cac acg agg tcc tac tgg 595
 Leu Thr Pro Glu Glu Ile Ile Gln Leu Ala His Thr Arg Ser Tyr Trp
 150 155 160 165
 tta aac gcg tca gag aaa atc aaa gag cgt gtt gat cag aac ctt cag 643
 Leu Asn Ala Ser Glu Lys Ile Lys Glu Arg Val Asp Gln Asn Leu Gln
 170 175 180
 tgg tat ctc tac gag cat ttg ggt ttc agt ccc gac aat cca gtg gaa 691
 Trp Tyr Leu Tyr Glu His Leu Gly Phe Ser Pro Asp Asn Pro Val Glu
 185 190 195
 ctt ccc tat cgc tgt gat gca ttt tta ctt tca cgt tcc ggt acc ctg 739
 Leu Pro Tyr Arg Cys Asp Ala Phe Leu Leu Ser Arg Ser Gly Thr Leu
 200 205 210
 gca ggc aga tct tcc aat ctt taggagccct cgccatgtac ctg 783
 Ala Gly Arg Ser Ser Asn Leu
 215 220

<210> 248

<211> 220

<212> PRT

<213> Corynebacterium glutamicum

<400> 248

Val Glu Leu Ala Arg Gly Phe Gly Arg Val Leu Asp Val Gly Ala Gly
 1 5 10 15

Thr Gly Lys Leu Thr Ser Glu Leu Thr Ala Asp Gln Val Leu Ala Leu
 20 25 30

Asp Pro Ser Met Asp Met Leu Arg Val Phe Arg Ser Ala Leu Pro Ala
 35 40 45

Val Pro Cys Trp Gln Ala Thr Ala Glu His Thr Gly Ile Arg Asp Asn
 50 55 60

Ala Val Asp Leu Ile Thr Cys Ala Gln Thr Trp His Trp Val Asp Val
 65 70 75 80

Thr Ala Ala Ser Ala Glu Phe Asp Arg Val Ile Ala Pro Glu Gly Ala
 85 90 95

Val Leu Leu Val Trp Asn Asn Leu Asp Thr Ser Ile Ala Trp Val His
 100 105 110

Arg Leu Ser Arg Ile Met His Ala Gly Asp Val Leu Lys Pro Gly Phe
 115 120 125

Thr Pro Glu Thr Ala Ala Pro Trp Ile Ile Asp Arg Glu Ile Arg Thr
 130 135 140

Thr Trp Asn Gln His Leu Thr Pro Glu Glu Ile Ile Gln Leu Ala His
 145 150 155 160

Thr Arg Ser Tyr Trp Leu Asn Ala Ser Glu Lys Ile Lys Glu Arg Val
 165 170 175

Asp Gln Asn Leu Gln Trp Tyr Leu Tyr Glu His Leu Gly Phe Ser Pro
 180 185 190

Asp Asn Pro Val Glu Leu Pro Tyr Arg Cys Asp Ala Phe Leu Leu Ser
 195 200 205

Arg Ser Gly Thr Leu Ala Gly Arg Ser Ser Asn Leu
 210 215 220

<210> 249

<211> 1134

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1111)

<223> RXS00288

<400> 249

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acacgggcat gaaacgtacc caagggctaa catcgggggc atg agc gcg caa atg 115
 Met Ser Ala Gln Met
 1 5

gat acc cct gat ccc act atg tct gct gtt gca atg tta gat tcc atc 163
 Asp Thr Pro Asp Pro Thr Met Ser Ala Val Ala Met Leu Asp Ser Ile
 10 15 20

cct tct gat caa cca gat ttc ctg atc gat gta gaa gta gat cga cca 211
 Pro Ser Asp Gln Pro Asp Phe Leu Ile Asp Val Glu Val Asp Arg Pro
 25 30 35

act ccc gga cca cat gat ctg cta gtc cac att gag gcg gtc tca att 259
 Thr Pro Gly Pro His Asp Leu Leu Val His Ile Glu Ala Val Ser Ile

40	45	50	
aac cct gtt gat acc aag gta cgc atg cgg gcc ggg aag caa aag cat Asn Pro Val Asp Thr Lys Val Arg Met Arg Ala Gly Lys Gln Lys His 55 60 65			307
cct aaa att tta ggt ttt gat gct gca ggt gag gtg gtg gct gtt gga Pro Lys Ile Leu Gly Phe Asp Ala Ala Gly Glu Val Val Ala Val Gly 70 75 80 85			355
tcg cag gtc acg ctc ttc aat gtt ggt gac aaa gtg ttc tac gca gga Ser Gln Val Thr Leu Phe Asn Val Gly Asp Lys Val Phe Tyr Ala Gly 90 95 100			403
tcc aat cag cgt cca gga agt aac gca gag tac cag gtg gtg gat gaa Ser Asn Gln Arg Pro Gly Ser Asn Ala Glu Tyr Gln Val Val Asp Glu 105 110 115			451
cgg ctg gtg ggt cac gca cca caa agc ttg ggg gca cac gac gcc gct Arg Leu Val Gly His Ala Pro Gln Ser Leu Gly Ala His Asp Ala Ala 120 125 130			499
gct ctc cca ctt gtc gcg ctc act gca tgg gag tca ctt ttt gac cga Ala Leu Pro Leu Val Ala Leu Thr Ala Trp Glu Ser Leu Phe Asp Arg 135 140 145			547
ttg gga gta act cag tca act act gga aca ctg ttg gtc ttg ggc ggt Leu Gly Val Thr Gln Ser Thr Thr Gly Thr Leu Leu Val Leu Gly Gly 150 155 160 165			595
tca gga ggt gtg cct tca gct ctt att caa ctt gct cga gct ctc act Ser Gly Gly Val Pro Ser Ala Leu Ile Gln Leu Ala Arg Ala Leu Thr 170 175 180			643
ggt ctg aaa gta gtg gca aca gct tct cgc cct gaa tca caa gaa tgg Gly Leu Lys Val Val Ala Thr Ala Ser Arg Pro Glu Ser Gln Glu Trp 185 190 195			691
gtg aca aag ctc ggt gct cat gag gtg att gat cac tcc aag gat ttg Val Thr Lys Leu Gly Ala His Glu Val Ile Asp His Ser Lys Asp Leu 200 205 210			739
agt gag caa atc tcc gac gtg gat ttt gtt ttc agc tcg tgg act act Ser Glu Gln Ile Ser Asp Val Asp Phe Val Phe Ser Ser Trp Thr Thr 215 220 225			787
ggg cgt gaa gta gag ctc gcc acg ttg atg aaa ccc cag tcc cac cta Gly Arg Glu Val Glu Leu Ala Thr Leu Met Lys Pro Gln Ser His Leu 230 235 240 245			835
gtg ctc atc gat gat cca gtg gat ccc aat ttg ggc gct ttt aag caa Val Leu Ile Asp Asp Pro Val Asp Pro Asn Leu Gly Ala Phe Lys Gln 250 255 260			883
aaa gcg atc gct ttg cac tgg gag ttc atg ttt acc cgc gct atg ttc Lys Ala Ile Ala Leu His Trp Glu Phe Met Phe Thr Arg Ala Met Phe 265 270 275			931
aac act cct gat atg ggt gaa caa ggg aaa att ctg aat aag atc gcc Asn Thr Pro Asp Met Gly Glu Gln Gly Lys Ile Leu Asn Lys Ile Ala 280 285 290			979

gac atg gtt gat cgg ggt cag ttt gag tcc gtg aca gca acg gtg ctg 1027
 Asp Met Val Asp Arg Gly Gln Phe Glu Ser Val Thr Ala Thr Val Leu
 295 300 305

gat ggg ctc aac gct gca aac atc atg gag ggg cac cgg ctc gtt gag 1075
 Asp Gly Leu Asn Ala Ala Asn Ile Met Glu Gly His Arg Leu Val Glu
 310 315 320 325

cag ggt aaa acc tca gga aaa att gtt gtg agg gta taaagaggac 1121
 Gln Gly Lys Thr Ser Gly Lys Ile Val Val Arg Val
 330 335

ttgaaaaatg cac 1134

<210> 250

<211> 337

<212> PRT

<213> Corynebacterium glutamicum

<400> 250

Met Ser Ala Gln Met Asp Thr Pro Asp Pro Thr Met Ser Ala Val Ala
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Met Leu Asp Ser Ile Pro Ser Asp Gln Pro Asp Phe Leu Ile Asp Val
 20 25 30

Glu Val Asp Arg Pro Thr Pro Gly Pro His Asp Leu Leu Val His Ile
 35 40 45

Glu Ala Val Ser Ile Asn Pro Val Asp Thr Lys Val Arg Met Arg Ala
 50 55 60

Gly Lys Gln Lys His Pro Lys Ile Leu Gly Phe Asp Ala Ala Gly Glu
 65 70 75 80

Val Val Ala Val Gly Ser Gln Val Thr Leu Phe Asn Val Gly Asp Lys
 85 90 95

Val Phe Tyr Ala Gly Ser Asn Gln Arg Pro Gly Ser Asn Ala Glu Tyr
 100 105 110

Gln Val Val Asp Glu Arg Leu Val Gly His Ala Pro Gln Ser Leu Gly
 115 120 125

Ala His Asp Ala Ala Ala Leu Pro Leu Val Ala Leu Thr Ala Trp Glu
 130 135 140

Ser Leu Phe Asp Arg Leu Gly Val Thr Gln Ser Thr Thr Gly Thr Leu
 145 150 155 160

Leu Val Leu Gly Gly Ser Gly Gly Val Pro Ser Ala Leu Ile Gln Leu
 165 170 175

Ala Arg Ala Leu Thr Gly Leu Lys Val Val Ala Thr Ala Ser Arg Pro
 180 185 190

Glu Ser Gln Glu Trp Val Thr Lys Leu Gly Ala His Glu Val Ile Asp
 195 200 205

His Ser Lys Asp Leu Ser Glu Gln Ile Ser Asp Val Asp Phe Val Phe
 210 215 220
 Ser Ser Trp Thr Thr Gly Arg Glu Val Glu Leu Ala Thr Leu Met Lys
 225 230 235 240
 Pro Gln Ser His Leu Val Leu Ile Asp Asp Pro Val Asp Pro Asn Leu
 245 250 255
 Gly Ala Phe Lys Gln Lys Ala Ile Ala Leu His Trp Glu Phe Met Phe
 260 265 270
 Thr Arg Ala Met Phe Asn Thr Pro Asp Met Gly Glu Gln Gly Lys Ile
 275 280 285
 Leu Asn Lys Ile Ala Asp Met Val Asp Arg Gly Gln Phe Glu Ser Val
 290 295 300
 Thr Ala Thr Val Leu Asp Gly Leu Asn Ala Ala Asn Ile Met Glu Gly
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 His Arg Leu Val Glu Gln Gly Lys Thr Ser Gly Lys Ile Val Val Arg
 325 330 335

Val

<210> 251
 <211> 1347
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1324)
 <223> RXS01114

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 Met Asn Pro Gln Asp
 1 5

att gtc atc tgt tcc cca ttg cgc acc cca gtt ggt gct tac ggc gga 163
 Ile Val Ile Cys Ser Pro Leu Arg Thr Pro Val Gly Ala Tyr Gly Gly
 10 15 20

tcc ttc acc ggc gtc cct gtt gaa gaa ttg gcc acc acc gtg atc aac 211
 Ser Phe Thr Gly Val Pro Val Glu Glu Leu Ala Thr Thr Val Ile Asn
 25 30 35

gcg atc gtt gag gca acc ggc atc acc ggc gac gat gtg gac gat ctg 259
 Ala Ile Val Glu Ala Thr Gly Ile Thr Gly Asp Asp Val Asp Asp Leu
 40 45 50

atc ctc ggc cag gca tcc ccc aac ggt gcg gct cca gca ctg ggc cgt 307
 Ile Leu Gly Gln Ala Ser Pro Asn Gly Ala Ala Pro Ala Leu Gly Arg
 55 60 65

gtt gtt gct cta gat tcc aag ctt ggc caa aac gtt cca ggc atg cag Val Val Ala Leu Asp Ser Lys Leu Gly Gln Asn Val Pro Gly Met Gln 70 75 80 85	355
ctt gat cgc cgc tgt ggt tcc ggc ctg cag gca atc gtc acc gct gct Leu Asp Arg Arg Cys Gly Ser Gly Leu Gln Ala Ile Val Thr Ala Ala 90 95 100	403
gca cac gtt gca tcc ggc gct gct gat ctg atc atc gca ggt ggc gca Ala His Val Ala Ser Gly Ala Ala Asp Leu Ile Ile Ala Gly Gly Ala 105 110 115	451
gaa tcc atg agc cgc gtt gag tac acc gtg tcc ggc gat atc cgt tgg Glu Ser Met Ser Arg Val Glu Tyr Thr Val Ser Gly Asp Ile Arg Trp 120 125 130	499
ggt gtc aag ggc ggc gac atg cag ctt cgt gac cgc ctt gca gaa gca Gly Val Lys Gly Gly Asp Met Gln Leu Arg Asp Arg Leu Ala Glu Ala 135 140 145	547
cgc gaa acc gct ggc gga cgc aac cac ccg atc cct ggt ggc atg atc Arg Glu Thr Ala Gly Gly Arg Asn His Pro Ile Pro Gly Gly Met Ile 150 155 160 165	595
gag acc gct gag aac ctg cgt cgc gaa tac ggc atc tcc cgc gag gag Glu Thr Ala Glu Asn Leu Arg Arg Glu Tyr Gly Ile Ser Arg Glu Glu 170 175 180	643
cag gac aag atc tcc gca gcg tcc cag cag cgt tgg ggc aag gct gct Gln Asp Lys Ile Ser Ala Ala Ser Gln Gln Arg Trp Gly Lys Ala Ala 185 190 195	691
gat gcg ggg ctt ttc gac gac gag atc gtg cca gtc acc gtc cct gcc Asp Ala Gly Leu Phe Asp Asp Glu Ile Val Pro Val Thr Val Pro Ala 200 205 210	739
aag aag cgc ggc cag gag cca acc atc gtt tct cga gac gag cat ggt Lys Lys Arg Gly Gln Glu Pro Thr Ile Val Ser Arg Asp Glu His Gly 215 220 225	787
cga cca gga aca acc gtc gaa aag ctt gct gct ttg cgc ccc atc atg Arg Pro Gly Thr Thr Val Glu Lys Leu Ala Ala Leu Arg Pro Ile Met 230 235 240 245	835
ggc cgc cag gat gcg gaa gca acc gtc acc gct ggc aac gcg tcc ggc Gly Arg Gln Asp Ala Glu Ala Thr Val Thr Ala Gly Asn Ala Ser Gly 250 255 260	883
caa aat gat ggc gct gct gcc gtc atc gtg acc act cgc gcc aag gcc Gln Asn Asp Gly Ala Ala Ala Val Ile Val Thr Thr Arg Ala Lys Ala 265 270 275	931
gag gag aag ggc ctg cgc cca gtc atg cgt ttg gct ggc tgg tct gtg Glu Glu Lys Gly Leu Arg Pro Val Met Arg Leu Ala Gly Trp Ser Val 280 285 290	979
gct gct gtt ccc cca gag acc atg ggt att gga cct gtt cct gcc acc Ala Ala Val Pro Pro Glu Thr Met Gly Ile Gly Pro Val Pro Ala Thr 295 300 305	1027
aag aag gtc ctg gat cgt ttg ggc ctt acc ctg gag gac atc ggc gcg	1075

Lys Lys Val Leu Asp Arg Leu Gly Leu Thr Leu Glu Asp Ile Gly Ala
 310 315 320 325
 atc gaa ctc aac gaa gct ttc gca gct cag gca ctg tct gtg ctg aag 1123
 Ile Glu Leu Asn Glu Ala Phe Ala Ala Gln Ala Leu Ser Val Leu Lys
 330 335 340
 gaa tgg aac att tct tgg gaa gat gag cgc gtc aac cca ctg ggt tcc 1171
 Glu Trp Asn Ile Ser Trp Glu Asp Glu Arg Val Asn Pro Leu Gly Ser
 345 350 355
 ggt att tcc atg gga cac cca gtc ggt gcc acc ggt gct cgc atg gca 1219
 Gly Ile Ser Met Gly His Pro Val Gly Ala Thr Gly Ala Arg Met Ala
 360 365 370
 gta acc ttg gct cac cgc atg cag cgt gaa aac act cag tac gga ctg 1267
 Val Thr Leu Ala His Arg Met Gln Arg Glu Asn Thr Gln Tyr Gly Leu
 375 380 385
 gcc acc atg tgc atc ggt ggc ggc cag ggt ctt gca gct gtc ttt gaa 1315
 Ala Thr Met Cys Ile Gly Gly Gly Gln Gly Leu Ala Ala Val Phe Glu
 390 395 400 405
 aag gag aac taaaaatggc tattttgcac agc 1347
 Lys Glu Asn

<210> 252

<211> 408

<212> PRT

<213> Corynebacterium glutamicum

<400> 252

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 20 25 30
 Thr Thr Val Ile Asn Ala Ile Val Glu Ala Thr Gly Ile Thr Gly Asp
 35 40 45
 Asp Val Asp Asp Leu Ile Leu Gly Gln Ala Ser Pro Asn Gly Ala Ala
 50 55 60
 Pro Ala Leu Gly Arg Val Val Ala Leu Asp Ser Lys Leu Gly Gln Asn
 65 70 75 80
 Val Pro Gly Met Gln Leu Asp Arg Arg Cys Gly Ser Gly Leu Gln Ala
 85 90 95
 Ile Val Thr Ala Ala Ala His Val Ala Ser Gly Ala Ala Asp Leu Ile
 100 105 110
 Ile Ala Gly Gly Ala Glu Ser Met Ser Arg Val Glu Tyr Thr Val Ser
 115 120 125
 Gly Asp Ile Arg Trp Gly Val Lys Gly Gly Asp Met Gln Leu Arg Asp
 130 135 140

Arg Leu Ala Glu Ala Arg Glu Thr Ala Gly Gly Arg Asn His Pro Ile
 145 150 155 160
 Pro Gly Gly Met Ile Glu Thr Ala Glu Asn Leu Arg Arg Glu Tyr Gly
 165 170 175
 Ile Ser Arg Glu Glu Gln Asp Lys Ile Ser Ala Ala Ser Gln Gln Arg
 180 185 190
 Trp Gly Lys Ala Ala Asp Ala Gly Leu Phe Asp Asp Glu Ile Val Pro
 195 200 205
 Val Thr Val Pro Ala Lys Lys Arg Gly Gln Glu Pro Thr Ile Val Ser
 210 215 220
 Arg Asp Glu His Gly Arg Pro Gly Thr Thr Val Glu Lys Leu Ala Ala
 225 230 235 240
 Leu Arg Pro Ile Met Gly Arg Gln Asp Ala Glu Ala Thr Val Thr Ala
 245 250 255
 Gly Asn Ala Ser Gly Gln Asn Asp Gly Ala Ala Ala Val Ile Val Thr
 260 265 270
 Thr Arg Ala Lys Ala Glu Glu Lys Gly Leu Arg Pro Val Met Arg Leu
 275 280 285
 Ala Gly Trp Ser Val Ala Ala Val Pro Pro Glu Thr Met Gly Ile Gly
 290 295 300
 Pro Val Pro Ala Thr Lys Lys Val Leu Asp Arg Leu Gly Leu Thr Leu
 305 310 315 320
 Glu Asp Ile Gly Ala Ile Glu Leu Asn Glu Ala Phe Ala Ala Gln Ala
 325 330 335
 Leu Ser Val Leu Lys Glu Trp Asn Ile Ser Trp Glu Asp Glu Arg Val
 340 345 350
 Asn Pro Leu Gly Ser Gly Ile Ser Met Gly His Pro Val Gly Ala Thr
 355 360 365
 Gly Ala Arg Met Ala Val Thr Leu Ala His Arg Met Gln Arg Glu Asn
 370 375 380
 Thr Gln Tyr Gly Leu Ala Thr Met Cys Ile Gly Gly Gly Gln Gly Leu
 385 390 395 400
 Ala Ala Val Phe Glu Lys Glu Asn
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<210> 253

<211> 554

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(531)

<223> RXS01205

<400> 253

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Val Ser Ala Tyr Pro Pro Ala Ile Ile Ala Ala Ala Leu Val Gly Ile
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tgc gcg gga gtt ttg ccc cat aat ttt gaa ccc tcg cga ata ttt atg 96
Cys Ala Gly Val Leu Pro His Asn Phe Glu Pro Ser Arg Ile Phe Met
          20             25             30

ggc gat tcc gcc tcc atg ctc atc ggc ctg ctg ttg gct gca gca tcg 144
Gly Asp Ser Gly Ser Met Leu Ile Gly Leu Leu Leu Ala Ala Ala Ser
          35             40             45

acc tca gcg tca gga aaa atc aac atg agc ctg tat ggc gca gct gat 192
Thr Ser Ala Ser Gly Lys Ile Asn Met Ser Leu Tyr Gly Ala Ala Asp
          50             55             60

ttt atc gca ttg atc tca ccc atc atc gtt gtt ctc gcc gcc gtg gcc 240
Phe Ile Ala Leu Ile Ser Pro Ile Ile Val Val Leu Ala Ala Val Ala
  65             70             75             80

atc cca ctg ctc gac ctc gtg atg gca gtg gtt agg cgc gtg ggc agg 288
Ile Pro Leu Leu Asp Leu Val Met Ala Val Val Arg Arg Val Gly Arg
          85             90             95

gga gca tca ccc ttt tcc ccg gac aaa atg cat ctg cac cac cga ctg 336
Gly Ala Ser Pro Phe Ser Pro Asp Lys Met His Leu His His Arg Leu
          100             105             110

ctg tcc atc gga cac acc cat agg cgc gtg gtc cta gtg ctc tac acc 384
Leu Ser Ile Gly His Thr His Arg Arg Val Val Leu Val Leu Tyr Thr
          115             120             125

tgg gcg agc gcc gtg gca ttc ggc gca gtg agc ttc tcc gtc gtt ccg 432
Trp Ala Ser Ala Val Ala Phe Gly Ala Val Ser Phe Ser Val Val Pro
          130             135             140

cca ctg ttt gcc acc gga tcg agc atc tgt ggc atc ctc atc gcc gtc 480
Pro Leu Phe Ala Thr Gly Ser Ser Ile Cys Gly Ile Leu Ile Ala Val
          145             150             155             160

gct gtc aca gcc gtg cca gtg atg aaa agc cgg cga gcc gcc aaa ctt 528
Ala Val Thr Ala Val Pro Val Met Lys Ser Arg Arg Ala Ala Lys Leu
          165             170             175

gat taagtgattg tcactttgga ttg 554
Asp

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<210> 254

<211> 177

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 254

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Val Ser Ala Tyr Pro Pro Ala Ile Ile Ala Ala Ala Leu Val Gly Ile
  1             5             10             15

Cys Ala Gly Val Leu Pro His Asn Phe Glu Pro Ser Arg Ile Phe Met

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20										25					30				
Gly	Asp	Ser	Gly	Ser	Met	Leu	Ile	Gly	Leu	Leu	Leu	Leu	Ala	Ala	Ala	Ser			
					35						40						45		
Thr	Ser	Ala	Ser	Gly	Lys	Ile	Asn	Met	Ser	Leu	Tyr	Gly	Ala	Ala	Ala	Asp			
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Phe	Ile	Ala	Leu	Ile	Ser	Pro	Ile	Ile	Val	Val	Leu	Ala	Ala	Val	Ala				
					65						70						75	80	
Ile	Pro	Leu	Leu	Asp	Leu	Val	Met	Ala	Val	Val	Arg	Arg	Val	Gly	Arg				
					85						90						95		
Gly	Ala	Ser	Pro	Phe	Ser	Pro	Asp	Lys	Met	His	Leu	His	His	Arg	Leu				
					100						105						110		
Leu	Ser	Ile	Gly	His	Thr	His	Arg	Arg	Val	Val	Leu	Val	Leu	Tyr	Thr				
					115						120						125		
Trp	Ala	Ser	Ala	Val	Ala	Phe	Gly	Ala	Val	Ser	Phe	Ser	Val	Val	Pro				
					130						135						140		
Pro	Leu	Phe	Ala	Thr	Gly	Ser	Ser	Ile	Cys	Gly	Ile	Leu	Ile	Ala	Val				
					145						150						155	160	
Ala	Val	Thr	Ala	Val	Pro	Val	Met	Lys	Ser	Arg	Arg	Ala	Ala	Lys	Leu				
					165						170						175		

Asp

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 <211> 564
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(541)
 <223> RXS01269

<400> 255
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tccgattcta tttcgtcaac cagcacctgg gaaagacggt gtg gta ttt gag atg 115
 Val Val Phe Glu Met
 1 5

att aag ttt cga acc atg ctt gaa cca gat gaa aaa cat gta act gat 163
 Ile Lys Phe Arg Thr Met Leu Glu Pro Asp Glu Lys His Val Thr Asp
 10 15 20

gaa cag cgt cta act aaa gtt gga aag ctt ctg cgg gaa acg agt tta 211
 Glu Gln Arg Leu Thr Lys Val Gly Lys Leu Leu Arg Glu Thr Ser Leu

25 30 35

gat gag tta cct aca ctc tgg aat gta ttt aaa ggt gat atg agc ctt 259
 Asp Glu Leu Pro Thr Leu Trp Asn Val Phe Lys Gly Asp Met Ser Leu
 40 45 50

gta ggg cct cga cct ttg ctt gtt agc tat ctg gaa cat tac tct tct 307
 Val Gly Pro Arg Pro Leu Leu Val Ser Tyr Leu Glu His Tyr Ser Ser
 55 60 65

gaa caa gct cga cgc cat gaa gtt cgt cct ggg att act ggt ttg gct 355
 Glu Gln Ala Arg Arg His Glu Val Arg Pro Gly Ile Thr Gly Leu Ala
 70 75 80 85

cag gtg aat ggc cgt aat caa act act tgg gat gaa cga ctt aag ttg 403
 Gln Val Asn Gly Arg Asn Gln Thr Thr Trp Asp Glu Arg Leu Lys Leu
 90 95 100

gat gtc gaa tat gtg gat cgc tgt agt ttg aaa cta gat ttc aaa ata 451
 Asp Val Glu Tyr Val Asp Arg Cys Ser Leu Lys Leu Asp Phe Lys Ile
 105 110 115

tta atc gcc act gta aaa aca gtt ctt tct aaa aag ggc att agt aat 499
 Leu Ile Ala Thr Val Lys Thr Val Leu Ser Lys Lys Gly Ile Ser Asn
 120 125 130

gaa ggt cat gtc acg atg cca tcc ttc att gaa gaa aga aaa 541
 Glu Gly His Val Thr Met Pro Ser Phe Ile Glu Glu Arg Lys
 135 140 145

tagcaggtaa aaattttact ttc 564

<210> 256

<211> 147

<212> PRT

<213> Corynebacterium glutamicum

<400> 256

Val Val Phe Glu Met Ile Lys Phe Arg Thr Met Leu Glu Pro Asp Glu
 1 5 10 15

Lys His Val Thr Asp Glu Gln Arg Leu Thr Lys Val Gly Lys Leu Leu
 20 25 30

Arg Glu Thr Ser Leu Asp Glu Leu Pro Thr Leu Trp Asn Val Phe Lys
 35 40 45

Gly Asp Met Ser Leu Val Gly Pro Arg Pro Leu Leu Val Ser Tyr Leu
 50 55 60

Glu His Tyr Ser Ser Glu Gln Ala Arg Arg His Glu Val Arg Pro Gly
 65 70 75 80

Ile Thr Gly Leu Ala Gln Val Asn Gly Arg Asn Gln Thr Thr Trp Asp
 85 90 95

Glu Arg Leu Lys Leu Asp Val Glu Tyr Val Asp Arg Cys Ser Leu Lys
 100 105 110

Leu Asp Phe Lys Ile Leu Ile Ala Thr Val Lys Thr Val Leu Ser Lys
 115 120 125

Lys Gly Ile Ser Asn Glu Gly His Val Thr Met Pro Ser Phe Ile Glu
 130 135 140

Glu Arg Lys
145

<210> 257
<211> 510
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(487)
<223> RXS01421

<400> 257
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ttactgcagg gatcctgcga gatcgagtaa acgcctaaaag atg acg tcg aaa agc 115
Met Thr Ser Lys Ser
1 5

att agc ggc aag cgc ccg aat ctg ccg tcg ctc act gga gcg cgg tgg 163
Ile Ser Gly Lys Arg Pro Asn Leu Pro Ser Leu Thr Gly Ala Arg Trp
10 15 20

ctc gcg gcg ctc gct gtt tat ttt ttg cat gcg ttg gtg ttt ttg tcg 211
Leu Ala Ala Leu Ala Val Tyr Phe Leu His Ala Leu Val Phe Leu Ser
25 30 35

gtg tat ccg ttc cag cag tcg gaa ctg ttt gcc aca atc cat aaa ttt 259
Val Tyr Pro Phe Gln Gln Ser Glu Leu Phe Ala Thr Ile His Lys Phe
40 45 50

gtc ccc atg cag ctg ggt tca gct ggt gta acc ttc ttc ttt atc ttg 307
Val Pro Met Gln Leu Gly Ser Ala Gly Val Thr Phe Phe Phe Ile Leu
55 60 65

tcc gga ttt ttg atc tat tgg tca aat agc cag ctc aag ggc atg aag 355
Ser Gly Phe Leu Ile Tyr Trp Ser Asn Ser Gln Leu Lys Gly Met Lys
70 75 80 85

aat gtg ctg tat tac tgc aag cgc cgc atc acc aag att tat ccc atg 403
Asn Val Leu Tyr Tyr Cys Lys Arg Arg Ile Thr Lys Ile Tyr Pro Met
90 95 100

cac ttg att gcg ttg ccg atg ttt att gag gcg tcg gcg aag ttc acg 451
His Leu Ile Ala Leu Pro Met Phe Ile Glu Ala Ser Ala Lys Phe Thr
105 110 115

act aca ggc att acc tgg gtg ctg att ttg cgc gag taaagctgtg 497
Thr Thr Gly Ile Thr Trp Val Leu Ile Leu Arg Glu
120 125

gctgcggaat gcg 510

<210> 258
<211> 129
<212> PRT
<213> Corynebacterium glutamicum

<400> 258

Met Thr Ser Lys Ser Ile Ser Gly Lys Arg Pro Asn Leu Pro Ser Leu
 1 5 10 15

Thr Gly Ala Arg Trp Leu Ala Ala Leu Ala Val Tyr Phe Leu His Ala
 20 25 30

Leu Val Phe Leu Ser Val Tyr Pro Phe Gln Gln Ser Glu Leu Phe Ala
 35 40 45

Thr Ile His Lys Phe Val Pro Met Gln Leu Gly Ser Ala Gly Val Thr
 50 55 60

Phe Phe Phe Ile Leu Ser Gly Phe Leu Ile Tyr Trp Ser Asn Ser Gln
 65 70 75 80

Leu Lys Gly Met Lys Asn Val Leu Tyr Tyr Cys Lys Arg Arg Ile Thr
 85 90 95

Lys Ile Tyr Pro Met His Leu Ile Ala Leu Pro Met Phe Ile Glu Ala
 100 105 110

Ser Ala Lys Phe Thr Thr Thr Gly Ile Thr Trp Val Leu Ile Leu Arg
 115 120 125

Glu

<210> 259

<211> 774

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(751)

<223> RXS01491

<400> 259

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gggcagcatg tgtggccata tccagtgatg gaggtggaca atg ctg gat gag tct 115
 Met Leu Asp Glu Ser
 1 5

ttg ttt cca aat tcg gca aag ttt tct ttc att aaa act ggc gat gct 163
 Leu Phe Pro Asn Ser Ala Lys Phe Ser Phe Ile Lys Thr Gly Asp Ala
 10 15 20

gtt aat tta gac cat ttc cat cag ttg cat ccg ttg gaa aag gca ctg 211
 Val Asn Leu Asp His Phe His Gln Leu His Pro Leu Glu Lys Ala Leu
 25 30 35

gta gcg cac tcg gtt gat att aga aaa gca gag ttt gga gat gcc agg 259
 Val Ala His Ser Val Asp Ile Arg Lys Ala Glu Phe Gly Asp Ala Arg
 40 45 50

tgg tgt gca cat cag gca ctc caa gct ttg gga cga gat agc ggt gat 307
 Trp Cys Ala His Gln Ala Leu Gln Ala Leu Gly Arg Asp Ser Gly Asp
 55 60 65

ccc att ttg cgt ggg gaa cga gga atg cca ttg tgg cct tct tcg gtg 355
 Pro Ile Leu Arg Gly Glu Arg Gly Met Pro Leu Trp Pro Ser Ser Val
 70 75 80 85

tct ggt tca ttg acc cac act gac gga ttc cga gct gct gtt gtg gcg 403
 Ser Gly Ser Leu Thr His Thr Asp Gly Phe Arg Ala Ala Val Val Ala
 90 95 100

cca cga ttg ttg gtg cgt tct atg gga ttg gat gcc gaa cct gcg gag 451
 Pro Arg Leu Leu Val Arg Ser Met Gly Leu Asp Ala Glu Pro Ala Glu
 105 110 115

ccg ttg ccc aag gat gtt ttg ggt tca atc gct cgg gtg ggg gag att 499
 Pro Leu Pro Lys Asp Val Leu Gly Ser Ile Ala Arg Val Gly Glu Ile
 120 125 130

cct caa ctt aag cgc ttg gag gaa caa ggt gtg cac tgc gcg gat cgc 547
 Pro Gln Leu Lys Arg Leu Glu Glu Gln Gly Val His Cys Ala Asp Arg
 135 140 145

ctg ctg ttt tgt gcc aag gaa gca aca tac aaa gcg tgg ttc ccg ctg 595
 Leu Leu Phe Cys Ala Lys Glu Ala Thr Tyr Lys Ala Trp Phe Pro Leu
 150 155 160 165

acg cat agg tgg ctt ggt ttt gaa caa gct gag atc gac ttg cgt gat 643
 Thr His Arg Trp Leu Gly Phe Glu Gln Ala Glu Ile Asp Leu Arg Asp
 170 175 180

gat ggc act ttt gtg tcc tat ttg ctg gtt cga cca act cca gtg ccg 691
 Asp Gly Thr Phe Val Ser Tyr Leu Leu Val Arg Pro Thr Pro Val Pro
 185 190 195

ttt att tca ggt aaa tgg gta ctg cgt gat ggt tat gtc ata gct gcg 739
 Phe Ile Ser Gly Lys Trp Val Leu Arg Asp Gly Tyr Val Ile Ala Ala
 200 205 210

act gca gtg act tgaactggat ggagaggata cct 774
 Thr Ala Val Thr
 215

<210> 260

<211> 217

<212> PRT

<213> Corynebacterium glutamicum

<400> 260

Met Leu Asp Glu Ser Leu Phe Pro Asn Ser Ala Lys Phe Ser Phe Ile
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Lys Thr Gly Asp Ala Val Asn Leu Asp His Phe His Gln Leu His Pro
 20 25 30

Leu Glu Lys Ala Leu Val Ala His Ser Val Asp Ile Arg Lys Ala Glu
 35 40 45

Phe Gly Asp Ala Arg Trp Cys Ala His Gln Ala Leu Gln Ala Leu Gly
 50 55 60

Arg Asp Ser Gly Asp Pro Ile Leu Arg Gly Glu Arg Gly Met Pro Leu

65		70		75		80									
Trp	Pro	Ser	Ser	Val	Ser	Gly	Ser	Leu	Thr	His	Thr	Asp	Gly	Phe	Arg
				85					90					95	
Ala	Ala	Val	Val	Ala	Pro	Arg	Leu	Leu	Val	Arg	Ser	Met	Gly	Leu	Asp
			100					105					110		
Ala	Glu	Pro	Ala	Glu	Pro	Leu	Pro	Lys	Asp	Val	Leu	Gly	Ser	Ile	Ala
		115					120					125			
Arg	Val	Gly	Glu	Ile	Pro	Gln	Leu	Lys	Arg	Leu	Glu	Glu	Gln	Gly	Val
	130					135					140				
His	Cys	Ala	Asp	Arg	Leu	Leu	Phe	Cys	Ala	Lys	Glu	Ala	Thr	Tyr	Lys
145					150					155					160
Ala	Trp	Phe	Pro	Leu	Thr	His	Arg	Trp	Leu	Gly	Phe	Glu	Gln	Ala	Glu
				165					170					175	
Ile	Asp	Leu	Arg	Asp	Asp	Gly	Thr	Phe	Val	Ser	Tyr	Leu	Leu	Val	Arg
			180					185					190		
Pro	Thr	Pro	Val	Pro	Phe	Ile	Ser	Gly	Lys	Trp	Val	Leu	Arg	Asp	Gly
		195					200					205			
Tyr	Val	Ile	Ala	Ala	Thr	Ala	Val	Thr							
	210					215									

<210> 261

<211> 615

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(592)

<223> RXS01572

<400> 261

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gacaaagtag	cagtcattggg	cctcggcggg	actcggacac	atg	ggt	gtc	cag	atc		115
				Met	Gly	Val	Gln	Ile		
				1				5		

gct	gca	gcc	aag	ggt	gct	gag	gtt	acc	gtt	ctg	tcc	cgt	tcc	ctg	cgc	163
Ala	Ala	Ala	Lys	Gly	Ala	Glu	Val	Thr	Val	Leu	Ser	Arg	Ser	Leu	Arg	
			10					15						20		

aag	gca	gaa	ctt	gcc	aag	gaa	ctc	ggc	gca	gct	cgc	acg	ctt	gcg	act	211
Lys	Ala	Glu	Leu	Ala	Lys	Glu	Leu	Gly	Ala	Ala	Arg	Thr	Leu	Ala	Thr	
			25					30					35			

tct	gat	gag	gat	ttc	ttc	acc	gaa	cac	gcc	ggt	gaa	ttc	gac	ttc	atc	259
Ser	Asp	Glu	Asp	Phe	Phe	Thr	Glu	His	Ala	Gly	Glu	Phe	Asp	Phe	Ile	
		40					45					50				

ctc	aac	acc	att	agc	gca	tcc	atc	cca	gtc	gac	aag	tac	ctg	agc	ctt	307
Leu	Asn	Thr	Ile	Ser	Ala	Ser	Ile	Pro	Val	Asp	Lys	Tyr	Leu	Ser	Leu	

55	60	65	
ctc aag cca cac ggt gtc atg gct gtt gtc ggt ctg cca cca gag aag			355
Leu Lys Pro His Gly Val Met Ala Val Val Gly Leu Pro Pro Glu Lys			
70	75	80	85
cag cca ctg agc ttc ggt gcg ctc atc ggc ggc gga aaa gtc ctc acc			403
Gln Pro Leu Ser Phe Gly Ala Leu Ile Gly Gly Gly Lys Val Leu Thr			
90	95		100
gga tcc aac att ggc ggc atc cct gaa acc cag gaa atg ctc gac ttc			451
Gly Ser Asn Ile Gly Gly Ile Pro Glu Thr Gln Glu Met Leu Asp Phe			
105	110		115
tgt gca aaa cac ggc ctc ggt gcg atg atc gaa act gtc ggc gtc aac			499
Cys Ala Lys His Gly Leu Gly Ala Met Ile Glu Thr Val Gly Val Asn			
120	125		130
gat gtt gat gca gcc tac gac cgt gtt gtt gcc ggc gac gtt cag ttc			547
Asp Val Asp Ala Ala Tyr Asp Arg Val Val Ala Gly Asp Val Gln Phe			
135	140		145
cgc gtt gtc att gat act gct tcg ttt gct gag gtt gag gcg gtt			592
Arg Val Val Ile Asp Thr Ala Ser Phe Ala Glu Val Glu Ala Val			
150	155		160
taggtttact gaagttcaga ctt			615

<210> 262

<211> 164

<212> PRT

<213> Corynebacterium glutamicum

<400> 262

Met Gly Val Gln Ile Ala Ala Ala Lys Gly Ala Glu Val Thr Val Leu
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Ser Arg Ser Leu Arg Lys Ala Glu Leu Ala Lys Glu Leu Gly Ala Ala
20 25 30

Arg Thr Leu Ala Thr Ser Asp Glu Asp Phe Phe Thr Glu His Ala Gly
35 40 45

Glu Phe Asp Phe Ile Leu Asn Thr Ile Ser Ala Ser Ile Pro Val Asp
50 55 60

Lys Tyr Leu Ser Leu Leu Lys Pro His Gly Val Met Ala Val Val Gly
65 70 75 80

Leu Pro Pro Glu Lys Gln Pro Leu Ser Phe Gly Ala Leu Ile Gly Gly
85 90 95

Gly Lys Val Leu Thr Gly Ser Asn Ile Gly Gly Ile Pro Glu Thr Gln
100 105 110

Glu Met Leu Asp Phe Cys Ala Lys His Gly Leu Gly Ala Met Ile Glu
115 120 125

Thr Val Gly Val Asn Asp Val Asp Ala Ala Tyr Asp Arg Val Val Ala
130 135 140

Gly Asp Val Gln Phe Arg Val Val Ile Asp Thr Ala Ser Phe Ala Glu
 145 150 155 160

Val Glu Ala Val

<210> 263

<211> 876

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(853)

<223> RXS02453

<400> 263

aaccaacaaa ggtcatctca accggcttaa gaaaattctg ccagctttct gctgattgaa 60

tcgtgccagc tcagggcata tctcacctaa agtaaacacc atg aaa tca atc ttc 115
 Met Lys Ser Ile Phe
 1 5

att tcc ggt gcg gcg aac gga att ggc aaa gct gtg gcg ttg aaa ttt 163
 Ile Ser Gly Ala Ala Asn Gly Ile Gly Lys Ala Val Ala Leu Lys Phe
 10 15 20

ctt cac gaa ggt tgg ctc gtt gga gcc tac gac ctc gcg gaa atc acc 211
 Leu His Glu Gly Trp Leu Val Gly Ala Tyr Asp Leu Ala Glu Ile Thr
 25 30 35

tac tca cac ccc aat ctt cgc tgg ggc tac ctc aat gtt cga cag tcc 259
 Tyr Ser His Pro Asn Leu Arg Trp Gly Tyr Leu Asn Val Arg Gln Ser
 40 45 50

gag tcg tgg gac aaa gcc cta gaa gac ttt gcg acg cac acc gga ggc 307
 Glu Ser Trp Asp Lys Ala Leu Glu Asp Phe Ala Thr His Thr Gly Gly
 55 60 65

acc atc gat gtg gtg gac aat aat gcc ggc gta att att gag gga ccg 355
 Thr Ile Asp Val Val Asp Asn Asn Ala Gly Val Ile Ile Glu Gly Pro
 70 75 80 85

ctg cag gac gca gag gag ggg agc gtc gac aag ctt ctt gca atc aac 403
 Leu Gln Asp Ala Glu Glu Gly Ser Val Asp Lys Leu Leu Ala Ile Asn
 90 95 100

gtc aat ggc gtg act ctt ggt gcc cgc gcc gct cat cct tat ttg gcg 451
 Val Asn Gly Val Thr Leu Gly Ala Arg Ala Ala His Pro Tyr Leu Ala
 105 110 115

cgc acg ccg ggc gcc cag ttg tta aac atg tcc tcg gcg tcg gcg gtg 499
 Arg Thr Pro Gly Ala Gln Leu Leu Asn Met Ser Ser Ala Ser Ala Val
 120 125 130

tac ggg cag ccc cag atc gcg gtg tat tcg gct tcg aag ttt tac gtc 547
 Tyr Gly Gln Pro Gln Ile Ala Val Tyr Ser Ala Ser Lys Phe Tyr Val
 135 140 145

gca ggt ctt act gag gcg ctg aat ttg gag tgg cgg aaa gac gat att 595
 Ala Gly Leu Thr Glu Ala Leu Asn Leu Glu Trp Arg Lys Asp Asp Ile
 150 155 160 165

 cgc gtg gtc gat gtt tgg cct ttg tgg gcg aaa acc gat ttg gtg aac 643
 Arg Val Val Asp Val Trp Pro Leu Trp Ala Lys Thr Asp Leu Val Asn
 170 175 180

 ggc gtg aag gct aag tca ctg aag cgt ttg ggt gtc cgg atc act ccg 691
 Gly Val Lys Ala Lys Ser Leu Lys Arg Leu Gly Val Arg Ile Thr Pro
 185 190 195

 gaa cag gtg gca cag gcg gta tgg gat gcg gtg cat ccg aaa tct ccg 739
 Glu Gln Val Ala Gln Ala Val Trp Asp Ala Val His Pro Lys Ser Arg
 200 205 210

 tgg gcg aag gga aag gtg cat cac ggg gtg tca aag ttg gat aag gcg 787
 Trp Ala Lys Gly Lys Val His His Gly Val Ser Lys Leu Asp Lys Ala
 215 220 225

 ctg tat ctc atg aaa tct ctg tgc cct gat cgg gta gcg atg tgt ttt 835
 Leu Tyr Leu Met Lys Ser Leu Ser Pro Asp Arg Val Ala Met Cys Phe
 230 235 240 245

 gcg cga cta atc gcc gga taaatgaatt gattatttta ggc 876
 Ala Arg Leu Ile Ala Gly
 250

<210> 264

<211> 251

<212> PRT

<213> Corynebacterium glutamicum

<400> 264

Met Lys Ser Ile Phe Ile Ser Gly Ala Ala Asn Gly Ile Gly Lys Ala
 1 5 10 15

 Val Ala Leu Lys Phe Leu His Glu Gly Trp Leu Val Gly Ala Tyr Asp
 20 25 30

 Leu Ala Glu Ile Thr Tyr Ser His Pro Asn Leu Arg Trp Gly Tyr Leu
 35 40 45

 Asn Val Arg Gln Ser Glu Ser Trp Asp Lys Ala Leu Glu Asp Phe Ala
 50 55 60

 Thr His Thr Gly Gly Thr Ile Asp Val Val Asp Asn Asn Ala Gly Val
 65 70 75 80

 Ile Ile Glu Gly Pro Leu Gln Asp Ala Glu Glu Gly Ser Val Asp Lys
 85 90 95

 Leu Leu Ala Ile Asn Val Asn Gly Val Thr Leu Gly Ala Arg Ala Ala
 100 105 110

 His Pro Tyr Leu Ala Arg Thr Pro Gly Ala Gln Leu Leu Asn Met Ser
 115 120 125

 Ser Ala Ser Ala Val Tyr Gly Gln Pro Gln Ile Ala Val Tyr Ser Ala
 130 135 140

Ser Lys Phe Tyr Val Ala Gly Leu Thr Glu Ala Leu Asn Leu Glu Trp
 145 150 155 160

Arg Lys Asp Asp Ile Arg Val Val Asp Val Trp Pro Leu Trp Ala Lys
 165 170 175

Thr Asp Leu Val Asn Gly Val Lys Ala Lys Ser Leu Lys Arg Leu Gly
 180 185 190

Val Arg Ile Thr Pro Glu Gln Val Ala Gln Ala Val Trp Asp Ala Val
 195 200 205

His Pro Lys Ser Arg Trp Ala Lys Gly Lys Val His His Gly Val Ser
 210 215 220

Lys Leu Asp Lys Ala Leu Tyr Leu Met Lys Ser Leu Ser Pro Asp Arg
 225 230 235 240

Val Ala Met Cys Phe Ala Arg Leu Ile Ala Gly
 245 250

<210> 265
 <211> 897
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(874)
 <223> RXS02474

<400> 265
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aatcttgaga atttattttg aggaagcaag aggaagtgtc atg agc aaa gtt gca 115
 Met Ser Lys Val Ala
 1 5

atg gtt acc ggt ggt gca caa ggc atc ggt cgt gga att tca gag aag 163
 Met Val Thr Gly Gly Ala Gln Gly Ile Gly Arg Gly Ile Ser Glu Lys
 10 15 20

ctg gca gca gat ggt ttc gat att gcc gta gcc gac ctg cca caa cag 211
 Leu Ala Ala Asp Gly Phe Asp Ile Ala Val Ala Asp Leu Pro Gln Gln
 25 30 35

gaa gaa caa gct gca gag acc atc aag ttg att gaa gct gca ggt caa 259
 Glu Glu Gln Ala Ala Glu Thr Ile Lys Leu Ile Glu Ala Ala Gly Gln
 40 45 50

aag gct gta ttc gtt gga tta gat gtc acc gat aag gct aat ttc gac 307
 Lys Ala Val Phe Val Gly Leu Asp Val Thr Asp Lys Ala Asn Phe Asp
 55 60 65

agt gca att gat gag gca gca gag aaa ctt ggc ggc ttc gat gtg cta 355
 Ser Ala Ile Asp Glu Ala Ala Glu Lys Leu Gly Gly Phe Asp Val Leu
 70 75 80 85

gta aac aac gcc ggc atc gca caa att aag cca ctt ctg gaa gtc acc 403

Val Asn Asn Ala Gly Ile Ala Gln Ile Lys Pro Leu Leu Glu Val Thr
 90 95 100
 gaa gaa gac cta aag cag atc tac tcc gtg aac gtt ttt agc gta ttt 451
 Glu Glu Asp Leu Lys Gln Ile Tyr Ser Val Asn Val Phe Ser Val Phe
 105 110 115
 ttt ggt att caa gca gca tcc cga aag ttc gat gag ctt ggc gta aaa 499
 Phe Gly Ile Gln Ala Ala Ser Arg Lys Phe Asp Glu Leu Gly Val Lys
 120 125 130
 ggc aag atc atc aac gct gca tca atc gct gct atc caa ggt ttc cca 547
 Gly Lys Ile Ile Asn Ala Ala Ser Ile Ala Ala Ile Gln Gly Phe Pro
 135 140 145
 atc ttg agc gcc tac tcc acc acc aaa ttc gcg gtt cgt ggc ctc acc 595
 Ile Leu Ser Ala Tyr Ser Thr Thr Lys Phe Ala Val Arg Gly Leu Thr
 150 155 160 165
 cag gct gct gcg caa gaa ctc gca ccc aag ggt cac acc gtg aat gcc 643
 Gln Ala Ala Ala Gln Glu Leu Ala Pro Lys Gly His Thr Val Asn Ala
 170 175 180
 tac gca cct ggc atc gtg ggc acc gga atg tgg gag caa atc gat gcc 691
 Tyr Ala Pro Gly Ile Val Gly Thr Gly Met Trp Glu Gln Ile Asp Ala
 185 190 195
 gag ctt tcc aag atc aac ggc aag cca atc ggt gag aac ttc aag gag 739
 Glu Leu Ser Lys Ile Asn Gly Lys Pro Ile Gly Glu Asn Phe Lys Glu
 200 205 210
 tac tcc tcc tca atc gca ttg ggc cga cca tca gta cct gag gat gta 787
 Tyr Ser Ser Ser Ile Ala Leu Gly Arg Pro Ser Val Pro Glu Asp Val
 215 220 225
 gcc ggt ctg gtt tcg ttc ctg gct tct gaa aac tcc aac tac atc acc 835
 Ala Gly Leu Val Ser Phe Leu Ala Ser Glu Asn Ser Asn Tyr Ile Thr
 230 235 240 245
 gga cag gtc atg ctt gtc gac ggc ggc atg ctc tac aac tagggggttc 884
 Gly Gln Val Met Leu Val Asp Gly Gly Met Leu Tyr Asn
 250 255
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<210> 266

<211> 258

<212> PRT

<213> Corynebacterium glutamicum

<400> 266

Met Ser Lys Val Ala Met Val Thr Gly Gly Ala Gln Gly Ile Gly Arg
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Gly Ile Ser Glu Lys Leu Ala Ala Asp Gly Phe Asp Ile Ala Val Ala
 20 25 30

Asp Leu Pro Gln Gln Glu Glu Gln Ala Ala Glu Thr Ile Lys Leu Ile
 35 40 45

Glu Ala Ala Gly Gln Lys Ala Val Phe Val Gly Leu Asp Val Thr Asp
 50 55 60
 Lys Ala Asn Phe Asp Ser Ala Ile Asp Glu Ala Ala Glu Lys Leu Gly
 65 70 75 80
 Gly Phe Asp Val Leu Val Asn Asn Ala Gly Ile Ala Gln Ile Lys Pro
 85 90 95
 Leu Leu Glu Val Thr Glu Glu Asp Leu Lys Gln Ile Tyr Ser Val Asn
 100 105 110
 Val Phe Ser Val Phe Phe Gly Ile Gln Ala Ala Ser Arg Lys Phe Asp
 115 120 125
 Glu Leu Gly Val Lys Gly Lys Ile Ile Asn Ala Ala Ser Ile Ala Ala
 130 135 140
 Ile Gln Gly Phe Pro Ile Leu Ser Ala Tyr Ser Thr Thr Lys Phe Ala
 145 150 155 160
 Val Arg Gly Leu Thr Gln Ala Ala Ala Gln Glu Leu Ala Pro Lys Gly
 165 170 175
 His Thr Val Asn Ala Tyr Ala Pro Gly Ile Val Gly Thr Gly Met Trp
 180 185 190
 Glu Gln Ile Asp Ala Glu Leu Ser Lys Ile Asn Gly Lys Pro Ile Gly
 195 200 205
 Glu Asn Phe Lys Glu Tyr Ser Ser Ser Ile Ala Leu Gly Arg Pro Ser
 210 215 220
 Val Pro Glu Asp Val Ala Gly Leu Val Ser Phe Leu Ala Ser Glu Asn
 225 230 235 240
 Ser Asn Tyr Ile Thr Gly Gln Val Met Leu Val Asp Gly Gly Met Leu
 245 250 255

Tyr Asn

<210> 267

<211> 1224

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1201)

<223> RXS02485

<400> 267

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tacgcgttgc catgaggata agactaccgt tagtgggggtg ttg gat tca tcg cta 115
 Leu Asp Ser Ser Leu
 1 5

gcc cag gaa atc gcc gcg atc gac ggc gtc gaa ctc gat tcg gaa gtc 163

Ala	Gln	Glu	Ile	Ala	Ala	Ile	Asp	Gly	Val	Glu	Leu	Asp	Ser	Glu	Val		
				10					15					20			
act	ttc	gcc	gat	ctg	acg	acc	ctc	cgc	atc	ggc	gga	aaa	ccc	cgc	agc	211	
Thr	Phe	Ala	Asp	Leu	Thr	Thr	Leu	Arg	Ile	Gly	Gly	Lys	Pro	Arg	Ser		
			25					30					35				
gcc	gta	cgt	tgc	cag	acc	acg	gag	gcg	ctg	gtc	agc	gcc	ata	aaa	ttg	259	
Ala	Val	Arg	Cys	Gln	Thr	Thr	Glu	Ala	Leu	Val	Ser	Ala	Ile	Lys	Leu		
		40					45				50						
ctt	gac	gac	gcc	tcc	ctc	ccc	ctc	ctc	att	gtc	ggc	ggc	ggg	tcc	aat	307	
Leu	Asp	Asp	Ala	Ser	Leu	Pro	Leu	Leu	Ile	Val	Gly	Gly	Gly	Ser	Asn		
	55					60					65						
ctc	gtc	gtg	gcc	gac	ggc	gat	ctg	gat	gtt	att	gcc	gtc	atc	atc	gaa	355	
Leu	Val	Val	Ala	Asp	Gly	Asp	Leu	Asp	Val	Ile	Ala	Val	Ile	Ile	Glu		
70					75					80					85		
acc	gac	gac	gtc	tcc	atc	aac	ctc	acc	gac	ggc	ctc	ctc	acc	gcc	gat	403	
Thr	Asp	Asp	Val	Ser	Ile	Asn	Leu	Thr	Asp	Gly	Leu	Leu	Thr	Ala	Asp		
				90					95					100			
gca	ggc	gct	gtt	tgg	gac	gat	gtt	gtc	cac	ctt	tcg	gtg	gat	gcc	ggc	451	
Ala	Gly	Ala	Val	Trp	Asp	Asp	Val	Val	His	Leu	Ser	Val	Asp	Ala	Gly		
			105					110					115				
ctc	ggc	gga	att	gaa	tgc	ctc	tcc	gga	atc	ccc	ggc	tcc	gcc	ggc	gcc	499	
Leu	Gly	Gly	Ile	Glu	Cys	Leu	Ser	Gly	Ile	Pro	Gly	Ser	Ala	Gly	Ala		
	120						125					130					
acc	cca	gtc	caa	aac	gtg	ggc	gcc	tac	ggc	acg	gaa	gtt	tcc	gat	gta	547	
Thr	Pro	Val	Gln	Asn	Val		Ala	Tyr	Gly	Thr	Glu	Val	Ser	Asp	Val		
	135					140					145						
ctc	acc	cgc	gtc	cag	ctt	ctc	gac	cgc	acc	acc	cac	caa	gtc	tcc	tgg	595	
Leu	Thr	Arg	Val	Gln	Leu	Leu	Asp	Arg	Thr	Thr	His	Gln	Val	Ser	Trp		
150					155					160					165		
gtc	gac	gcc	tcc	gaa	ctc	gac	ctc	tct	tac	cga	tac	tcc	aat	ctc	aaa	643	
Val	Asp	Ala	Ser	Glu	Leu	Asp	Leu	Ser	Tyr	Arg	Tyr	Ser	Asn	Leu	Lys		
				170					175					180			
ttc	acc	aac	cgc	gca	gtc	gtc	ttg	gcg	atc	gaa	ctc	cag	ctc	ctc	acc	691	
Phe	Thr	Asn	Arg	Ala	Val	Val	Leu	Ala	Ile	Glu	Leu	Gln	Leu	Leu	Thr		
			185					190					195				
gac	gga	ttg	tcc	gcg	ccg	cta	cgt	ttt	ggc	gaa	ttg	gga	cgt	cga	tta	739	
Asp	Gly	Leu	Ser	Ala	Pro	Leu	Arg	Phe	Gly	Glu	Leu	Gly	Arg	Arg	Leu		
		200					205					210					
gcg	atc	tcc	gag	gcc	gaa	ccc	cac	cca	cgt	cgc	ccc	gtc	cgc	atg	gtc	787	
Ala	Ile	Ser	Glu	Ala	Glu	Pro	His	Pro	Arg	Arg	Pro	Val	Arg	Met	Val		
	215					220					225						
cgc	gac	gcc	gtc	cta	gaa	ctc	cgc	cgc	gcc	aaa	ggc	atg	gtc	gtg	gaa	835	
Arg	Asp	Ala	Val	Leu	Glu	Leu	Arg	Arg	Ala	Lys	Gly	Met	Val	Val	Glu		
230					235					240					245		
cac	acc	gac	cac	gac	acc	tgg	tcc	gcc	gga	tcc	ttc	ttc	acc	aac	cca	883	
His	Thr	Asp	His	Asp	Thr	Trp	Ser	Ala	Gly	Ser	Phe	Phe	Thr	Asn	Pro		

250										255					260					
atc gtc gac cca gcc ctt gcc gac gca gtc ttt gaa aaa gtc ggc gaa	931																			
Ile Val Asp Pro Ala Leu Ala Asp Ala Val Phe Glu Lys Val Gly Glu																				
265	270	275																		
ccc acc atg ccc cgc ttc cca gcc ggc gat ggc aaa gaa aaa ctc tcc	979																			
Pro Thr Met Pro Arg Phe Pro Ala Gly Asp Gly Lys Glu Lys Leu Ser																				
280	285	290																		
gca gcc tgg ctc atc gaa cgc gcc ggc ttc aaa aag gga cac ccc ggc	1027																			
Ala Ala Trp Leu Ile Glu Arg Ala Gly Phe Lys Lys Gly His Pro Gly																				
295	300	305																		
gca ggc gca aaa gcc tcc ctg agc acc aaa cac acc ctc gca ctc acc	1075																			
Ala Gly Ala Lys Ala Ser Leu Ser Thr Lys His Thr Leu Ala Leu Thr																				
310	315	320	325																	
aac cgt ggc gac gcc cgc gcc tcc gac ctc gtc gca tta gcc aaa gaa	1123																			
Asn Arg Gly Asp Ala Arg Ala Ser Asp Leu Val Ala Leu Ala Lys Glu																				
330	335	340																		
atc cgc gac gga gtc ctc gaa acc ttc ggc gtc acc ctc gtc cca gaa	1171																			
Ile Arg Asp Gly Val Leu Glu Thr Phe Gly Val Thr Leu Val Pro Glu																				
345	350	355																		
ccc gtc tgg att gga atc agc atc gat gac tgaattttcc gacgtccctg	1221																			
Pro Val Trp Ile Gly Ile Ser Ile Asp Asp																				
360	365																			
gca	1224																			
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<211> 367																				
<212> PRT																				
<213> Corynebacterium glutamicum																				
<400> 268																				
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Leu Asp Ser Glu Val Thr Phe Ala Asp Leu Thr Thr Leu Arg Ile Gly																				
20	25	30																		
Gly Lys Pro Arg Ser Ala Val Arg Cys Gln Thr Thr Glu Ala Leu Val																				
35	40	45																		
Ser Ala Ile Lys Leu Leu Asp Asp Ala Ser Leu Pro Leu Leu Ile Val																				
50	55	60																		
Gly Gly Gly Ser Asn Leu Val Val Ala Asp Gly Asp Leu Asp Val Ile																				
65	70	75	80																	
Ala Val Ile Ile Glu Thr Asp Asp Val Ser Ile Asn Leu Thr Asp Gly																				
85	90	95																		
Leu Leu Thr Ala Asp Ala Gly Ala Val Trp Asp Asp Val Val His Leu																				
100	105	110																		
Ser Val Asp Ala Gly Leu Gly Gly Ile Glu Cys Leu Ser Gly Ile Pro																				

115					120					125					
Gly	Ser	Ala	Gly	Ala	Thr	Pro	Val	Gln	Asn	Val	Gly	Ala	Tyr	Gly	Thr
130						135					140				
Glu	Val	Ser	Asp	Val	Leu	Thr	Arg	Val	Gln	Leu	Leu	Asp	Arg	Thr	Thr
145					150					155					160
His	Gln	Val	Ser	Trp	Val	Asp	Ala	Ser	Glu	Leu	Asp	Leu	Ser	Tyr	Arg
				165					170					175	
Tyr	Ser	Asn	Leu	Lys	Phe	Thr	Asn	Arg	Ala	Val	Val	Leu	Ala	Ile	Glu
			180					185					190		
Leu	Gln	Leu	Leu	Thr	Asp	Gly	Leu	Ser	Ala	Pro	Leu	Arg	Phe	Gly	Glu
		195					200					205			
Leu	Gly	Arg	Arg	Leu	Ala	Ile	Ser	Glu	Ala	Glu	Pro	His	Pro	Arg	Arg
	210					215					220				
Pro	Val	Arg	Met	Val	Arg	Asp	Ala	Val	Leu	Glu	Leu	Arg	Arg	Ala	Lys
225					230					235					240
Gly	Met	Val	Val	Glu	His	Thr	Asp	His	Asp	Thr	Trp	Ser	Ala	Gly	Ser
				245					250					255	
Phe	Phe	Thr	Asn	Pro	Ile	Val	Asp	Pro	Ala	Leu	Ala	Asp	Ala	Val	Phe
			260					265					270		
Glu	Lys	Val	Gly	Glu	Pro	Thr	Met	Pro	Arg	Phe	Pro	Ala	Gly	Asp	Gly
		275					280					285			
Lys	Glu	Lys	Leu	Ser	Ala	Ala	Trp	Leu	Ile	Glu	Arg	Ala	Gly	Phe	Lys
	290					295					300				
Lys	Gly	His	Pro	Gly	Ala	Gly	Ala	Lys	Ala	Ser	Leu	Ser	Thr	Lys	His
305					310					315					320
Thr	Leu	Ala	Leu	Thr	Asn	Arg	Gly	Asp	Ala	Arg	Ala	Ser	Asp	Leu	Val
				325					330					335	
Ala	Leu	Ala	Lys	Glu	Ile	Arg	Asp	Gly	Val	Leu	Glu	Thr	Phe	Gly	Val
			340					345					350		
Thr	Leu	Val	Pro	Glu	Pro	Val	Trp	Ile	Gly	Ile	Ser	Ile	Asp	Asp	
		355					360					365			

<210> 269

<211> 1641

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1618)

<223> RXS02539

<400> 269

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aat cca gga acc gaa ggc tcg atc gtt aac tat											gaa Glu	aag Lys	cgc Arg	tac Tyr	gag Glu	163 20	
Asn Pro Gly Thr 10											Val 15	Tyr					
aac tac att ggt ggc aag tgg gtt cca ccg gta											gag Glu	ggc Gly	cag Gln	tac Tyr	ctt Leu	211 35	
Asn Tyr Ile 25											Pro 30	Pro	Val				
gag aac att tca cct gtc act ggt gaa gtt ttc tgt											gag Glu	gtc Val	gca Ala	cgt Arg	259 50		
Glu Asn Ile Ser Pro Val Thr Gly 45											Glu	Val	Phe	Cys			
ggc acc gca gcg gac gtg gag ctt gca ctg gat gct											gca Ala	cat His	gca Ala	gcc Ala	307 65		
Gly Thr Ala Ala Asp Val Glu Leu 60											Ala	Leu	Asp				
gct gat gcg tgg ggc aag act tct gtc gct gaa cgt											gct Ala	ctg Leu	atc Ile	ctg Leu	355 85		
Ala Asp Ala Trp Gly Lys Thr Ser Val Ala Glu Arg 70 75 80																	
cac cgc att gcg gac cgc atg gaa gag cac ctg gaa gaa atc											gca Ala	gtt Val	403 100				
His Arg Ile Ala Asp Arg Met Glu Glu His Leu Glu Glu Ile 90 95																	
gca gaa acc tgg gag aac ggc aag gca gtc cgt gag act ctt											gct Ala	gca Ala	451 115				
Ala Glu Thr Trp Glu Asn Gly Lys Ala Val Arg Glu Thr Leu 105 110																	
gat atc cca ctg gca atc gac cac ttc cgc tac ttt gct ggc gcg atc											gct Ala	gca Ala	499 130				
Asp Ile Pro Leu Ala Ile Asp His Phe Arg Tyr Phe Ala Gly Ala Ile 120 125																	
cgt gct cag gaa gat cgt tcc tca cag atc gac cac aac act gtt gct											gct Ala	gca Ala	547 145				
Arg Ala Gln Glu Asp Arg Ser Ser Gln Ile Asp His Asn Thr Val Ala 135 140																	
tac cac ttc aac gag cca atc ggt gtt gtt ggt cag atc att cct tgg											gct Ala	gca Ala	595 165				
Tyr His Phe Asn Glu Pro Ile Gly Val Val Gly Gln Ile Ile Pro Trp 150 155 160																	
aac ttc cca atc ctc atg gct acc tgg aag ctc gca ccg gca ctt gct											gct Ala	gca Ala	643 180				
Asn Phe Pro Ile Leu Met Ala Thr Trp Lys Leu Ala Pro Ala Leu Ala 170 175																	
gca ggt aac gcg atc gtc atg aag cca gct gag cag acc cca gca tcc											gct Ala	gca Ala	691 195				
Ala Gly Asn Ala Ile Val Met Lys Pro Ala Glu Gln Thr Pro Ala Ser 185 190																	
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Ile Leu Tyr Leu Ile Asn Ile Ile Gly Asp Leu Ile Pro Glu Gly Val 200 205																	
ctc aac atc gtc aac gga ctc ggc ggt gaa gca ggc gct gca ctg tcc											gct Ala	gca Ala	787 225				
Leu Asn Ile Val Asn Gly Leu Gly Gly Glu Ala Gly Ala Ala Leu Ser 215 220																	
ggc tct aat cgg att ggc aag att gct ttc acc ggt tcc acc gag gtc											gct Ala	gca Ala	835				

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Gly	Lys	Leu	Ile	Asn 250	Arg	Ala	Ala	Ser	Asp 255	Lys	Ile	Ile	Pro	Val 260	Thr	
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Leu	Glu	Leu	Gly 265	Gly	Lys	Ser	Pro	Ser 270	Ile	Phe	Phe	Ser	Asp 275	Val	Leu	
tca	cag	gat	gac	gcc	ttc	gca	gag	aag	gca	gtt	gaa	ggc	ttc	gcg	atg	979
Ser	Gln	Asp 280	Asp	Ala	Phe	Ala	Glu 285	Lys	Ala	Val	Glu	Gly 290	Phe	Ala	Met	
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Phe	Ala 295	Leu	Asn	Gln	Gly 300	Glu	Val	Cys	Thr	Cys	Pro 305	Ser	Arg	Ala	Leu	
gtt	cat	gag	tcc	atc	gct	gat	gaa	ttc	ctc	gag	ctt	ggc	gtg	aag	cga	1075
Val	His	Glu	Ser	Ile	Ala 315	Asp	Glu	Phe	Leu	Glu 320	Leu	Gly	Val	Lys	Arg 325	
gtt	cag	aac	atc	aag	ctg	ggg	aac	cca	ctt	gat	act	gaa	acc	atg	atg	1123
Val	Gln	Asn	Ile	Lys 330	Leu	Gly	Asn	Pro 335	Leu	Asp	Thr	Glu	Thr	Met 340	Met	
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Gly	Ala	Gln 345	Ala	Ser	Gln	Glu	Gln	Met 350	Asp	Lys	Ile	Ser	Ser	Tyr	Leu	
aag	atc	ggc	cca	gaa	gaa	ggc	gct	caa	acc	ctc	act	ggg	ggc	aag	gtc	1219
Lys	Ile	Gly 360	Pro	Glu	Glu	Gly	Ala 365	Gln	Thr	Leu	Thr	Gly 370	Gly	Lys	Val	
aac	aag	gtt	gat	ggc	atg	gag	aac	ggg	tac	tac	att	gag	cca	acc	gtt	1267
Asn	Lys	Val	Asp	Gly	Met	Glu	Asn 380	Gly	Tyr	Tyr	Ile 385	Glu	Pro	Thr	Val	
ttc	cgc	ggc	acc	aac	gac	atg	agg	atc	ttc	cgc	gag	gaa	atc	ttc	gga	1315
Phe	Arg	Gly	Thr	Asn	Asp 395	Met	Arg	Ile	Phe	Arg 400	Glu	Glu	Ile	Phe	Gly 405	
cca	gtc	ctt	tct	gtt	gct	acc	ttc	agc	gac	ttc	gat	gag	gcc	atc	cgt	1363
Pro	Val	Leu	Ser	Val 410	Ala	Thr	Phe	Ser	Asp 415	Phe	Asp	Glu	Ala	Ile	Arg 420	
att	gca	aac	gac	acc	aac	tac	ggc	ctc	ggc	gct	ggg	gtc	tgg	agc	cgt	1411
Ile	Ala	Asn	Asp 425	Thr	Asn	Tyr	Gly 430	Leu	Gly	Ala	Gly	Val	Trp 435	Ser	Arg	
gac	caa	aac	acc	att	tat	cgt	gca	ggg	cgc	gca	atc	cag	gct	ggg	cga	1459
Asp	Gln	Asn 440	Thr	Ile	Tyr	Arg	Ala 445	Gly	Arg	Ala	Ile	Gln	Ala	Gly	Arg	
gtt	tgg	gtc	aac	cag	tac	cac	aac	tac	cca	gcg	cac	tcc	gct	ttc	ggg	1507
Val	Trp 455	Val	Asn	Gln	Tyr	His 460	Asn	Tyr	Pro	Ala	His 465	Ser	Ala	Phe	Gly	
gga	tac	aag	gag	tcc	ggc	atc	ggc	cgt	gag	aac	cac	ctc	atg	atg	ctg	1555
Gly	Tyr	Lys	Glu	Ser	Gly	Ile	Gly	Arg	Glu	Asn	His	Leu	Met	Met	Leu	

470 475 480 485
 aac cac tac cag cag acc aag aac ctg ttg gtc tcc tac gat cca aac 1603
 Asn His Tyr Gln Gln Thr Lys Asn Leu Leu Val Ser Tyr Asp Pro Asn
 490 495 500

cca acc gga ctg ttc tgatctaagc gttaagtcct aga 1641
 Pro Thr Gly Leu Phe
 505

<210> 270
 <211> 506
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 270
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 20 25 30

Glu Gly Gln Tyr Leu Glu Asn Ile Ser Pro Val Thr Gly Glu Val Phe
 35 40 45

Cys Glu Val Ala Arg Gly Thr Ala Ala Asp Val Glu Leu Ala Leu Asp
 50 55 60

Ala Ala His Ala Ala Ala Asp Ala Trp Gly Lys Thr Ser Val Ala Glu
 65 70 75 80

Arg Ala Leu Ile Leu His Arg Ile Ala Asp Arg Met Glu Glu His Leu
 85 90 95

Glu Glu Ile Ala Val Ala Glu Thr Trp Glu Asn Gly Lys Ala Val Arg
 100 105 110

Glu Thr Leu Ala Ala Asp Ile Pro Leu Ala Ile Asp His Phe Arg Tyr
 115 120 125

Phe Ala Gly Ala Ile Arg Ala Gln Glu Asp Arg Ser Ser Gln Ile Asp
 130 135 140

His Asn Thr Val Ala Tyr His Phe Asn Glu Pro Ile Gly Val Val Gly
 145 150 155 160

Gln Ile Ile Pro Trp Asn Phe Pro Ile Leu Met Ala Thr Trp Lys Leu
 165 170 175

Ala Pro Ala Leu Ala Ala Gly Asn Ala Ile Val Met Lys Pro Ala Glu
 180 185 190

Gln Thr Pro Ala Ser Ile Leu Tyr Leu Ile Asn Ile Ile Gly Asp Leu
 195 200 205

Ile Pro Glu Gly Val Leu Asn Ile Val Asn Gly Leu Gly Gly Glu Ala
 210 215 220

Gly Ala Ala Leu Ser Gly Ser Asn Arg Ile Gly Lys Ile Ala Phe Thr
 225 230 235 240

Gly Ser Thr Glu Val Gly Lys Leu Ile Asn Arg Ala Ala Ser Asp Lys
 245 250 255
 Ile Ile Pro Val Thr Leu Glu Leu Gly Gly Lys Ser Pro Ser Ile Phe
 260 265 270
 Phe Ser Asp Val Leu Ser Gln Asp Asp Ala Phe Ala Glu Lys Ala Val
 275 280 285
 Glu Gly Phe Ala Met Phe Ala Leu Asn Gln Gly Glu Val Cys Thr Cys
 290 295 300
 Pro Ser Arg Ala Leu Val His Glu Ser Ile Ala Asp Glu Phe Leu Glu
 305 310 315 320
 Leu Gly Val Lys Arg Val Gln Asn Ile Lys Leu Gly Asn Pro Leu Asp
 325 330 335
 Thr Glu Thr Met Met Gly Ala Gln Ala Ser Gln Glu Gln Met Asp Lys
 340 345 350
 Ile Ser Ser Tyr Leu Lys Ile Gly Pro Glu Glu Gly Ala Gln Thr Leu
 355 360 365
 Thr Gly Gly Lys Val Asn Lys Val Asp Gly Met Glu Asn Gly Tyr Tyr
 370 375 380
 Ile Glu Pro Thr Val Phe Arg Gly Thr Asn Asp Met Arg Ile Phe Arg
 385 390 395 400
 Glu Glu Ile Phe Gly Pro Val Leu Ser Val Ala Thr Phe Ser Asp Phe
 405 410 415
 Asp Glu Ala Ile Arg Ile Ala Asn Asp Thr Asn Tyr Gly Leu Gly Ala
 420 425 430
 Gly Val Trp Ser Arg Asp Gln Asn Thr Ile Tyr Arg Ala Gly Arg Ala
 435 440 445
 Ile Gln Ala Gly Arg Val Trp Val Asn Gln Tyr His Asn Tyr Pro Ala
 450 455 460
 His Ser Ala Phe Gly Gly Tyr Lys Glu Ser Gly Ile Gly Arg Glu Asn
 465 470 475 480
 His Leu Met Met Leu Asn His Tyr Gln Gln Thr Lys Asn Leu Leu Val
 485 490 495
 Ser Tyr Asp Pro Asn Pro Thr Gly Leu Phe
 500 505

<210> 271

<211> 1227

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1204)

<223> RXS02578

<400> 271

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ggcaaaaatg aggaacagca cgcccgcaat aatgaggacc gttgcagatc gcttcataaa 60

aacagcccac acctttccgc taaactcgca tggtgaaata atg tct acc caa tca 115
                                         Met Ser Thr Gln Ser
                                         1 5

tat gca ccc atc cgc cat cgc gga ttc atc agc tca ctc gag gga cta 163
Tyr Ala Pro Ile Arg His Arg Gly Phe Ile Ser Ser Leu Glu Gly Leu
                        10 15 20

cgc gca atc gcc tcc ctg gga gtc ttg gcg acc cac gtt gca ttc caa 211
Arg Ala Ile Ala Ser Leu Gly Val Leu Ala Thr His Val Ala Phe Gln
                        25 30 35

acc tcc gtc gac ccc gcc agc aac atc ggt gca gta ctc gcg cgt ttc 259
Thr Ser Val Asp Pro Ala Ser Asn Ile Gly Ala Val Leu Ala Arg Phe
                        40 45 50

gac ttt ttc gtc gcc gtc ttc ttc gcc ctc tcc gcc ttc gtt ctt tgg 307
Asp Phe Phe Val Ala Val Phe Phe Ala Leu Ser Ala Phe Val Leu Trp
                        55 60 65

cga cgc cgc gcc ggg caa cca gtg gga ctg tac tac ctc aaa cgc cta 355
Arg Arg Arg Ala Gly Gln Pro Val Gly Leu Tyr Tyr Leu Lys Arg Leu
                        70 75 80 85

gcc cgc atc atg ccc gca tac tgg gca acg gtc att gca gtc ctg ctg 403
Ala Arg Ile Met Pro Ala Tyr Trp Ala Thr Val Ile Ala Val Leu Leu
                        90 95 100

ttt att ccc acc ggc ccc tgg tta gcc aac ctg acg atg acc caa atc 451
Phe Ile Pro Thr Gly Pro Trp Leu Ala Asn Leu Thr Met Thr Gln Ile
                        105 110 115

tac tgg cca gac ggg ctc atg aca ggc ctc acc cac ctt tgg tcc ctg 499
Tyr Trp Pro Asp Gly Leu Met Thr Gly Leu Thr His Leu Trp Ser Leu
                        120 125 130

tgc gtg gaa gtg gcg ttt tac ctg gtg atg ccg ctt ctc gcg tgg gtg 547
Cys Val Glu Val Ala Phe Tyr Leu Val Met Pro Leu Leu Ala Trp Val
                        135 140 145

ttg gat agg ttt ggt cgg ccg gtg cgc atc ctg ttg att gtt ggt ggg 595
Leu Asp Arg Phe Gly Arg Pro Val Arg Ile Leu Leu Ile Val Gly Gly
                        150 155 160 165

gca gtg ttg agt ctg gcg tgg ccg tgg att ccc ctt gtg gag cat gcg 643
Ala Val Leu Ser Leu Ala Trp Pro Trp Ile Pro Leu Val Glu His Ala
                        170 175 180

ttg gac gag ggg tgg gcg aac atg cag atc tgg cca ccc gct tac gct 691
Leu Asp Glu Gly Trp Ala Asn Met Gln Ile Trp Pro Pro Ala Tyr Ala
                        185 190 195

tgc tgg ttt gca gtc ggc atg atc gcc gca gaa att gaa gga gtt cga 739
Cys Trp Phe Ala Val Gly Met Ile Ala Ala Glu Ile Glu Gly Val Arg
                        200 205 210

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ttc cca cgg gtt ccg agc ttt gtg tgg gtg ggt tta gct tta gtg gtc 787
Phe Pro Arg Val Pro Ser Phe Val Trp Val Gly Leu Ala Leu Val Val
215 220 225

gct tgg atc gcg ggc caa gaa tgg ttc gga cca cta ggt tta gtg cac 835
Ala Trp Ile Ala Gly Gln Glu Trp Phe Gly Pro Leu Gly Leu Val His
230 235 240 245

ccc agc ccc tgg gaa ttc aac tta aga gtc ctc gcg ggc aca ctt ttc 883
Pro Ser Pro Trp Glu Phe Asn Leu Arg Val Leu Ala Gly Thr Leu Phe
250 255 260

gct gta ttt ctg gtg gtt ccc tac gcg ctg ggt acg ccc tct cgg ctt 931
Ala Val Phe Leu Val Val Pro Tyr Ala Leu Gly Thr Pro Ser Arg Leu
265 270 275

ctt gat tcc agt tgg atg aaa acg ctc ggc acc tgg tcg tat tcc atc 979
Leu Asp Ser Ser Trp Met Lys Thr Leu Gly Thr Trp Ser Tyr Ser Ile
280 285 290

ttc ctc tgg cac ctt ccc gtg ctg acg att gtg ttc cca ctg ctc ggg 1027
Phe Leu Trp His Leu Pro Val Leu Thr Ile Val Phe Pro Leu Leu Gly
295 300 305

ttg cct tta ttt agt gga aat ttc ctg ttg gtg ttc atc gtg acg gtc 1075
Leu Pro Leu Phe Ser Gly Asn Phe Leu Leu Val Phe Ile Val Thr Val
310 315 320 325

ttg ttg acg atc cca gtt gcc gcc atc agc tac acc ttc atc gaa gag 1123
Leu Leu Thr Ile Pro Val Ala Ala Ile Ser Tyr Thr Phe Ile Glu Glu
330 335 340

ccc atc agc ggt gga ccc ggc gcg cca ttc agg ctg ggg gtc gtt agg 1171
Pro Ile Ser Gly Gly Pro Gly Ala Pro Phe Arg Leu Gly Val Val Arg
345 350 355

att cac cat ttt tct ggg ggt agg tct gga aaa tgatgaattg gcaccacgtc 1224
Ile His His Phe Ser Gly Gly Arg Ser Gly Lys
360 365

aag 1227

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<210> 272

<211> 368

<212> PRT

<213> Corynebacterium glutamicum

<400> 272

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Met Ser Thr Gln Ser Tyr Ala Pro Ile Arg His Arg Gly Phe Ile Ser
1 5 10 15

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Ser Leu Glu Gly Leu Arg Ala Ile Ala Ser Leu Gly Val Leu Ala Thr
20 25 30

```

```

His Val Ala Phe Gln Thr Ser Val Asp Pro Ala Ser Asn Ile Gly Ala
35 40 45

```

```

Val Leu Ala Arg Phe Asp Phe Phe Val Ala Val Phe Phe Ala Leu Ser
50 55 60

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Ala	Phe	Val	Leu	Trp	Arg	Arg	Arg	Ala	Gly	Gln	Pro	Val	Gly	Leu	Tyr	65	70	75	80
Tyr	Leu	Lys	Arg	Leu	Ala	Arg	Ile	Met	Pro	Ala	Tyr	Trp	Ala	Thr	Val	85	90	95	
Ile	Ala	Val	Leu	Leu	Phe	Ile	Pro	Thr	Gly	Pro	Trp	Leu	Ala	Asn	Leu	100	105	110	
Thr	Met	Thr	Gln	Ile	Tyr	Trp	Pro	Asp	Gly	Leu	Met	Thr	Gly	Leu	Thr	115	120	125	
His	Leu	Trp	Ser	Leu	Cys	Val	Glu	Val	Ala	Phe	Tyr	Leu	Val	Met	Pro	130	135	140	
Leu	Leu	Ala	Trp	Val	Leu	Asp	Arg	Phe	Gly	Arg	Pro	Val	Arg	Ile	Leu	145	150	155	160
Leu	Ile	Val	Gly	Gly	Ala	Val	Leu	Ser	Leu	Ala	Trp	Pro	Trp	Ile	Pro	165	170	175	
Leu	Val	Glu	His	Ala	Leu	Asp	Glu	Gly	Trp	Ala	Asn	Met	Gln	Ile	Trp	180	185	190	
Pro	Pro	Ala	Tyr	Ala	Cys	Trp	Phe	Ala	Val	Gly	Met	Ile	Ala	Ala	Glu	195	200	205	
Ile	Glu	Gly	Val	Arg	Phe	Pro	Arg	Val	Pro	Ser	Phe	Val	Trp	Val	Gly	210	215	220	
Leu	Ala	Leu	Val	Val	Ala	Trp	Ile	Ala	Gly	Gln	Glu	Trp	Phe	Gly	Pro	225	230	235	240
Leu	Gly	Leu	Val	His	Pro	Ser	Pro	Trp	Glu	Phe	Asn	Leu	Arg	Val	Leu	245	250	255	
Ala	Gly	Thr	Leu	Phe	Ala	Val	Phe	Leu	Val	Val	Pro	Tyr	Ala	Leu	Gly	260	265	270	
Thr	Pro	Ser	Arg	Leu	Leu	Asp	Ser	Ser	Trp	Met	Lys	Thr	Leu	Gly	Thr	275	280	285	
Trp	Ser	Tyr	Ser	Ile	Phe	Leu	Trp	His	Leu	Pro	Val	Leu	Thr	Ile	Val	290	295	300	
Phe	Pro	Leu	Leu	Gly	Leu	Pro	Leu	Phe	Ser	Gly	Asn	Phe	Leu	Leu	Val	305	310	315	320
Phe	Ile	Val	Thr	Val	Leu	Leu	Thr	Ile	Pro	Val	Ala	Ala	Ile	Ser	Tyr	325	330	335	
Thr	Phe	Ile	Glu	Glu	Pro	Ile	Ser	Gly	Gly	Pro	Gly	Ala	Pro	Phe	Arg	340	345	350	
Leu	Gly	Val	Val	Arg	Ile	His	His	Phe	Ser	Gly	Gly	Arg	Ser	Gly	Lys	355	360	365	

<210> 273

<211> 1089

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1066)

<223> RXS02741

<400> 273

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ttcccaacct	tgtcttttcag	tcattgggttag	tgtgggaacc	atg	aag	gca	atc	tta	115
				Met	Lys	Ala	Ile	Leu	
				1				5	

ggt	tcc	cgc	acc	ggc	gga	cca	gag	gtg	ttg	gag	ttc	acc	gac	act	gac	163
Val	Ser	Arg	Thr	Gly	Gly	Pro	Glu	Val	Leu	Glu	Phe	Thr	Asp	Thr	Asp	
			10					15						20		

gcc	cca	aag	ccc	act	gat	gat	cag	ggt	tta	ggt	gaa	ggt	gat	atg	gct	211
Ala	Pro	Lys	Pro	Thr	Asp	Asp	Gln	Val	Leu	Val	Glu	Val	Asp	Met	Ala	
			25					30					35			

ggc	gtc	aac	ttt	att	gat	act	tac	tat	cgc	cag	ggt	gaa	tat	cac	gct	259
Gly	Val	Asn	Phe	Ile	Asp	Thr	Tyr	Tyr	Arg	Gln	Gly	Glu	Tyr	His	Ala	
		40					45					50				

cgc	ctg	ccg	ttt	atc	cca	ggt	ttt	gaa	ggc	act	ggt	cgg	gtg	ttg	gag	307
Arg	Leu	Pro	Phe	Ile	Pro	Gly	Phe	Glu	Gly	Thr	Gly	Arg	Val	Leu	Glu	
	55					60					65					

gat	ccg	cag	ggg	ttg	att	gcg	gcg	ggt	acc	aag	gtg	gcg	tgg	tgt	gat	355
Asp	Pro	Gln	Gly	Leu	Ile	Ala	Ala	Gly	Thr	Lys	Val	Ala	Trp	Cys	Asp	
70					75					80					85	

gcc	atg	ggt	tcg	tat	gct	cag	cag	gtg	tgt	gtg	ccg	cgg	gat	cgc	ttg	403
Ala	Met	Gly	Ser	Tyr	Ala	Gln	Gln	Val	Cys	Val	Pro	Arg	Asp	Arg	Leu	
				90					95					100		

gtg	gcg	ggt	ccc	gag	ggc	gtg	agt	tcg	gaa	gtg	gct	gcg	tcg	atg	ttg	451
Val	Ala	Val	Pro	Glu	Gly	Val	Ser	Ser	Glu	Val	Ala	Ala	Ser	Met	Leu	
			105					110					115			

atg	cag	gga	atc	act	gcg	cat	tat	cta	acc	aat	ggt	gtg	tat	gag	ctt	499
Met	Gln	Gly	Ile	Thr	Ala	His	Tyr	Leu	Thr	Asn	Gly	Val	Tyr	Glu	Leu	
		120					125					130				

gaa	gag	ggc	gat	tct	tgc	ctc	atc	act	gct	ggc	gcg	ggt	ggt	gtt	gga	547
Glu	Glu	Gly	Asp	Ser	Cys	Leu	Ile	Thr	Ala	Gly	Ala	Gly	Gly	Val	Gly	
	135					140					145					

ttg	ttg	gct	acg	cag	atg	gcg	gcg	gcc	aag	gga	gtg	cgc	gtg	tac	agc	595
Leu	Leu	Ala	Thr	Gln	Met	Ala	Ala	Ala	Lys	Gly	Val	Arg	Val	Tyr	Ser	
150				155						160					165	

gtg	gtg	tcc	acg	gat	gaa	aaa	gct	gag	ctt	gct	ttg	gat	gcc	ggt	gct	643
Val	Val	Ser	Thr	Asp	Glu	Lys	Ala	Glu	Leu	Ala	Leu	Asp	Ala	Gly	Ala	
						170			175				180			

tat	gag	gtg	ttt	cgt	tat	tcc	gat	aat	ttg	gcg	gag	cag	gtt	cgt	cgg	691
Tyr	Glu	Val	Phe	Arg	Tyr	Ser	Asp	Asn	Leu	Ala	Glu	Gln	Val	Arg	Arg	
			185					190					195			

cac aac ggg ggt cgc gga gtt gat gtg gtg tat gac ggt gtc ggc cag 739
 His Asn Gly Gly Arg Gly Val Asp Val Val Tyr Asp Gly Val Gly Gln
 200 205 210
 tcc acg ttc aat gag tcc tta gag gct gtt cgt ccg cgc ggc act gtg 787
 Ser Thr Phe Asn Glu Ser Leu Glu Ala Val Arg Pro Arg Gly Thr Val
 215 220 225
 tgt ttg ttt ggt gcg gcg tcg ggt cct gtg gag cct ttt gat ccg cag 835
 Cys Leu Phe Gly Ala Ala Ser Gly Pro Val Glu Pro Phe Asp Pro Gln
 230 235 240 245
 ctg ttg aac act cac ggt tcg atc ttc ttg acc cgc cca agc att ggc 883
 Leu Leu Asn Thr His Gly Ser Ile Phe Leu Thr Arg Pro Ser Ile Gly
 250 255 260
 gcg tgg acg tct gag gag ggc gaa ttt gcc aag cgt gca cag gcg gtc 931
 Ala Trp Thr Ser Glu Glu Gly Glu Phe Ala Lys Arg Ala Gln Ala Val
 265 270 275
 acg cag gcc atc gtc gaa ggc acc ttg cgg gtt cgc gtt act ggc aca 979
 Thr Gln Ala Ile Val Glu Gly Thr Leu Arg Val Arg Val Thr Gly Thr
 280 285 290
 tat tcg ctt gcc gac gcc tac atc gcc cac cgc gac ctt cag gcg cgt 1027
 Tyr Ser Leu Ala Asp Ala Tyr Ile Ala His Arg Asp Leu Gln Ala Arg
 295 300 305
 agc acg agc ggt tct ttg gtc ttg gaa atc ccg aag gac taaacacgca 1076
 Ser Thr Ser Gly Ser Leu Val Leu Glu Ile Pro Lys Asp
 310 315 320
 taaaaagatc ctg 1089

<210> 274

<211> 322

<212> PRT

<213> Corynebacterium glutamicum

<400> 274

Met Lys Ala Ile Leu Val Ser Arg Thr Gly Gly Pro Glu Val Leu Glu
 1 5 10 15

Phe Thr Asp Thr Asp Ala Pro Lys Pro Thr Asp Asp Gln Val Leu Val
 20 25 30

Glu Val Asp Met Ala Gly Val Asn Phe Ile Asp Thr Tyr Tyr Arg Gln
 35 40 45

Gly Glu Tyr His Ala Arg Leu Pro Phe Ile Pro Gly Phe Glu Gly Thr
 50 55 60

Gly Arg Val Leu Glu Asp Pro Gln Gly Leu Ile Ala Ala Gly Thr Lys
 65 70 75 80

Val Ala Trp Cys Asp Ala Met Gly Ser Tyr Ala Gln Gln Val Cys Val
 85 90 95

Pro Arg Asp Arg Leu Val Ala Val Pro Glu Gly Val Ser Ser Glu Val

100	105	110
Ala Ala Ser Met Leu Met Gln Gly Ile Thr Ala His Tyr Leu Thr Asn		
115	120	125
Gly Val Tyr Glu Leu Glu Glu Gly Asp Ser Cys Leu Ile Thr Ala Gly		
130	135	140
Ala Gly Gly Val Gly Leu Leu Ala Thr Gln Met Ala Ala Ala Lys Gly		
145	150	155
Val Arg Val Tyr Ser Val Val Ser Thr Asp Glu Lys Ala Glu Leu Ala		
165	170	175
Leu Asp Ala Gly Ala Tyr Glu Val Phe Arg Tyr Ser Asp Asn Leu Ala		
180	185	190
Glu Gln Val Arg Arg His Asn Gly Gly Arg Gly Val Asp Val Val Tyr		
195	200	205
Asp Gly Val Gly Gln Ser Thr Phe Asn Glu Ser Leu Glu Ala Val Arg		
210	215	220
Pro Arg Gly Thr Val Cys Leu Phe Gly Ala Ala Ser Gly Pro Val Glu		
225	230	235
Pro Phe Asp Pro Gln Leu Leu Asn Thr His Gly Ser Ile Phe Leu Thr		
245	250	255
Arg Pro Ser Ile Gly Ala Trp Thr Ser Glu Glu Gly Glu Phe Ala Lys		
260	265	270
Arg Ala Gln Ala Val Thr Gln Ala Ile Val Glu Gly Thr Leu Arg Val		
275	280	285
Arg Val Thr Gly Thr Tyr Ser Leu Ala Asp Ala Tyr Ile Ala His Arg		
290	295	300
Asp Leu Gln Ala Arg Ser Thr Ser Gly Ser Leu Val Leu Glu Ile Pro		
305	310	315
		320

Lys Asp

<210> 275

<211> 430

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(430)

<223> RXS03061

<400> 275

ctgccaccac tggtcattgc agaggacact ctccgtgatg gtcttcaggt gttagtcgca 60

gccctagagc	gcgaaaccgc	gcaccagaag	gtgggctaaa	gtg tct ttg acc ttc	115
				Val Ser Leu Thr Phe	
				1 5	

cca gta atc aac ccc agc gat ggc tcc acc atc acc gag cta gaa aac 163
 Pro Val Ile Asn Pro Ser Asp Gly Ser Thr Ile Thr Glu Leu Glu Asn
 10 15 20

cac gat tcc acc cag tgg atg tcc gcg ctc tct gat gca gtt gca gct 211
 His Asp Ser Thr Gln Trp Met Ser Ala Leu Ser Asp Ala Val Ala Ala
 25 30 35

ggg cct tca tgg gct gcg aaa act ccc cgc gaa aga tcc gtg gta ctc 259
 Gly Pro Ser Trp Ala Ala Lys Thr Pro Arg Glu Arg Ser Val Val Leu
 40 45 50

acc gca atc ttc gaa gca ctg acc gaa cgc gcc caa gaa ctt gca gag 307
 Thr Ala Ile Phe Glu Ala Leu Thr Glu Arg Ala Gln Glu Leu Ala Glu
 55 60 65

atc atc cac ctg gaa gct gga aaa tcc gat gca gaa gct ctt ggt gaa 355
 Ile Ile His Leu Glu Ala Gly Lys Ser Asp Ala Glu Ala Leu Gly Glu
 70 75 80 85

gtc gct tat ggt gca gaa tac ttc cgt tgg ttt gcg gaa gaa gca gtg 403
 Val Ala Tyr Gly Ala Glu Tyr Phe Arg Trp Phe Ala Glu Glu Ala Val
 90 95 100

cgc ctg ccc ggc cgc tac gga cag tca 430
 Arg Leu Pro Gly Arg Tyr Gly Gln Ser
 105 110

<210> 276

<211> 110

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 276

Val Ser Leu Thr Phe Pro Val Ile Asn Pro Ser Asp Gly Ser Thr Ile
 1 5 10 15

Thr Glu Leu Glu Asn His Asp Ser Thr Gln Trp Met Ser Ala Leu Ser
 20 25 30

Asp Ala Val Ala Ala Gly Pro Ser Trp Ala Ala Lys Thr Pro Arg Glu
 35 40 45

Arg Ser Val Val Leu Thr Ala Ile Phe Glu Ala Leu Thr Glu Arg Ala
 50 55 60

Gln Glu Leu Ala Glu Ile Ile His Leu Glu Ala Gly Lys Ser Asp Ala
 65 70 75 80

Glu Ala Leu Gly Glu Val Ala Tyr Gly Ala Glu Tyr Phe Arg Trp Phe
 85 90 95

Ala Glu Glu Ala Val Arg Leu Pro Gly Arg Tyr Gly Gln Ser
 100 105 110

<210> 277

<211> 747

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(724)

<223> RXS03150

<400> 277

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ttaaacagag tgcgtttcaa tgctgtagt gttccggcaa ttttgaatgt cgttacggtt 60
acccaaggct gaattcctga gctcaccttg tacaagatca gtg gaa gcc cag ttc 115
                               Val Glu Ala Gln Phe
                               1                               5

acc tct ccc ctg ctc aac aat ggg caa acc tgt ttc ctt ggt acc cga 163
Thr Ser Pro Leu Leu Asn Asn Gly Gln Thr Cys Phe Leu Gly Thr Arg
                               10                               15                               20

atc ctt gct cca aaa tca cgt tac gcg gaa gta gtc gat gca ttc acc 211
Ile Leu Ala Pro Lys Ser Arg Tyr Ala Glu Val Val Asp Ala Phe Thr
                               25                               30                               35

gct ttc gct ggc agc ctg cag gtt gga gtc acg tcc tcc cct gac act 259
Ala Phe Ala Gly Ser Leu Gln Val Gly Val Thr Ser Ser Pro Asp Thr
                               40                               45                               50

cag atc gga ccg atg gcg act gcc cgg cag cgt gag cgc gtg gaa tcc 307
Gln Ile Gly Pro Met Ala Thr Ala Arg Gln Arg Glu Arg Val Glu Ser
                               55                               60                               65

tac att tcc caa ggc aaa aat gct gga gcc cgc atc act gtc ggt ggc 355
Tyr Ile Ser Gln Gly Lys Asn Ala Gly Ala Arg Ile Thr Val Gly Gly
                               70                               75                               80                               85

agc cgt cca cga gat ctt gac gcc gga ttc ttc gtt gag cca aca gtg 403
Ser Arg Pro Arg Asp Leu Asp Ala Gly Phe Phe Val Glu Pro Thr Val
                               90                               95                               100

ttc gcc gat gta gac aat cgc gca gcc att gcc caa gat gaa atc ttc 451
Phe Ala Asp Val Asp Asn Arg Ala Ala Ile Ala Gln Asp Glu Ile Phe
                               105                               110                               115

gga ccg gtg ccc tct gtt gtt tcc tac caa gac gat gaa cac gcc atc 499
Gly Pro Val Pro Ser Val Val Ser Tyr Gln Asp Asp Glu His Ala Ile
                               120                               125                               130

caa cta gcc aac gat tcc gaa ttc ggt ctc ggc gga act gtc tgg acg 547
Gln Leu Ala Asn Asp Ser Glu Phe Gly Leu Gly Gly Thr Val Trp Thr
                               135                               140                               145

agc gat ccc gag cgc ggc gct gca ttg gcc cgc cga gtt cac aca gga 595
Ser Asp Pro Glu Arg Gly Ala Ala Leu Ala Arg Arg Val His Thr Gly
150                               155                               160                               165

acc att ggc atc aac cgc tat atc cct gat ccc gcc gca cca ttt gga 643
Thr Ile Gly Ile Asn Arg Tyr Ile Pro Asp Pro Ala Ala Pro Phe Gly
170                               175                               180

ggt gtg aaa aac agt ggc ctt ggc aga gaa ctc ggc ccc gaa ggt ctt 691
Gly Val Lys Asn Ser Gly Leu Gly Arg Glu Leu Gly Pro Glu Gly Leu
185                               190                               195

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gct tcc tac caa gaa acc caa acc att tat ctc taatccaaac tgcacctata 744
 Ala Ser Tyr Gln Glu Thr Gln Thr Ile Tyr Leu
 200 205

tat

747

<210> 278

<211> 208

<212> PRT

<213> Corynebacterium glutamicum

<400> 278

Val Glu Ala Gln Phe Thr Ser Pro Leu Leu Asn Asn Gly Gln Thr Cys
 1 5 10 15

Phe Leu Gly Thr Arg Ile Leu Ala Pro Lys Ser Arg Tyr Ala Glu Val
 20 25 30

Val Asp Ala Phe Thr Ala Phe Ala Gly Ser Leu Gln Val Gly Val Thr
 35 40 45

Ser Ser Pro Asp Thr Gln Ile Gly Pro Met Ala Thr Ala Arg Gln Arg
 50 55 60

Glu Arg Val Glu Ser Tyr Ile Ser Gln Gly Lys Asn Ala Gly Ala Arg
 65 70 75 80

Ile Thr Val Gly Gly Ser Arg Pro Arg Asp Leu Asp Ala Gly Phe Phe
 85 90 95

Val Glu Pro Thr Val Phe Ala Asp Val Asp Asn Arg Ala Ala Ile Ala
 100 105 110

Gln Asp Glu Ile Phe Gly Pro Val Pro Ser Val Val Ser Tyr Gln Asp
 115 120 125

Asp Glu His Ala Ile Gln Leu Ala Asn Asp Ser Glu Phe Gly Leu Gly
 130 135 140

Gly Thr Val Trp Thr Ser Asp Pro Glu Arg Gly Ala Ala Leu Ala Arg
 145 150 155 160

Arg Val His Thr Gly Thr Ile Gly Ile Asn Arg Tyr Ile Pro Asp Pro
 165 170 175

Ala Ala Pro Phe Gly Gly Val Lys Asn Ser Gly Leu Gly Arg Glu Leu
 180 185 190

Gly Pro Glu Gly Leu Ala Ser Tyr Gln Glu Thr Gln Thr Ile Tyr Leu
 195 200 205

<210> 279

<211> 747

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(724)

<223> RXS02554

<400> 279

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ggataggctc cataaaaaata accaaaggcg gaaaatttca atg tca cac act aag 115
Met Ser His Thr Lys
1 5

cca tcc att gcc atc ctc ggt gct ggc cga gtg ggt tct tca ctt gcc 163
Pro Ser Ile Ala Ile Leu Gly Ala Gly Arg Val Gly Ser Ser Leu Ala
10 15 20

agg tca gcg gtc gcc gca ggc tat gag gta aag gtt gct ggt tca ggt 211
Arg Ser Ala Val Ala Ala Gly Tyr Glu Val Lys Val Ala Gly Ser Gly
25 30 35

gct gtg gac aaa atc gct ctt acc gct gag atc ctt atg ccc ggc gcg 259
Ala Val Asp Lys Ile Ala Leu Thr Ala Glu Ile Leu Met Pro Gly Ala
40 45 50

gtt cca agc act gct gac cag gct gta aag gat gca gat att gtg ttc 307
Val Pro Ser Thr Ala Asp Gln Ala Val Lys Asp Ala Asp Ile Val Phe
55 60 65

ttg gct gtt ccc ctg cat aaa ttc cgc agt gtc aat cca gcc act tta 355
Leu Ala Val Pro Leu His Lys Phe Arg Ser Val Asn Pro Ala Thr Leu
70 75 80 85

gag ggc aag atc gtt att gac acg atg aac cac tgg gtt ccg gtc aat 403
Glu Gly Lys Ile Val Ile Asp Thr Met Asn His Trp Val Pro Val Asn
90 95 100

ggt gag ttg gag gaa att gat cag gat ccg cgc agc act tcg gag att 451
Gly Glu Leu Glu Glu Ile Asp Gln Asp Pro Arg Ser Thr Ser Glu Ile
105 110 115

att gcg gag ttt ttc gcg gga tca acc atg gtg aag tct ttt aac cac 499
Ile Ala Glu Phe Phe Ala Gly Ser Thr Met Val Lys Ser Phe Asn His
120 125 130

att ggt tat cac gag att gag cag gat gcg ggt acc ggg cgt gcg att 547
Ile Gly Tyr His Glu Ile Glu Gln Asp Ala Gly Thr Gly Arg Ala Ile
135 140 145

gcg tat gcc acg gat gat gtg gat gca ggt gcc cag gtt gca cag cta 595
Ala Tyr Ala Thr Asp Asp Val Asp Ala Gly Ala Gln Val Ala Gln Leu
150 155 160 165

att aag agt ttt ggg ttt gtt cct tta aat att ggc gca ttg gaa aac 643
Ile Lys Ser Phe Gly Phe Val Pro Leu Asn Ile Gly Ala Leu Glu Asn
170 175 180

ggc cgt att ctg gaa cct ggc caa gaa gct ttc ggc gcg cac ctt aat 691
Gly Arg Ile Leu Glu Pro Gly Gln Glu Ala Phe Gly Ala His Leu Asn
185 190 195

aaa gat tcg cgc cta gaa ctt gtt aat cag cgg tagtacctcg atcttcagcc 744
Lys Asp Ser Arg Leu Glu Leu Val Asn Gln Arg
200 205

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aac

747

<210> 280

<211> 208

<212> PRT

<213> Corynebacterium glutamicum

<400> 280

Met Ser His Thr Lys Pro Ser Ile Ala Ile Leu Gly Ala Gly Arg Val
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Gly Ser Ser Leu Ala Arg Ser Ala Val Ala Ala Gly Tyr Glu Val Lys
 20 25 30

Val Ala Gly Ser Gly Ala Val Asp Lys Ile Ala Leu Thr Ala Glu Ile
 35 40 45

Leu Met Pro Gly Ala Val Pro Ser Thr Ala Asp Gln Ala Val Lys Asp
 50 55 60

Ala Asp Ile Val Phe Leu Ala Val Pro Leu His Lys Phe Arg Ser Val
 65 70 75 80

Asn Pro Ala Thr Leu Glu Gly Lys Ile Val Ile Asp Thr Met Asn His
 85 90 95

Trp Val Pro Val Asn Gly Glu Leu Glu Glu Ile Asp Gln Asp Pro Arg
 100 105 110

Ser Thr Ser Glu Ile Ile Ala Glu Phe Phe Ala Gly Ser Thr Met Val
 115 120 125

Lys Ser Phe Asn His Ile Gly Tyr His Glu Ile Glu Gln Asp Ala Gly
 130 135 140

Thr Gly Arg Ala Ile Ala Tyr Ala Thr Asp Asp Val Asp Ala Gly Ala
 145 150 155 160

Gln Val Ala Gln Leu Ile Lys Ser Phe Gly Phe Val Pro Leu Asn Ile
 165 170 175

Gly Ala Leu Glu Asn Gly Arg Ile Leu Glu Pro Gly Gln Glu Ala Phe
 180 185 190

Gly Ala His Leu Asn Lys Asp Ser Arg Leu Glu Leu Val Asn Gln Arg
 195 200 205

<210> 281

<211> 606

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(583)

<223> RXS03058

<400> 281

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gcccatttgg aatcacaaca ccgcatatcg gccatggctg gtg tca aag ctc aaa 115
 Val Ser Lys Leu Lys
 1 5

ggc tca aga tcg ctt ctc gac gtc ggc tcc ggc gat cac tcc ttc gcc 163
 Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly Asp His Ser Phe Ala
 10 15 20

gac ctg gcc ggc cgc cag gtc gcg cat gtc gat gtc gtg gat cct ctt 211
 Asp Leu Ala Gly Arg Gln Val Ala His Val Asp Val Val Asp Pro Leu
 25 30 35

att aat aca acc ttt gaa gaa ttc cag ccg acc caa agc tac gat gcc 259
 Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr Gln Ser Tyr Asp Ala
 40 45 50

atc acg ttc atc gcg tcc ctc cat cac atg aac gcg gaa gaa gga ctt 307
 Ile Thr Phe Ile Ala Ser Leu His His Met Asn Ala Glu Glu Gly Leu
 55 60 65

aac aaa gca gtc cga atc ctc aat cct ggc ggc aag ctc ctc atc gta 355
 Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly Lys Leu Leu Ile Val
 70 75 80 85

ggc ctc gcc aaa aac aaa acc gcc tcc gac tgg atc atc tcc gga cta 403
 Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp Ile Ile Ser Gly Leu
 90 95 100

caa gct ttt ctc tcc cga cca atc agc ctc atc aat agg gaa caa caa 451
 Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile Asn Arg Glu Gln Gln
 105 110 115

atc tac ccc ttc cct acc aaa gaa ccc tca gag agt ctc cac gaa ata 499
 Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu Ser Leu His Glu Ile
 120 125 130

cga caa ctc acc aag cag ctc ctc cct cac cgc cgt att cgc cgt gga 547
 Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg Arg Ile Arg Arg Gly
 135 140 145

atc cac ttc cga tac ctc ctc gag tgg aca aag cct taaacagccc 593
 Ile His Phe Arg Tyr Leu Leu Glu Trp Thr Lys Pro
 150 155 160

tataaaccaa aaa 606

<210> 282

<211> 161

<212> PRT

<213> Corynebacterium glutamicum

<400> 282

Val Ser Lys Leu Lys Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly
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Asp His Ser Phe Ala Asp Leu Ala Gly Arg Gln Val Ala His Val Asp
 20 25 30

<400> 283																
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atcaacaatt gccctttaac caggagtatt cttagcttct																
											atg	act	cct	gat	ctt	115
											Met	Thr	Pro	Asp	Leu	
											1				5	
gca gct ttt ctg gac aaa ctt tat gcc gag ggg cag gaa ttt gat gca																163
Ala	Ala	Phe	Leu	Asp	Lys	Leu	Tyr	Ala	Glu	Gly	Gln	Glu	Phe	Asp	Ala	
				10					15					20		
gag caa ccg gat cgg ctt gat cgc agg aga aac ctt gaa tct gaa agc																211
Glu	Gln	Pro	Asp	Arg	Leu	Asp	Arg	Arg	Arg	Asn	Leu	Glu	Ser	Glu	Ser	
			25					30					35			
gct gcg cta ctt cgc tcg ctc atc tac gga att agt cca aag tca gtt																259
Ala	Ala	Leu	Leu	Arg	Ser	Leu	Ile	Tyr	Gly	Ile	Ser	Pro	Lys	Ser	Val	
		40					45					50				
ctc gag cta ggc аса тcc аат ggt tac tcg act att tgg atg gca gat																307
Leu	Glu	Leu	Gly	Thr	Ser	Asn	Gly	Tyr	Ser	Thr	Ile	Trp	Met	Ala	Asp	
	55					60					65					

gtc gtg aat tta aca aca gta gac aat gat cct gag cgg tct ttg gat 355
 Val Val Asn Leu Thr Thr Val Asp Asn Asp Pro Glu Arg Ser Leu Asp
 70 75 80 85

gct gca gca aac ctt cgc gcc gct gga gtt gaa gaa aaa gtt caa cga 403
 Ala Ala Ala Asn Leu Arg Ala Ala Gly Val Glu Glu Lys Val Gln Arg
 90 95 100

atc gtc gcc gat gga gca acc gta ctt gcc gat tcc gcc gat gaa caa 451
 Ile Val Ala Asp Gly Ala Thr Val Leu Ala Asp Ser Ala Asp Glu Gln
 105 110 115

tgg gat ttc att ttc ctt gat gcc gaa caa tca ctc tat gta aat tgg 499
 Trp Asp Phe Ile Phe Leu Asp Ala Glu Gln Ser Leu Tyr Val Asn Trp
 120 125 130

tgg cct gac ctg caa tgagttctag caaatggcgg cttgttagtg 544
 Trp Pro Asp Leu Gln
 135

<210> 284

<211> 138

<212> PRT

<213> Corynebacterium glutamicum

<400> 284

Met Thr Pro Asp Leu Ala Ala Phe Leu Asp Lys Leu Tyr Ala Glu Gly
 1 5 10 15

Gln Glu Phe Asp Ala Glu Gln Pro Asp Arg Leu Asp Arg Arg Arg Asn
 20 25 30

Leu Glu Ser Glu Ser Ala Ala Leu Leu Arg Ser Leu Ile Tyr Gly Ile
 35 40 45

Ser Pro Lys Ser Val Leu Glu Leu Gly Thr Ser Asn Gly Tyr Ser Thr
 50 55 60

Ile Trp Met Ala Asp Val Val Asn Leu Thr Thr Val Asp Asn Asp Pro
 65 70 75 80

Glu Arg Ser Leu Asp Ala Ala Ala Asn Leu Arg Ala Ala Gly Val Glu
 85 90 95

Glu Lys Val Gln Arg Ile Val Ala Asp Gly Ala Thr Val Leu Ala Asp
 100 105 110

Ser Ala Asp Glu Gln Trp Asp Phe Ile Phe Leu Asp Ala Glu Gln Ser
 115 120 125

Leu Tyr Val Asn Trp Trp Pro Asp Leu Gln
 130 135

<210> 285

<211> 537

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(514)

<223> FRXA01918

<400> 285

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atcaacaatt gccctttaac caggagtatt cttagcttct	atg act cct gat ctt	115
	Met Thr Pro Asp Leu	
	1 5	

gca gct ttt ctg gac aaa ctt tat gcc gag ggg cag gaa ttt gat gca	163
Ala Ala Phe Leu Asp Lys Leu Tyr Ala Glu Gly Gln Glu Phe Asp Ala	
10 15 20	

gag caa ccg gat cgg ctt gat cgc agg aga aac ctt gaa tct gaa agc	211
Glu Gln Pro Asp Arg Leu Asp Arg Arg Arg Asn Leu Glu Ser Glu Ser	
25 30 35	

gct gcg cta ctt cgc tcg ctc atc tac gga att agt cca aag tca gtt	259
Ala Ala Leu Leu Arg Ser Leu Ile Tyr Gly Ile Ser Pro Lys Ser Val	
40 45 50	

ctc gag cta ggc aca tcc aat ggt tac tcg act att tgg atg gca gat	307
Leu Glu Leu Gly Thr Ser Asn Gly Tyr Ser Thr Ile Trp Met Ala Asp	
55 60 65	

gtc gtg aat tta aca aca gta gac aat gat cct gag cgg tct ttg gat	355
Val Val Asn Leu Thr Thr Val Asp Asn Asp Pro Glu Arg Ser Leu Asp	
70 75 80 85	

gct gca gca aac ctt cgc gcc gct gga gtt gaa gaa aaa gtt caa cga	403
Ala Ala Ala Asn Leu Arg Ala Ala Gly Val Glu Glu Lys Val Gln Arg	
90 95 100	

atc gtc gcc gat gga gca acc gta ctt gcc gat tcc gcc gat gaa caa	451
Ile Val Ala Asp Gly Ala Thr Val Leu Ala Asp Ser Ala Asp Glu Gln	
105 110 115	

tgg gat ttc att ttc ctt gat gcc gaa caa tca ctc tat gta aat tgg	499
Trp Asp Phe Ile Phe Leu Asp Ala Glu Gln Ser Leu Tyr Val Asn Trp	
120 125 130	

tgg cct gac ctg caa tgagttctag caaatggcgg ctt	537
Trp Pro Asp Leu Gln	
135	

<210> 286

<211> 138

<212> PRT

<213> Corynebacterium glutamicum

<400> 286

Met Thr Pro Asp Leu Ala Ala Phe Leu Asp Lys Leu Tyr Ala Glu Gly
1 5 10 15

Gln Glu Phe Asp Ala Glu Gln Pro Asp Arg Leu Asp Arg Arg Arg Asn
20 25 30

Leu Glu Ser Glu Ser Ala Ala Leu Leu Arg Ser Leu Ile Tyr Gly Ile

35	40	45
Ser Pro Lys Ser Val Leu Glu Leu Gly Thr Ser Asn Gly Tyr Ser Thr		
50	55	60
Ile Trp Met Ala Asp Val Val Asn Leu Thr Thr Val Asp Asn Asp Pro		
65	70	75 80
Glu Arg Ser Leu Asp Ala Ala Ala Asn Leu Arg Ala Ala Gly Val Glu		
	85	90 95
Glu Lys Val Gln Arg Ile Val Ala Asp Gly Ala Thr Val Leu Ala Asp		
	100	105 110
Ser Ala Asp Glu Gln Trp Asp Phe Ile Phe Leu Asp Ala Glu Gln Ser		
	115	120 125
Leu Tyr Val Asn Trp Trp Pro Asp Leu Gln		
130	135	

<210> 287
 <211> 672
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(649)
 <223> RXC00110

<400> 287
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 aataacgaac gctaatttta aacactggag gagcttccac gtg agc aac aaa gac 115
 Val Ser Asn Lys Asp
 1 5
 ggc ctt ttt act gac ggt aac agc acg ttt gca cct aag gtg gat tca 163
 Gly Leu Phe Thr Asp Gly Asn Ser Thr Phe Ala Pro Lys Val Asp Ser
 10 15 20
 att ccc ctc agc gat gtg gat acc agc gtt agc ggt gaa gcc tcc atc 211
 Ile Pro Leu Ser Asp Val Asp Thr Ser Val Ser Gly Glu Ala Ser Ile
 25 30 35
 ggc acg ctg atc tcc aac gca acc tcc caa atg tcc agc ctt ttc cgc 259
 Gly Thr Leu Ile Ser Asn Ala Thr Ser Gln Met Ser Ser Leu Phe Arg
 40 45 50
 gca gaa gtt gag ctg gcg aag act gaa ctc gca ggc gaa gcc aag aaa 307
 Ala Glu Val Glu Leu Ala Lys Thr Glu Leu Ala Gly Glu Ala Lys Lys
 55 60 65
 gct gcc atc ggc ggc ggc gca ttc agc gtt gct ggc gta atc gca ctg 355
 Ala Ala Ile Gly Gly Gly Ala Phe Ser Val Ala Gly Val Ile Ala Leu
 70 75 80 85
 tac agc tcc ttc ttc ttt ttc ttc ttc gtc gca gca ctg ctg agc gag 403
 Tyr Ser Ser Phe Phe Phe Phe Phe Phe Val Ala Ala Leu Leu Ser Glu
 90 95 100

tgg att aag cct tgg gca gca ttc ctc atc gtg ttc ctc ttc atg ctg 451
 Trp Ile Lys Pro Trp Ala Ala Phe Leu Ile Val Phe Leu Phe Met Leu
 105 110 115
 gtc atc gcc gca gct ctc gca ctg ttc ggc tgg cgc aag gtg aag aag 499
 Val Ile Ala Ala Ala Leu Ala Leu Phe Gly Trp Arg Lys Val Lys Lys
 120 125 130
 atg ggc gct ccg aag aac acc atc caa tcg gtc aac caa ctg aag aac 547
 Met Gly Ala Pro Lys Asn Thr Ile Gln Ser Val Asn Gln Leu Lys Asn
 135 140 145
 ctg gtc cca ggt cag gca tcc gag aag ctg gag aag gcc aac aag cgt 595
 Leu Val Pro Gly Gln Ala Ser Glu Lys Leu Glu Lys Ala Asn Lys Arg
 150 155 160 165
 ggc ctc tac acc tcc gcg tcc ttc cac agc ccc ggc gcc atc act ggc 643
 Gly Leu Tyr Thr Ser Ala Ser Phe His Ser Pro Gly Ala Ile Thr Gly
 170 175 180
 gac cac taaaaaagga gacttcgatg gcc 672
 Asp His

<210> 288

<211> 183

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 288

Val Ser Asn Lys Asp Gly Leu Phe Thr Asp Gly Asn Ser Thr Phe Ala
 1 5 10 15
 Pro Lys Val Asp Ser Ile Pro Leu Ser Asp Val Asp Thr Ser Val Ser
 20 25 30
 Gly Glu Ala Ser Ile Gly Thr Leu Ile Ser Asn Ala Thr Ser Gln Met
 35 40 45
 Ser Ser Leu Phe Arg Ala Glu Val Glu Leu Ala Lys Thr Glu Leu Ala
 50 55 60
 Gly Glu Ala Lys Lys Ala Ala Ile Gly Gly Gly Ala Phe Ser Val Ala
 65 70 75 80
 Gly Val Ile Ala Leu Tyr Ser Ser Phe Phe Phe Phe Phe Phe Val Ala
 85 90 95
 Ala Leu Leu Ser Glu Trp Ile Lys Pro Trp Ala Ala Phe Leu Ile Val
 100 105 110
 Phe Leu Phe Met Leu Val Ile Ala Ala Ala Leu Ala Leu Phe Gly Trp
 115 120 125
 Arg Lys Val Lys Lys Met Gly Ala Pro Lys Asn Thr Ile Gln Ser Val
 130 135 140
 Asn Gln Leu Lys Asn Leu Val Pro Gly Gln Ala Ser Glu Lys Leu Glu
 145 150 155 160

Lys Ala Asn Lys Arg Gly Leu Tyr Thr Ser Ala Ser Phe His Ser Pro
 165 170 175

Gly Ala Ile Thr Gly Asp His
 180

<210> 289

<211> 954

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(931)

<223> RXC01971

<400> 289

aggctcttggt tatttcggct actgattcag tagctgcgct ccgataggat tcttagtttt 60

cagttcagta tctttgagcc acggctagaa tgtgaatcct atg tct aag aag aag 115
 Met Ser Lys Lys Lys
 1 5

cct cgc ccc att ccg gtt cct gcc caa ttt atc cct ggt ctc att gat 163
 Pro Arg Pro Ile Pro Val Pro Ala Gln Phe Ile Pro Gly Leu Ile Asp
 10 15 20

gcg cat aca cat ttg gca tcg tgt gga gga gat ctt gca ggg ttg gtg 211
 Ala His Thr His Leu Ala Ser Cys Gly Gly Asp Leu Ala Gly Leu Val
 25 30 35

gaa agg gcc aag gag gcg ggc gtc gaa aag ctt tgt acc gtc ggt gat 259
 Glu Arg Ala Lys Glu Ala Gly Val Glu Lys Leu Cys Thr Val Gly Asp
 40 45 50

ggt ttg gct gag gcc gag ctt gcg ctg gag gcc gcg caa cag ttt ggc 307
 Gly Leu Ala Glu Ala Glu Leu Ala Leu Glu Ala Ala Gln Gln Phe Gly
 55 60 65

aat gtg ttt gct gcg tgt gcg att cat ccg acg aag gct gat cag ttg 355
 Asn Val Phe Ala Ala Cys Ala Ile His Pro Thr Lys Ala Asp Gln Leu
 70 75 80 85

gat ggg gct gcg cgt gcg cgg ctg acg cag atg gcg gcg gat ccg aat 403
 Asp Gly Ala Ala Arg Ala Arg Leu Thr Gln Met Ala Ala Asp Pro Asn
 90 95 100

tgt gtg gcc att ggt gag act ggt ttg gat tcg tat tgg atc aag cac 451
 Cys Val Ala Ile Gly Glu Thr Gly Leu Asp Ser Tyr Trp Ile Lys His
 105 110 115

gat cca gag gac acg gcg gcg ttg gat gtg caa gag gag gcg ctg cgc 499
 Asp Pro Glu Asp Thr Ala Ala Leu Asp Val Gln Glu Glu Ala Leu Arg
 120 125 130

tgg cat att gat ttg gca att agt gcg gat aag ccg ttg atg att cac 547
 Trp His Ile Asp Leu Ala Ile Ser Ala Asp Lys Pro Leu Met Ile His
 135 140 145

aat cgt gag gcg gat gct gat ttg atg cga gtg ttg gcg gat gct cca 595
 Asn Arg Glu Ala Asp Ala Asp Leu Met Arg Val Leu Ala Asp Ala Pro
 150 155 160 165

 cct cca aaa gat acg att ctg cat tgt ttt tct tcg ccg ttg gac gtg 643
 Pro Pro Lys Asp Thr Ile Leu His Cys Phe Ser Ser Pro Leu Asp Val
 170 175 180

 gcg aag gaa gcg ttg gat cgt gga tat gtg ttg agt ttt gcg ggc aat 691
 Ala Lys Glu Ala Leu Asp Arg Gly Tyr Val Leu Ser Phe Ala Gly Asn
 185 190 195

 gtg acg ttt aag cgt aat gag gag ttg cgg gag gct gct cgt att gcg 739
 Val Thr Phe Lys Arg Asn Glu Glu Leu Arg Glu Ala Ala Arg Ile Ala
 200 205 210

 ccg att tcc cag att ttg att gaa acc gat gcg ccg tat atg acg ccg 787
 Pro Ile Ser Gln Ile Leu Ile Glu Thr Asp Ala Pro Tyr Met Thr Pro
 215 220 225

 gag ccg ttt cgg ggg agt agg aat gag ccg tcg ttg att ggt cat acg 835
 Glu Pro Phe Arg Gly Ser Arg Asn Glu Pro Ser Leu Ile Gly His Thr
 230 235 240 245

 gcg cta tgc att gcg gag gtt cgg ggg atg gct gtg gag gat gtt gcg 883
 Ala Leu Cys Ile Ala Glu Val Arg Gly Met Ala Val Glu Asp Val Ala
 250 255 260

 gcg gct ttg aat gag aat ttt gat cgc gtt tat ggg gtc aca aat cta 931
 Ala Ala Leu Asn Glu Asn Phe Asp Arg Val Tyr Gly Val Thr Asn Leu
 265 270 275

 taacgtgagg tagctcacag tca 954

<210> 290

<211> 277

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 290

Met Ser Lys Lys Lys Pro Arg Pro Ile Pro Val Pro Ala Gln Phe Ile
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 Pro Gly Leu Ile Asp Ala His Thr His Leu Ala Ser Cys Gly Gly Asp
 20 25 30

 Leu Ala Gly Leu Val Glu Arg Ala Lys Glu Ala Gly Val Glu Lys Leu
 35 40 45

 Cys Thr Val Gly Asp Gly Leu Ala Glu Ala Glu Leu Ala Leu Glu Ala
 50 55 60

 Ala Gln Gln Phe Gly Asn Val Phe Ala Ala Cys Ala Ile His Pro Thr
 65 70 75 80

 Lys Ala Asp Gln Leu Asp Gly Ala Ala Arg Ala Arg Leu Thr Gln Met
 85 90 95

 Ala Ala Asp Pro Asn Cys Val Ala Ile Gly Glu Thr Gly Leu Asp Ser
 100 105 110

Tyr Trp Ile Lys His Asp Pro Glu Asp Thr Ala Ala Leu Asp Val Gln
 115 120 125
 Glu Glu Ala Leu Arg Trp His Ile Asp Leu Ala Ile Ser Ala Asp Lys
 130 135 140
 Pro Leu Met Ile His Asn Arg Glu Ala Asp Ala Asp Leu Met Arg Val
 145 150 155 160
 Leu Ala Asp Ala Pro Pro Pro Lys Asp Thr Ile Leu His Cys Phe Ser
 165 170 175
 Ser Pro Leu Asp Val Ala Lys Glu Ala Leu Asp Arg Gly Tyr Val Leu
 180 185 190
 Ser Phe Ala Gly Asn Val Thr Phe Lys Arg Asn Glu Glu Leu Arg Glu
 195 200 205
 Ala Ala Arg Ile Ala Pro Ile Ser Gln Ile Leu Ile Glu Thr Asp Ala
 210 215 220
 Pro Tyr Met Thr Pro Glu Pro Phe Arg Gly Ser Arg Asn Glu Pro Ser
 225 230 235 240
 Leu Ile Gly His Thr Ala Leu Cys Ile Ala Glu Val Arg Gly Met Ala
 245 250 255
 Val Glu Asp Val Ala Ala Ala Leu Asn Glu Asn Phe Asp Arg Val Tyr
 260 265 270
 Gly Val Thr Asn Leu
 275

<210> 291
 <211> 465
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(442)
 <223> RXA02118

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tagtgctgtt accagggaca tcggctagaa tctgctgaat atg tct gat caa tta 115
 Met Ser Asp Gln Leu
 1 5

gct ccc tgc cct gag tgc agc agt gaa tat acc tac gaa aac ggc ggc 163
 Ala Pro Cys Pro Glu Cys Ser Ser Glu Tyr Thr Tyr Glu Asn Gly Gly
 10 15 20

gtt ctg gtc tgc cca atg tgt gcc cac gaa tgg gtc gaa ggt gaa gta 211
 Val Leu Val Cys Pro Met Cys Ala His Glu Trp Val Glu Gly Glu Val
 25 30 35

gcg gaa gaa acc gcg act gtc atc aaa gac tct gtg gga aat atc ctc 259

Ala Glu Glu Thr Ala Thr Val Ile Lys Asp Ser Val Gly Asn Ile Leu
 40 45 50

aat gat ggc gat tcc gta tcg att gtg aag agc ctc aaa gtc aag ggt 307
 Asn Asp Gly Asp Ser Val Ser Ile Val Lys Ser Leu Lys Val Lys Gly
 55 60 65

ggc ggt gcc atc aag att ggc acc aaa gtc agc gga att cgt ctt ctt 355
 Gly Gly Ala Ile Lys Ile Gly Thr Lys Val Ser Gly Ile Arg Leu Leu
 70 75 80 85

gaa gag cca gtt gac ggc cac gac atc gac gct aag gtc cct gga ttt 403
 Glu Glu Pro Val Asp Gly His Asp Ile Asp Ala Lys Val Pro Gly Phe
 90 95 100

ggt caa atg cga ctc aag tcc agt gtt gta aag aag gcc taaacccttt 452
 Gly Gln Met Arg Leu Lys Ser Ser Val Val Lys Lys Ala
 105 110

taaggagctt tag 465

<210> 292
 <211> 114
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 292
 Met Ser Asp Gln Leu Ala Pro Cys Pro Glu Cys Ser Ser Glu Tyr Thr
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Tyr Glu Asn Gly Gly Val Leu Val Cys Pro Met Cys Ala His Glu Trp
 20 25 30

Val Glu Gly Glu Val Ala Glu Glu Thr Ala Thr Val Ile Lys Asp Ser
 35 40 45

Val Gly Asn Ile Leu Asn Asp Gly Asp Ser Val Ser Ile Val Lys Ser
 50 55 60

Leu Lys Val Lys Gly Gly Gly Ala Ile Lys Ile Gly Thr Lys Val Ser
 65 70 75 80

Gly Ile Arg Leu Leu Glu Glu Pro Val Asp Gly His Asp Ile Asp Ala
 85 90 95

Lys Val Pro Gly Phe Gly Gln Met Arg Leu Lys Ser Ser Val Val Lys
 100 105 110

Lys Ala

<210> 293
 <211> 537
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(514)

<400> 293

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Met Lys Ala Asp Leu
1 5

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acc ccg tac cgt cag ttc aat gga aat gcc aaa gaa gca atg gag ttc 163
Thr Pro Tyr Arg Gln Phe Asn Gly Asn Ala Lys Glu Ala Met Glu Phe
      10                      15                      20
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tac	caa	aca	gtt	ttt	ggg	ggc	gag	ctt	cag	atg	atg	ccg	ttt	tcc	gcc	211
Tyr	Gln	Thr	Val	Phe	Gly	Gly	Glu	Leu	Gln	Met	Met	Pro	Phe	Ser	Ala	
			25					30					35			

atg	cat	tct	gag	gag	gaa	gtt	ggt	ggt	gac	ggc	gag	aaa	atc	atg	cac	259
Met	His	Ser	Glu	Glu	Glu	Val	Gly	Gly	Asp	Gly	Glu	Lys	Ile	Met	His	
		40					45					50				

gct gag ctg gtc gtt gat ggt cag aag ttg ctt ttt gcc agt gat att 307
Ala Glu Leu Val Val Asp Gly Gln Lys Leu Leu Phe Ala Ser Asp Ile
55 60 65

ccg cgc gtg atg caa cga atg aag ggc gag gac act ccg ttg tcg ctg 355
Pro Arg Val Met Gln Arg Met Lys Gly Glu Asp Thr Pro Leu Ser Leu
70 75 80 85

act ggt ggc gct gag ctg gaa gag gaa att. cgt ggc tac tgg gag aag 403
Thr Gly Gly Ala Glu Leu Glu Glu Glu Ile Arg Gly Tyr Trp Glu Lys
90 95 100

ttg tct gag ggc ggc acc gtg acc atg cct ttg gaa gct gtt cct tgg 451
Leu Ser Glu Gly Gly Thr Val Thr Met Pro Leu Glu Ala Val Pro Trp
105 110 115

ggt gcg gtt tat ggt gcg ctg gag gat cgc ttt gga act cac tgg atg 499
Gly Ala Val Tyr Gly Ala Leu Glu Asp Arg Phe Gly Thr His Trp Met
120 125 130

ttc aac atc ggt ggc taaaactttt ggaaacttat tga 537
Phe Asn Ile Gly Gly
135

<210> 294

<211> 138

<212> PRT

<213> Corynebacterium glutamicum

<400> 294

Met Lys Ala Asp Leu Thr Pro Tyr Arg Gln Phe Asn Gly Asn Ala Lys
1 5 10 15

Glu Ala Met Glu Phe Tyr Gln Thr Val Phe Gly Gly Glu Leu Gln Met
20 25 30

Met Pro Phe Ser Ala Met His Ser Glu Glu Glu Val Gly Gly Asp Gly
35 40 45

Glu Lys Ile Met His Ala Glu Leu Val Val Asp Gly Gln Lys Leu Leu
 50 55 60
 Phe Ala Ser Asp Ile Pro Arg Val Met Gln Arg Met Lys Gly Glu Asp
 65 70 75 80
 Thr Pro Leu Ser Leu Thr Gly Gly Ala Glu Leu Glu Glu Glu Ile Arg
 85 90 95
 Gly Tyr Trp Glu Lys Leu Ser Glu Gly Gly Thr Val Thr Met Pro Leu
 100 105 110
 Glu Ala Val Pro Trp Gly Ala Val Tyr Gly Ala Leu Glu Asp Arg Phe
 115 120 125
 Gly Thr His Trp Met Phe Asn Ile Gly Gly
 130 135

<210> 295

<211> 391

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(391)

<223> RXA02105

<400> 295

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 gcggttgaa aattccgtaa cttctttgag ggagaaaccc atg gtc ggc acg att 115
 Met Val Gly Thr Ile 5
 tcc acc tac atc gca ttc aat gga aac acc acg gaa gct ctg aaa cat 163
 Ser Thr Tyr Ile Ala Phe Asn Gly Asn Thr Thr Glu Ala Leu Lys His 20
 10 15
 tgg caa gag gtt ttt ggt ggt gaa ctt aat ctt tta acc tac ggt cag 211
 Trp Gln Glu Val Phe Gly Gly Glu Leu Asn Leu Leu Thr Tyr Gly Gln 35
 25 30
 ctc acc ttg gaa ggt atg ccg ttt gat cct cca gcg gat gcg ttg gcg 259
 Leu Thr Leu Glu Gly Met Pro Phe Asp Pro Pro Ala Asp Ala Leu Ala 50
 40 45
 cac ggc gtc ctc acg ttg gac aat ggt ggt ttg att tct ggc agt gat 307
 His Gly Val Leu Thr Leu Asp Asn Gly Gly Leu Ile Ser Gly Ser Asp 65
 55 60
 tct ttt gag gga gaa atg ctc gtc aaa gac acc gcg tac tcc atg ttg 355
 Ser Phe Glu Gly Glu Met Leu Val Lys Asp Thr Ala Tyr Ser Met Leu 85
 70 75 80
 tat aac gcg gag tca gtg gaa gat ggt cgc gcg cgg 391
 Tyr Asn Ala Glu Ser Val Glu Asp Gly Arg Ala Arg 95
 90 95

<210> 296
 <211> 97
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 296
 Met Val Gly Thr Ile Ser Thr Tyr Ile Ala Phe Asn Gly Asn Thr Thr
 1 5 10 15
 Glu Ala Leu Lys His Trp Gln Glu Val Phe Gly Gly Glu Leu Asn Leu
 20 25 30
 Leu Thr Tyr Gly Gln Leu Thr Leu Glu Gly Met Pro Phe Asp Pro Pro
 35 40 45
 Ala Asp Ala Leu Ala His Gly Val Leu Thr Leu Asp Asn Gly Gly Leu
 50 55 60
 Ile Ser Gly Ser Asp Ser Phe Glu Gly Glu Met Leu Val Lys Asp Thr
 65 70 75 80
 Ala Tyr Ser Met Leu Tyr Asn Ala Glu Ser Val Glu Asp Gly Arg Ala
 85 90 95

Arg

<210> 297
 <211> 1497
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1474)
 <223> RXN00663

<400> 297
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 actactaccg tgggcgacaa gccacttag aggaggactt gtg aca acc acc tat 115
 Val Thr Thr Thr Tyr
 1 5
 cca gat ttc ctt gga aat tct tcg ctc caa aca gat acg gag cac tgg 163
 Pro Asp Phe Leu Gly Asn Ser Ser Leu Gln Thr Asp Thr Glu His Trp
 10 15 20
 gaa atg gaa gga ggt gcg cag gaa gtc tct gtt act tat gtt ttg gac 211
 Glu Met Glu Gly Gly Ala Gln Glu Val Ser Val Thr Tyr Val Leu Asp
 25 30 35
 acg tca gtg ttg ctg tct gat ccg ttg tcg ttg aca cgg ttc gcg gag 259
 Thr Ser Val Leu Leu Ser Asp Pro Leu Ser Leu Thr Arg Phe Ala Glu
 40 45 50
 cac gat gta gtt ctg cca att gtt gta att acg gaa tta gaa gcc aag 307
 His Asp Val Val Leu Pro Ile Val Val Ile Thr Glu Leu Glu Ala Lys
 55 60 65

cgt cat cac ccg gac ctt ggc ttt ttt gct cgc caa gcg ctt cgg atg	355
Arg His His Pro Asp Leu Gly Phe Phe Ala Arg Gln Ala Leu Arg Met	
70 75 80 85	
ctg gat gag ctg cgt gag atc cat ggg gat ttg tcc aag cca ctg cca	403
Leu Asp Glu Leu Arg Glu Ile His Gly Asp Leu Ser Lys Pro Leu Pro	
90 95 100	
att ggc gat gaa ggc gga cac atc cat gtt gag ctg aat cac caa aac	451
Ile Gly Asp Glu Gly Gly His Ile His Val Glu Leu Asn His Gln Asn	
105 110 115	
acg ggg tcc ttg ccc gtg gga ttc cgc ctt ggt gac aat gac acc cgc	499
Thr Gly Ser Leu Pro Val Gly Phe Arg Leu Gly Asp Asn Asp Thr Arg	
120 125 130	
atc ctt gca gtg gcc aag aat ctg cag gaa gag ggc cac aat gtg gtt	547
Ile Leu Ala Val Ala Lys Asn Leu Gln Glu Glu Gly His Asn Val Val	
135 140 145	
ctg gtg tcg aag gac ctg ccg atg cgg att aag gcg tcg gca agc gga	595
Leu Val Ser Lys Asp Leu Pro Met Arg Ile Lys Ala Ser Ala Ser Gly	
150 155 160 165	
atc gcc gca cag gaa tac cgc gct gcc ctg gcg cgc gac cgt ggt tac	643
Ile Ala Ala Gln Glu Tyr Arg Ala Ala Leu Ala Arg Asp Arg Gly Tyr	
170 175 180	
acc ggc atg acc cac gcc aat atc acc gat gac cag ctc agc gag ctc	691
Thr Gly Met Thr His Ala Asn Ile Thr Asp Asp Gln Leu Ser Glu Leu	
185 190 195	
tac gac acc ggc gag gtg cgc att gag gag ctc gaa aag ctg ccc gtc	739
Tyr Asp Thr Gly Glu Val Arg Ile Glu Glu Leu Glu Lys Leu Pro Val	
200 205 210	
aac cac ggc ttc acc ctc aaa tcc aac agc ggt tcg gcg ctt ggt cgt	787
Asn His Gly Phe Thr Leu Lys Ser Asn Ser Gly Ser Ala Leu Gly Arg	
215 220 225	
atg aat tcc gac aag atc atc gag ctt gtc ccc ggc gac cag cag gta	835
Met Asn Ser Asp Lys Ile Ile Glu Leu Val Pro Gly Asp Gln Gln Val	
230 235 240 245	
ttc ggt atc agc ggg cgt agc gct gag cag cgg gtt gcc att gat ttg	883
Phe Gly Ile Ser Gly Arg Ser Ala Glu Gln Arg Val Ala Ile Asp Leu	
250 255 260	
ctt aac gac gac gcc gtc ggc atc gta tcc atc ggc ggc ccc gcg ggt	931
Leu Asn Asp Asp Ala Val Gly Ile Val Ser Ile Gly Gly Pro Ala Gly	
265 270 275	
aca ggt aaa agc gca ctc gca ctg tgt gcc ggc ctg gaa gct gtg atg	979
Thr Gly Lys Ser Ala Leu Ala Leu Cys Ala Gly Leu Glu Ala Val Met	
280 285 290	
gag cgt cgc att cag cgc aag att atc gtg ttc cgc cca ctc ttt gcc	1027
Glu Arg Arg Ile Gln Arg Lys Ile Ile Val Phe Arg Pro Leu Phe Ala	
295 300 305	
ggt ggc gga cag gaa ctt ggc tac ctg cct ggc gac caa gaa gaa aaa	1075

Val Gly Gly Gln Glu Leu Gly Tyr Leu Pro Gly Asp Gln Glu Glu Lys
 310 315 320 325
 atg ggg cct tgg gcg caa gcg gtt ttt gac acc cta agc tcc atg gtc 1123
 Met Gly Pro Trp Ala Gln Ala Val Phe Asp Thr Leu Ser Ser Met Val
 330 335 340
 agc caa aac atc atc gat gaa gcc ctc tcc cgc ggc ctc atc gaa gtt 1171
 Ser Gln Asn Ile Ile Asp Glu Ala Leu Ser Arg Gly Leu Ile Glu Val
 345 350 355
 ctc cca ctt act cac atc cgc gga cgc tca ctc cac gat gct ttc gtc 1219
 Leu Pro Leu Thr His Ile Arg Gly Arg Ser Leu His Asp Ala Phe Val
 360 365 370
 atc gtc gac gag gcc caa tcc cta gaa cgc aac gtg ttg ctc acc atg 1267
 Ile Val Asp Glu Ala Gln Ser Leu Glu Arg Asn Val Leu Leu Thr Met
 375 380 385
 ctg tct cgc atc ggc cag aat tcc cga gta gtt ctc acc cat gac gta 1315
 Leu Ser Arg Ile Gly Gln Asn Ser Arg Val Val Leu Thr His Asp Val
 390 395 400 405
 gcg cag cgc gac aac ctg cgc gtt ggt cgc tac gac ggc atc gtc tct 1363
 Ala Gln Arg Asp Asn Leu Arg Val Gly Arg Tyr Asp Gly Ile Val Ser
 410 415 420
 gtg gtg gaa gca ctc aag gat cac gaa ctg ttt ggc cac atc acg ttg 1411
 Val Val Glu Ala Leu Lys Asp His Glu Leu Phe Gly His Ile Thr Leu
 425 430 435
 cag cgt tcc gaa cgc tcc cga atc gct gag ttg gtc acc caa gtt ttg 1459
 Gln Arg Ser Glu Arg Ser Arg Ile Ala Glu Leu Val Thr Gln Val Leu
 440 445 450
 gat gcg ccg tct ctg tagtcgcgca gtctgtggcg att 1497
 Asp Ala Pro Ser Leu
 455

<210> 298

<211> 458

<212> PRT

<213> Corynebacterium glutamicum

<400> 298

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 Asp Thr Glu His Trp Glu Met Glu Gly Gly Ala Gln Glu Val Ser Val
 20 25 30
 Thr Tyr Val Leu Asp Thr Ser Val Leu Leu Ser Asp Pro Leu Ser Leu
 35 40 45
 Thr Arg Phe Ala Glu His Asp Val Val Leu Pro Ile Val Val Ile Thr
 50 55 60
 Glu Leu Glu Ala Lys Arg His His Pro Asp Leu Gly Phe Phe Ala Arg
 65 70 75 80

Gln Ala Leu Arg Met Leu Asp Glu Leu Arg Glu Ile His Gly Asp Leu
 85 90 95
 Ser Lys Pro Leu Pro Ile Gly Asp Glu Gly Gly His Ile His Val Glu
 100 105 110
 Leu Asn His Gln Asn Thr Gly Ser Leu Pro Val Gly Phe Arg Leu Gly
 115 120 125
 Asp Asn Asp Thr Arg Ile Leu Ala Val Ala Lys Asn Leu Gln Glu Glu
 130 135 140
 Gly His Asn Val Val Leu Val Ser Lys Asp Leu Pro Met Arg Ile Lys
 145 150 155 160
 Ala Ser Ala Ser Gly Ile Ala Ala Gln Glu Tyr Arg Ala Ala Leu Ala
 165 170 175
 Arg Asp Arg Gly Tyr Thr Gly Met Thr His Ala Asn Ile Thr Asp Asp
 180 185 190
 Gln Leu Ser Glu Leu Tyr Asp Thr Gly Glu Val Arg Ile Glu Glu Leu
 195 200 205
 Glu Lys Leu Pro Val Asn His Gly Phe Thr Leu Lys Ser Asn Ser Gly
 210 215 220
 Ser Ala Leu Gly Arg Met Asn Ser Asp Lys Ile Ile Glu Leu Val Pro
 225 230 235 240
 Gly Asp Gln Gln Val Phe Gly Ile Ser Gly Arg Ser Ala Glu Gln Arg
 245 250 255
 Val Ala Ile Asp Leu Leu Asn Asp Asp Ala Val Gly Ile Val Ser Ile
 260 265 270
 Gly Gly Pro Ala Gly Thr Gly Lys Ser Ala Leu Ala Leu Cys Ala Gly
 275 280 285
 Leu Glu Ala Val Met Glu Arg Arg Ile Gln Arg Lys Ile Ile Val Phe
 290 295 300
 Arg Pro Leu Phe Ala Val Gly Gly Gln Glu Leu Gly Tyr Leu Pro Gly
 305 310 315 320
 Asp Gln Glu Glu Lys Met Gly Pro Trp Ala Gln Ala Val Phe Asp Thr
 325 330 335
 Leu Ser Ser Met Val Ser Gln Asn Ile Ile Asp Glu Ala Leu Ser Arg
 340 345 350
 Gly Leu Ile Glu Val Leu Pro Leu Thr His Ile Arg Gly Arg Ser Leu
 355 360 365
 His Asp Ala Phe Val Ile Val Asp Glu Ala Gln Ser Leu Glu Arg Asn
 370 375 380

Val Leu Leu Thr Met Leu Ser Arg Ile Gly Gln Asn Ser Arg Val Val
 385 390 395 400
 Leu Thr His Asp Val Ala Gln Arg Asp Asn Leu Arg Val Gly Arg Tyr

	405		410		415
Asp Gly Ile Val Ser Val Val Glu Ala Leu Lys Asp His Glu Leu Phe					
	420		425		430
Gly His Ile Thr Leu Gln Arg Ser Glu Arg Ser Arg Ile Ala Glu Leu					
	435		440		445
Val Thr Gln Val Leu Asp Ala Pro Ser Leu					
	450		455		

<210> 299

<211> 1019

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(996)

<223> FRXA00663

<400> 299

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1 5 10 15	
gaa gag ggc cac aat gtg gtt ctg gtg tcg aag gac ctg ccg atg cgg	96
Glu Glu Gly His Asn Val Val Leu Val Ser Lys Asp Leu Pro Met Arg	
20 25 30	
att aag gcg tcg gca agc gga atc gcc gca cag gaa tac cgc gct gcc	144
Ile Lys Ala Ser Ala Ser Gly Ile Ala Ala Gln Glu Tyr Arg Ala Ala	
35 40 45	
ctg gcg cgc gac cgt ggt tac acc ggc atg acc cac gcc aat atc acc	192
Leu Ala Arg Asp Arg Gly Tyr Thr Gly Met Thr His Ala Asn Ile Thr	
50 55 60	
gat gac cag ctc agc gag ctc tac gac acc ggc gag gtg cgc att gag	240
Asp Asp Gln Leu Ser Glu Leu Tyr Asp Thr Gly Glu Val Arg Ile Glu	
65 70 75 80	
gag ctc gaa aag ctg ccc gtc aac cac ggc ttc acc ctc aaa tcc aac	288
Glu Leu Glu Lys Leu Pro Val Asn His Gly Phe Thr Leu Lys Ser Asn	
85 90 95	
agc ggt tcg gcg ctt ggt cgt atg aat tcc gac aag atc atc gag ctt	336
Ser Gly Ser Ala Leu Gly Arg Met Asn Ser Asp Lys Ile Ile Glu Leu	
100 105 110	
gtc ccc ggc gac cag cag gta ttc ggt atc agc ggg cgt agc gct gag	384
Val Pro Gly Asp Gln Gln Val Phe Gly Ile Ser Gly Arg Ser Ala Glu	
115 120 125	
cag cgg gtt gcc att gat ttg ctt aac gac gac gcc gtc ggc atc gta	432
Gln Arg Val Ala Ile Asp Leu Leu Asn Asp Asp Ala Val Gly Ile Val	
130 135 140	
tcc atc ggc ggc ccc gcg ggt aca ggt aaa agc gca ctc gca ctg tgt	480
Ser Ile Gly Gly Pro Ala Gly Thr Gly Lys Ser Ala Leu Ala Leu Cys	

145	150	155	160	
gcc ggc ctg gaa gct gtg atg gag cgt cgc att cag cgc aag att atc				528
Ala Gly Leu Glu Ala Val Met Glu Arg Arg Ile Gln Arg Lys Ile Ile	165	170	175	
gtg ttc cgc cca ctc ttt gcc gtt ggc gga cag gaa ctt ggc tac ctg				576
Val Phe Arg Pro Leu Phe Ala Val Gly Gly Gln Glu Leu Gly Tyr Leu	180	185	190	
cct ggc gac caa gaa gaa aaa atg ggg cct tgg gcg caa gcg gtt ttt				624
Pro Gly Asp Gln Glu Glu Lys Met Gly Pro Trp Ala Gln Ala Val Phe	195	200	205	
gac acc cta agc tcc atg gtc agc caa aac atc atc gat gaa gcc ctc				672
Asp Thr Leu Ser Ser Met Val Ser Gln Asn Ile Ile Asp Glu Ala Leu	210	215	220	
tcc cgc ggc ctc atc gaa gtt ctc cca ctt act cac atc cgc gga cgc				720
Ser Arg Gly Leu Ile Glu Val Leu Pro Leu Thr His Ile Arg Gly Arg	225	230	235	240
tca ctc cac gat gct ttc gtc atc gtc gac gag gcc caa tcc cta gaa				768
Ser Leu His Asp Ala Phe Val Ile Val Asp Glu Ala Gln Ser Leu Glu	245	250	255	
cgc aac gtg ttg ctc acc atg ctg tct cgc atc ggc cag aat tcc cga				816
Arg Asn Val Leu Leu Thr Met Leu Ser Arg Ile Gly Gln Asn Ser Arg	260	265	270	
gta gtt ctc acc cat gac gta gcg cag cgc gac aac ctg cgc gtt ggt				864
Val Val Leu Thr His Asp Val Ala Gln Arg Asp Asn Leu Arg Val Gly	275	280	285	
cgc tac gac ggc atc gtc tct gtg gtg gaa gca ctc aag gat cac gaa				912
Arg Tyr Asp Gly Ile Val Ser Val Val Glu Ala Leu Lys Asp His Glu	290	295	300	
ctg ttt ggc cac atc acg ttg cag cgt tcc gaa cgc tcc cga atc gct				960
Leu Phe Gly His Ile Thr Leu Gln Arg Ser Glu Arg Ser Arg Ile Ala	305	310	315	320
gag ttg gtc acc caa gtt ttg gat gcg ccg tct ctg tagtcgcgca				1006
Glu Leu Val Thr Gln Val Leu Asp Ala Pro Ser Leu	325	330		
gtctgtggcg att				1019

<210> 300

<211> 332

<212> PRT

<213> Corynebacterium glutamicum

<400> 300

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1

5

10

15

Glu Glu Gly His Asn Val Val Leu Val Ser Lys Asp Leu Pro Met Arg

20

25

30

Ile Lys Ala Ser Ala Ser Gly Ile Ala Ala Gln Glu Tyr Arg Ala Ala
 35 40 45
 Leu Ala Arg Asp Arg Gly Tyr Thr Gly Met Thr His Ala Asn Ile Thr
 50 55 60
 Asp Asp Gln Leu Ser Glu Leu Tyr Asp Thr Gly Glu Val Arg Ile Glu
 65 70 75 80
 Glu Leu Glu Lys Leu Pro Val Asn His Gly Phe Thr Leu Lys Ser Asn
 85 90 95
 Ser Gly Ser Ala Leu Gly Arg Met Asn Ser Asp Lys Ile Ile Glu Leu
 100 105 110
 Val Pro Gly Asp Gln Gln Val Phe Gly Ile Ser Gly Arg Ser Ala Glu
 115 120 125
 Gln Arg Val Ala Ile Asp Leu Leu Asn Asp Asp Ala Val Gly Ile Val
 130 135 140
 Ser Ile Gly Gly Pro Ala Gly Thr Gly Lys Ser Ala Leu Ala Leu Cys
 145 150 155 160
 Ala Gly Leu Glu Ala Val Met Glu Arg Arg Ile Gln Arg Lys Ile Ile
 165 170 175
 Val Phe Arg Pro Leu Phe Ala Val Gly Gly Gln Glu Leu Gly Tyr Leu
 180 185 190
 Pro Gly Asp Gln Glu Glu Lys Met Gly Pro Trp Ala Gln Ala Val Phe
 195 200 205
 Asp Thr Leu Ser Ser Met Val Ser Gln Asn Ile Ile Asp Glu Ala Leu
 210 215 220
 Ser Arg Gly Leu Ile Glu Val Leu Pro Leu Thr His Ile Arg Gly Arg
 225 230 235 240
 Ser Leu His Asp Ala Phe Val Ile Val Asp Glu Ala Gln Ser Leu Glu
 245 250 255
 Arg Asn Val Leu Leu Thr Met Leu Ser Arg Ile Gly Gln Asn Ser Arg
 260 265 270
 Val Val Leu Thr His Asp Val Ala Gln Arg Asp Asn Leu Arg Val Gly
 275 280 285
 Arg Tyr Asp Gly Ile Val Ser Val Val Glu Ala Leu Lys Asp His Glu
 290 295 300
 Leu Phe Gly His Ile Thr Leu Gln Arg Ser Glu Arg Ser Arg Ile Ala
 305 310 315 320
 Glu Leu Val Thr Gln Val Leu Asp Ala Pro Ser Leu
 325 330

<210> 301
 <211> 1140
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1117)

<223> RXA00888

<400> 301

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acctttcttg aacattccga aagcaggccg aactagcact gtg act gcc ccg cga 115
                               Val Thr Ala Pro Arg
                               1 5

aaa acc cgc aca gaa gta atc acc act gtc ctc aat cta gaa cgc acg 163
Lys Thr Arg Thr Glu Val Ile Thr Thr Val Leu Asn Leu Glu Arg Thr
                               10 15 20

ctc gcg caa acc gtt tta gga atc aac gac gaa aac ctg cgt gtg ttg 211
Leu Ala Gln Thr Val Leu Gly Ile Asn Asp Glu Asn Leu Arg Val Leu
                               25 30 35

gac aat caa att gat tgc gat att cac gtg cgt ggc acc cac gtg gaa 259
Asp Asn Gln Ile Asp Cys Asp Ile His Val Arg Gly Thr His Val Glu
                               40 45 50

ctc acc ggg cca gcc cac gaa gtc tcc cgc gcc tcg aaa ata ttt gag 307
Leu Thr Gly Pro Ala His Glu Val Ser Arg Ala Ser Lys Ile Phe Glu
                               55 60 65

gaa ctg cag gcg att gcc cgt cga gga cat gtg att agc cct gag aca 355
Glu Leu Gln Ala Ile Ala Arg Arg Gly His Val Ile Ser Pro Glu Thr
                               70 75 80 85

gta aaa aat gtc atc agc atg att aac gtg gag acg ccg caa acc gtc 403
Val Lys Asn Val Ile Ser Met Ile Asn Val Glu Thr Pro Gln Thr Val
                               90 95 100

tct gaa atc ttg acc ggc gat atc ctt gct cgc cgt ggc aaa gtg atc 451
Ser Glu Ile Leu Thr Gly Asp Ile Leu Ala Arg Arg Gly Lys Val Ile
                               105 110 115

cgc cct aag acg ctt ggc caa aag cac tac gtg gac gcg att gat acc 499
Arg Pro Lys Thr Leu Gly Gln Lys His Tyr Val Asp Ala Ile Asp Thr
                               120 125 130

aac acg att gtg ttc ggt ctg ggc cca gcc ggt tcc ggt aaa acc tat 547
Asn Thr Ile Val Phe Gly Leu Gly Pro Ala Gly Ser Gly Lys Thr Tyr
                               135 140 145

ctg gcc atg gca aaa gcc gtc caa gcg ctg caa tca aag cag gtc agc 595
Leu Ala Met Ala Lys Ala Val Gln Ala Leu Gln Ser Lys Gln Val Ser
                               150 155 160 165

cgc atc atc ttg acc cgc ccc gca gtg gaa gcc ggc gag aaa ctc ggc 643
Arg Ile Ile Leu Thr Arg Pro Ala Val Glu Ala Gly Glu Lys Leu Gly
                               170 175 180

ttc ttg ccc ggc acc ctg aac gaa aag atc gac ccc tac ctg cgc ccg 691
Phe Leu Pro Gly Thr Leu Asn Glu Lys Ile Asp Pro Tyr Leu Arg Pro
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<400> 302
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Asn Leu Glu Arg Thr Leu Ala Gln Thr Val Leu Gly Ile Asn Asp Glu
          20                      25                      30
Asn Leu Arg Val Leu Asp Asn Gln Ile Asp Cys Asp Ile His Val Arg
          35                      40                      45
Gly Thr His Val Glu Leu Thr Gly Pro Ala His Glu Val Ser Arg Ala
  50                      55                      60
Ser Lys Ile Phe Glu Glu Leu Gln Ala Ile Ala Arg Arg Gly His Val
  65                      70                      75                      80

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Ile Ser Pro Glu Thr Val Lys Asn Val Ile Ser Met Ile Asn Val Glu
 85 90 95
 Thr Pro Gln Thr Val Ser Glu Ile Leu Thr Gly Asp Ile Leu Ala Arg
 100 105 110
 Arg Gly Lys Val Ile Arg Pro Lys Thr Leu Gly Gln Lys His Tyr Val
 115 120 125
 Asp Ala Ile Asp Thr Asn Thr Ile Val Phe Gly Leu Gly Pro Ala Gly
 130 135 140
 Ser Gly Lys Thr Tyr Leu Ala Met Ala Lys Ala Val Gln Ala Leu Gln
 145 150 155 160
 Ser Lys Gln Val Ser Arg Ile Ile Leu Thr Arg Pro Ala Val Glu Ala
 165 170 175
 Gly Glu Lys Leu Gly Phe Leu Pro Gly Thr Leu Asn Glu Lys Ile Asp
 180 185 190
 Pro Tyr Leu Arg Pro Leu His Asp Ala Leu Arg Asp Met Val Glu Pro
 195 200 205
 Glu Val Ile Pro Lys Leu Met Glu Ala Gly Ile Val Glu Val Ala Pro
 210 215 220
 Leu Ala Tyr Met Arg Gly Arg Thr Leu Asn Asp Ala Phe Val Ile Leu
 225 230 235 240
 Asp Glu Ala Gln Asn Thr Thr Pro Ala Gln Met Lys Met Phe Leu Thr
 245 250 255
 Arg Leu Gly Phe Gly Ser Lys Met Val Val Thr Gly Asp Ile Thr Gln
 260 265 270
 Val Asp Leu Pro Gly Gly Gln Lys Ser Gly Leu Arg Leu Val Arg His
 275 280 285
 Ile Leu Arg Gly Val Asp Asp Val His Phe Ser Glu Leu Thr Ser Ser
 290 295 300
 Asp Val Val Arg His Gln Leu Val Gly His Ile Val Asp Ala Tyr Glu
 305 310 315 320
 Asp Tyr Glu Glu Arg Glu Ala Arg Glu Leu Lys Arg Lys Arg Gln Glu
 325 330 335
 Thr Arg Pro

<210> 303

<211> 1506

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1483)

<223> RXA01437

<400> 303

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atcaatgaga aggttcaggc tgaaattaga aaggcgaatgt atg tct gac aca ccg 115
Met Ser Asp Thr Pro
1 5

acc tca gct ctg atc acc acg gtc aac cgc agc ttc gat gga ttc gat 163
Thr Ser Ala Leu Ile Thr Thr Val Asn Arg Ser Phe Asp Gly Phe Asp
10 15 20

ttg gaa gaa gta gca gca gac ctt gga gtt cgg ctc acc tac ctg ccc 211
Leu Glu Glu Val Ala Ala Asp Leu Gly Val Arg Leu Thr Tyr Leu Pro
25 30 35

gac gaa gaa cta gaa gta tcc aaa gtt ctc gcg gcg gac ctc ctc gct 259
Asp Glu Glu Leu Glu Val Ser Lys Val Leu Ala Ala Asp Leu Leu Ala
40 45 50

gag ggg cca gct ctc atc atc ggt gta gga aac acg ttt ttc gac gcc 307
Glu Gly Pro Ala Leu Ile Ile Gly Val Gly Asn Thr Phe Phe Asp Ala
55 60 65

cag gtc gcc gct gcc ctc ggc gtc cca gtg cta ctg ctg gta gac aag 355
Gln Val Ala Ala Ala Leu Gly Val Pro Val Leu Leu Val Asp Lys
70 75 80 85

caa ggc aag cac gtt gct ctt gct cgc acc cag gta aac aat gcc ggc 403
Gln Gly Lys His Val Ala Leu Ala Arg Thr Gln Val Asn Asn Ala Gly
90 95 100

gca gtt gtt gca gca gca ttt acc gct gaa caa gag cca atg ccg gat 451
Ala Val Val Ala Ala Ala Phe Thr Ala Glu Gln Glu Pro Met Pro Asp
105 110 115

aag ctg cgc aag gct gtg cgc aac cac agc aac ctc gaa cca gtc atg 499
Lys Leu Arg Lys Ala Val Arg Asn His Ser Asn Leu Glu Pro Val Met
120 125 130

agc gcc gaa ctc ttt gaa aac tgg ctg ctc aag cgc gca cgc gca gag 547
Ser Ala Glu Leu Phe Glu Asn Trp Leu Leu Lys Arg Ala Arg Ala Glu
135 140 145

cac tcc cac att gtg ctg cca gaa ggt gac gac gac cgc atc ttg atg 595
His Ser His Ile Val Leu Pro Glu Gly Asp Asp Asp Arg Ile Leu Met
150 155 160 165

gct gcc cac cag ctg ctt gat caa gac atc tgt gac atc acg atc ctg 643
Ala Ala His Gln Leu Leu Asp Gln Asp Ile Cys Asp Ile Thr Ile Leu
170 175 180

ggc gat cca gta aag atc aag gag cgc gct acc gaa ctt ggc ctg cac 691
Gly Asp Pro Val Lys Ile Lys Glu Arg Ala Thr Glu Leu Gly Leu His
185 190 195

ctt aac act gca tac ctg gtc aat ccg ctg aca gat cct cgc ctg gag 739
Leu Asn Thr Ala Tyr Leu Val Asn Pro Leu Thr Asp Pro Arg Leu Glu
200 205 210

gaa ttc gcc gaa caa ttc gcg gag ctg cgc aag tca aag agc gtc act 787

Glu 215	Phe	Ala	Glu	Gln	Phe	Ala	Glu	Leu	Arg	Lys	Ser	Lys	Ser	Val	Thr	
atc Ile 230	gat Asp	gaa Glu	gcc Ala	cgc Arg	gaa Glu 235	atc Ile	atg Met	aag Lys	gat Asp	att Ile 240	tcc Ser	tac Tyr	ttc Phe	ggc Gly	acc Thr 245	835
atg Met	atg Met	gtc Val	cac His	aac Asn 250	ggc Gly	gac Asp	gcc Ala	gac Asp	gga Gly 255	atg Met	gta Val	tcc Ser	ggg Gly	gca Ala 260	gca Ala	883
aac Asn	acc Thr	acc Thr	gca Ala 265	cac His	acc Thr	att Ile	aag Lys	cca Pro 270	agc Ser	ttc Phe	cag Gln	atc Ile 275	atc Ile	aaa Lys	act Thr	931
gtt Val	cca Pro	gaa Glu 280	gca Ala	tcc Ser	gtc Val	gtt Val	tct Ser 285	tcc Ser	atc Ile	ttc Phe	ctc Leu 290	atg Met	gtg Val	ctg Leu	cgc Arg	979
ggg Gly	cga Arg 295	ctg Leu	tgg Trp	gca Ala	ttc Phe	ggc Gly 300	gac Asp	tgt Cys	gct Ala	gtt Val	aac Asn 305	ccg Pro	aac Asn	cca Pro	act Thr	1027
gct Ala 310	gaa Glu	cag Gln	ctt Leu	ggg Gly	gaa Glu 315	atc Ile	gcc Ala	gtt Val	gtg Val	tca Ser 320	gca Ala	aaa Lys	act Thr	gca Ala 325	gca Ala	1075
caa Gln	ttt Phe	ggc Gly	att Ile	gat Asp 330	cct Pro	cgc Arg	gta Val	gcc Ala	atc Ile 335	ttg Leu	tcc Ser	tac Tyr	tcc Ser	act Thr 340	ggc Gly	1123
aac Asn	tcc Ser	ggc Gly	gga Gly 345	ggc Gly	tca Ser	gat Asp	gtg Val	gat Asp 350	cgc Arg	gcc Ala	atc Ile	gac Asp 355	gct Ala 355	ctt Leu	gca Ala	1171
gaa Glu	gca Ala	cgc Arg 360	cga Arg	ctt Leu	aac Asn	cca Pro	gaa Glu 365	cta Leu	tgc Cys	gtc Val	gat Asp 370	gga Gly 370	cca Pro	ctt Leu	cag Gln	1219
ttc Phe	gac Asp 375	gcc Ala	gcc Ala	gtc Val	gac Asp 380	ccg Pro	ggg Gly	gtg Val	gcg Ala	cgc Arg 385	aag Lys 385	aag Lys	atg Met	cca Pro	gac Asp	1267
tct Ser 390	gac Asp	gtc Val	gct Ala	ggc Gly	cag Gln 395	gca Ala	aat Asn	gtg Val	ttt Phe	atc Ile 400	ttc Phe	cct Pro	gac Asp	ctg Leu	gaa Glu 405	1315
gcc Ala	gga Gly	aac Asn	atc Ile	ggc Gly 410	tac Tyr	aaa Lys	act Thr	gca Ala	caa Gln 415	cgc Arg	acc Thr	ggg Gly	cac His	gcc Ala 420	ctg Leu	1363
gca Ala	gtt Val	ggg Gly	ccg Pro	att Ile	ctg Leu	cag Gln	ggc Gly	cta Leu 430	aac Asn	aaa Lys	cca Pro	gtc Val	aac Asn 435	gac Asp	ctt Leu	1411
tcc Ser	cgt Arg	ggc Gly 440	gca Ala	aca Thr	gtc Val	cct Pro	gac Asp 445	atc Ile	gtc Val	aac Asn	aca Thr	gta Val 450	gcc Ala	atc Ile	aca Thr	1459
gca Ala	att Ile	cag Gln	gca Ala	gga Gly	gga Gly	cgc Arg	agc Ser	taatggcatt	ggcacttg	ttg						1506

455

460

<210> 304

<211> 461

<212> PRT

<213> Corynebacterium glutamicum

<400> 304

Met Ser Asp Thr Pro Thr Ser Ala Leu Ile Thr Thr Val Asn Arg Ser
 1 5 10 15

Phe Asp Gly Phe Asp Leu Glu Glu Val Ala Ala Asp Leu Gly Val Arg
 20 25 30

Leu Thr Tyr Leu Pro Asp Glu Glu Leu Glu Val Ser Lys Val Leu Ala
 35 40 45

Ala Asp Leu Leu Ala Glu Gly Pro Ala Leu Ile Ile Gly Val Gly Asn
 50 55 60

Thr Phe Phe Asp Ala Gln Val Ala Ala Ala Leu Gly Val Pro Val Leu
 65 70 75 80

Leu Leu Val Asp Lys Gln Gly Lys His Val Ala Leu Ala Arg Thr Gln
 85 90 95

Val Asn Asn Ala Gly Ala Val Val Ala Ala Ala Phe Thr Ala Glu Gln
 100 105 110

Glu Pro Met Pro Asp Lys Leu Arg Lys Ala Val Arg Asn His Ser Asn
 115 120 125

Leu Glu Pro Val Met Ser Ala Glu Leu Phe Glu Asn Trp Leu Leu Lys
 130 135 140

Arg Ala Arg Ala Glu His Ser His Ile Val Leu Pro Glu Gly Asp Asp
 145 150 155 160

Asp Arg Ile Leu Met Ala Ala His Gln Leu Leu Asp Gln Asp Ile Cys
 165 170 175

Asp Ile Thr Ile Leu Gly Asp Pro Val Lys Ile Lys Glu Arg Ala Thr
 180 185 190

Glu Leu Gly Leu His Leu Asn Thr Ala Tyr Leu Val Asn Pro Leu Thr
 195 200 205

Asp Pro Arg Leu Glu Glu Phe Ala Glu Gln Phe Ala Glu Leu Arg Lys
 210 215 220

Ser Lys Ser Val Thr Ile Asp Glu Ala Arg Glu Ile Met Lys Asp Ile
 225 230 235 240

Ser Tyr Phe Gly Thr Met Met Val His Asn Gly Asp Ala Asp Gly Met
 245 250 255

Val Ser Gly Ala Ala Asn Thr Thr Ala His Thr Ile Lys Pro Ser Phe
 260 265 270

Gln Ile Ile Lys Thr Val Pro Glu Ala Ser Val Val Ser Ser Ile Phe

275	280	285
Leu Met Val Leu Arg Gly Arg Leu Trp Ala Phe Gly Asp Cys Ala Val		
290	295	300
Asn Pro Asn Pro Thr Ala Glu Gln Leu Gly Glu Ile Ala Val Val Ser		
305	310	315
Ala Lys Thr Ala Ala Gln Phe Gly Ile Asp Pro Arg Val Ala Ile Leu		
	325	330
Ser Tyr Ser Thr Gly Asn Ser Gly Gly Gly Ser Asp Val Asp Arg Ala		
	340	345
Ile Asp Ala Leu Ala Glu Ala Arg Arg Leu Asn Pro Glu Leu Cys Val		
	355	360
Asp Gly Pro Leu Gln Phe Asp Ala Ala Val Asp Pro Gly Val Ala Arg		
	370	375
Lys Lys Met Pro Asp Ser Asp Val Ala Gly Gln Ala Asn Val Phe Ile		
385	390	395
Phe Pro Asp Leu Glu Ala Gly Asn Ile Gly Tyr Lys Thr Ala Gln Arg		
	405	410
Thr Gly His Ala Leu Ala Val Gly Pro Ile Leu Gln Gly Leu Asn Lys		
	420	425
Pro Val Asn Asp Leu Ser Arg Gly Ala Thr Val Pro Asp Ile Val Asn		
	435	440
Thr Val Ala Ile Thr Ala Ile Gln Ala Gly Gly Arg Ser		
450	455	460

<210> 305
 <211> 1248
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1225)
 <223> RXN00778

<400> 305
 aggtcttagg tttttaagtc gtgagcaatc cggagggaaa ctagcccgcc tacaggatct 60

gctcagacga tgtcttcact taaaccggaa aggccttcccc gtg aac ctc act ctt 115
 Val Asn Leu Thr Leu
 1 5

aag cgc tcc atc gcc ctt gtg ggc gca gtt act gca ggc tcc ttc gct 163
 Lys Arg Ser Ile Ala Leu Val Gly Ala Val Thr Ala Gly Ser Phe Ala
 10 15 20

ctt gta gct tgc tcc gac tcc aat gag tct gat tcc acc tcc tca tct 211
 Leu Val Ala Cys Ser Asp Ser Asn Glu Ser Asp Ser Thr Ser Ser Ser
 25 30 35

gca gct tcc acc ggt tct tcc gat gct gca tcc att gag ggc ctt tcc	259
Ala Ala Ser Thr Gly Ser Ser Asp Ala Ala Ser Ile Glu Gly Leu Ser	
40 45 50	
ggt gtt acc ggt cag ctc gtt gct gaa ggt gca tct tcc cag cag tcc	307
Gly Val Thr Gly Gln Leu Val Ala Glu Gly Ala Ser Ser Gln Gln Ser	
55 60 65	
gca atg gac tac ttt ggt atc cgt tac tcc gag gct gtc agc ggt gca	355
Ala Met Asp Tyr Phe Gly Ile Arg Tyr Ser Glu Ala Val Ser Gly Ala	
70 75 80 85	
tct ctg gct tac acc cct tca ggt tcc ggt tcc ggc cgc acc aac ttc	403
Ser Leu Ala Tyr Thr Pro Ser Gly Ser Gly Ser Gly Arg Thr Asn Phe	
90 95 100	
gct gca ggc cag gtt gct ttc ggt ggc tcc gac tcc gca atg aag gac	451
Ala Ala Gly Gln Val Ala Phe Gly Gly Ser Asp Ser Ala Met Lys Asp	
105 110 115	
gac cag gct gca gaa gca gaa gca cgt tgc aac ggc aac gaa gca tgg	499
Asp Gln Ala Ala Glu Ala Glu Ala Arg Cys Asn Gly Asn Glu Ala Trp	
120 125 130	
cac ctg cca ttc gtt atc ggc cca gtt gca gtt gct tac aac ctg cct	547
His Leu Pro Phe Val Ile Gly Pro Val Ala Val Ala Tyr Asn Leu Pro	
135 140 145	
ggc gtt gac acc ctg aac ctg gac acc aac atc atc gct cag atc ttc	595
Gly Val Asp Thr Leu Asn Leu Asp Thr Asn Ile Ile Ala Gln Ile Phe	
150 155 160 165	
aag ggc gag atc acc aag tgg aac gac gaa gca atc gct tcc cag aac	643
Lys Gly Glu Ile Thr Lys Trp Asn Asp Glu Ala Ile Ala Ser Gln Asn	
170 175 180	
gag ggc acc gac ctc cca gac cag gac atc tcc gtt ctg tac cgt tcc	691
Glu Gly Thr Asp Leu Pro Asp Gln Asp Ile Ser Val Leu Tyr Arg Ser	
185 190 195	
gaa gag tcc ggt acc tcc gac aac ttc cag aag ttc ctc gga gct tcc	739
Glu Glu Ser Gly Thr Ser Asp Asn Phe Gln Lys Phe Leu Gly Ala Ser	
200 205 210	
acc gac atc tgg gag acc gaa ggc cag cag ttc cca acc gag gtt ggc	787
Thr Asp Ile Trp Glu Thr Glu Gly Gln Gln Phe Pro Thr Glu Val Gly	
215 220 225	
tcc ggt gcg cag ggc tcc aac ggt gta gct tct gag gct tcc aac atc	835
Ser Gly Ala Gln Gly Ser Asn Gly Val Ala Ser Glu Ala Ser Asn Ile	
230 235 240 245	
gag ggt gca atc acc tac gtt gaa gct ggt ttc gct aac cag tcc ggc	883
Glu Gly Ala Ile Thr Tyr Val Glu Ala Gly Phe Ala Asn Gln Ser Gly	
250 255 260	
ctg ggc gtt gca aac atc gac ttc ggt tcc ggc cca gtt gaa ctc aac	931
Leu Gly Val Ala Asn Ile Asp Phe Gly Ser Gly Pro Val Glu Leu Asn	
265 270 275	
gct gag tcc gtt ggc gtt gca ctt ggt gca ctc gac ttc ctg act gag	979

Ala Glu Ser Val Gly Val Ala Leu Gly Ala Leu Asp Phe Leu Thr Glu
 280 285 290

ggc cac aac atg gtt gtt gac acc gac gct atg ttc gca atg aac gaa 1027
 Gly His Asn Met Val Val Asp Thr Asp Ala Met Phe Ala Met Asn Glu
 295 300 305

gcc ggt gct tac cca ctg atc ctc acc acc tac gaa atc gtc tgc tcc 1075
 Ala Gly Ala Tyr Pro Leu Ile Leu Thr Thr Tyr Glu Ile Val Cys Ser
 310 315 320 325

gca ggc tac gac gag acc acc cgc gac cag gtc aag gac ttc ctg acc 1123
 Ala Gly Tyr Asp Glu Thr Thr Arg Asp Gln Val Lys Asp Phe Leu Thr
 330 335 340

gtt gca ctg gac tcc cag gat gac cag ctc gag gct ctc ggc tac atc 1171
 Val Ala Leu Asp Ser Gln Asp Asp Gln Leu Glu Ala Leu Gly Tyr Ile
 345 350 355

cca gtt acc ggc gag cac tac gat cgc ctc gtt gca gca gtt gaa gca 1219
 Pro Val Thr Gly Glu His Tyr Asp Arg Leu Val Ala Ala Val Glu Ala
 360 365 370

att cag taataaaccg ctgccgtagc ttc 1248
 Ile Gln
 375

<210> 306

<211> 375

<212> PRT

<213> Corynebacterium glutamicum

<400> 306

Val Asn Leu Thr Leu Lys Arg Ser Ile Ala Leu Val Gly Ala Val Thr
 1 5 10 15

Ala Gly Ser Phe Ala Leu Val Ala Cys Ser Asp Ser Asn Glu Ser Asp
 20 25 30

Ser Thr Ser Ser Ser Ala Ala Ser Thr Gly Ser Ser Asp Ala Ala Ser
 35 40 45

Ile Glu Gly Leu Ser Gly Val Thr Gly Gln Leu Val Ala Glu Gly Ala
 50 55 60

Ser Ser Gln Gln Ser Ala Met Asp Tyr Phe Gly Ile Arg Tyr Ser Glu
 65 70 75 80

Ala Val Ser Gly Ala Ser Leu Ala Tyr Thr Pro Ser Gly Ser Gly Ser
 85 90 95

Gly Arg Thr Asn Phe Ala Ala Gly Gln Val Ala Phe Gly Gly Ser Asp
 100 105 110

Ser Ala Met Lys Asp Asp Gln Ala Ala Glu Ala Glu Ala Arg Cys Asn
 115 120 125

Gly Asn Glu Ala Trp His Leu Pro Phe Val Ile Gly Pro Val Ala Val
 130 135 140

Ala Tyr Asn Leu Pro Gly Val Asp Thr Leu Asn Leu Asp Thr Asn Ile
 145 150 155 160
 Ile Ala Gln Ile Phe Lys Gly Glu Ile Thr Lys Trp Asn Asp Glu Ala
 165 170 175
 Ile Ala Ser Gln Asn Glu Gly Thr Asp Leu Pro Asp Gln Asp Ile Ser
 180 185 190
 Val Leu Tyr Arg Ser Glu Glu Ser Gly Thr Ser Asp Asn Phe Gln Lys
 195 200 205
 Phe Leu Gly Ala Ser Thr Asp Ile Trp Glu Thr Glu Gly Gln Gln Phe
 210 215 220
 Pro Thr Glu Val Gly Ser Gly Ala Gln Gly Ser Asn Gly Val Ala Ser
 225 230 235 240
 Glu Ala Ser Asn Ile Glu Gly Ala Ile Thr Tyr Val Glu Ala Gly Phe
 245 250 255
 Ala Asn Gln Ser Gly Leu Gly Val Ala Asn Ile Asp Phe Gly Ser Gly
 260 265 270
 Pro Val Glu Leu Asn Ala Glu Ser Val Gly Val Ala Leu Gly Ala Leu
 275 280 285
 Asp Phe Leu Thr Glu Gly His Asn Met Val Val Asp Thr Asp Ala Met
 290 295 300
 Phe Ala Met Asn Glu Ala Gly Ala Tyr Pro Leu Ile Leu Thr Thr Tyr
 305 310 315 320
 Glu Ile Val Cys Ser Ala Gly Tyr Asp Glu Thr Thr Arg Asp Gln Val
 325 330 335
 Lys Asp Phe Leu Thr Val Ala Leu Asp Ser Gln Asp Asp Gln Leu Glu
 340 345 350
 Ala Leu Gly Tyr Ile Pro Val Thr Gly Glu His Tyr Asp Arg Leu Val
 355 360 365
 Ala Ala Val Glu Ala Ile Gln
 370 375

<210> 307

<211> 857

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(834)

<223> FRXA00778

<400> 307

cgc aac aac ttc gct gca gcc cag gtt gct ttc ggt ggc tcc gac tcc 48
 Arg Asn Asn Phe Ala Ala Ala Gln Val Ala Phe Gly Gly Ser Asp Ser
 1 5 10 15

gca atg aag gac gac cag gct gca gaa gca gaa gca cgt tgc aac ggc	96
Ala Met Lys Asp Asp Gln Ala Ala Glu Ala Glu Ala Arg Cys Asn Gly	
20 25 30	
aac gaa gca tgg cac ctg cca ttc gtt atc ggc cca gtt gca gtt gct	144
Asn Glu Ala Trp His Leu Pro Phe Val Ile Gly Pro Val Ala Val Ala	
35 40 45	
tac aac ctg cct ggc gtt gac acc ctg aac ctg gac acc aac atc atc	192
Tyr Asn Leu Pro Gly Val Asp Thr Leu Asn Leu Asp Thr Asn Ile Ile	
50 55 60	
gct cag atc ttc aag ggc gag atc acc aag tgg aac gac gaa gca atc	240
Ala Gln Ile Phe Lys Gly Glu Ile Thr Lys Trp Asn Asp Glu Ala Ile	
65 70 75 80	
gct tcc cag aac gag ggc acc gac ctc cca gac cag gac atc tcc gtt	288
Ala Ser Gln Asn Glu Gly Thr Asp Leu Pro Asp Gln Asp Ile Ser Val	
85 90 95	
ctg tac cgt tcc gaa gag tcc ggt acc tcc gac aac ttc cag aag ttc	336
Leu Tyr Arg Ser Glu Glu Ser Gly Thr Ser Asp Asn Phe Gln Lys Phe	
100 105 110	
ctc gga gct tcc acc gac atc tgg gag acc gaa ggc cag cag ttc cca	384
Leu Gly Ala Ser Thr Asp Ile Trp Glu Thr Glu Gly Gln Gln Phe Pro	
115 120 125	
acc gag gtt ggc tcc ggt gcg cag ggc tcc aac ggt gta gct tct gag	432
Thr Glu Val Gly Ser Gly Ala Gln Gly Ser Asn Gly Val Ala Ser Glu	
130 135 140	
gct tcc aac atc gag ggt gca atc acc tac gtt gaa gct ggt ttc gct	480
Ala Ser Asn Ile Glu Gly Ala Ile Thr Tyr Val Glu Ala Gly Phe Ala	
145 150 155 160	
aac cag tcc ggc ctg ggc gtt gca aac atc gac ttc ggt tcc ggc cca	528
Asn Gln Ser Gly Leu Gly Val Ala Asn Ile Asp Phe Gly Ser Gly Pro	
165 170 175	
ggt gaa ctc aac gct gag tcc gtt ggc gtt gca ctt ggt gca ctc gac	576
Val Glu Leu Asn Ala Glu Ser Val Gly Val Ala Leu Gly Ala Leu Asp	
180 185 190	
ttc ctg act gag ggc cac aac atg gtt gtt gac acc gac gct atg ttc	624
Phe Leu Thr Glu Gly His Asn Met Val Val Asp Thr Asp Ala Met Phe	
195 200 205	
gca atg aac gaa gcc ggt gct tac cca ctg atc ctc acc acc tac gaa	672
Ala Met Asn Glu Ala Gly Ala Tyr Pro Leu Ile Leu Thr Thr Tyr Glu	
210 215 220	
atc gtc tgc tcc gca ggc tac gac gag acc acc cgc gac cag gtc aag	720
Ile Val Cys Ser Ala Gly Tyr Asp Glu Thr Thr Arg Asp Gln Val Lys	
225 230 235 240	
gac ttc ctg acc gtt gca ctg gac tcc cag gat gac cag ctc gag gct	768
Asp Phe Leu Thr Val Ala Leu Asp Ser Gln Asp Asp Gln Leu Glu Ala	
245 250 255	
ctc ggc tac atc cca gtt acc ggc gag cac tac gat cgc ctc gtt gca	816

Leu Gly Tyr Ile Pro Val Thr Gly Glu His Tyr Asp Arg Leu Val Ala
 260 265 270

gca gtt gaa gca att cag taataaacgcg ctgccgtagc ttc
 Ala Val Glu Ala Ile Gln
 275

857

<210> 308

<211> 278

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 308

Arg Asn Asn Phe Ala Ala Ala Gln Val Ala Phe Gly Gly Ser Asp Ser
 1 5 10 15

Ala Met Lys Asp Asp Gln Ala Ala Glu Ala Glu Ala Arg Cys Asn Gly
 20 25 30

Asn Glu Ala Trp His Leu Pro Phe Val Ile Gly Pro Val Ala Val Ala
 35 40 45

Tyr Asn Leu Pro Gly Val Asp Thr Leu Asn Leu Asp Thr Asn Ile Ile
 50 55 60

Ala Gln Ile Phe Lys Gly Glu Ile Thr Lys Trp Asn Asp Glu Ala Ile
 65 70 75 80

Ala Ser Gln Asn Glu Gly Thr Asp Leu Pro Asp Gln Asp Ile Ser Val
 85 90 95

Leu Tyr Arg Ser Glu Glu Ser Gly Thr Ser Asp Asn Phe Gln Lys Phe
 100 105 110

Leu Gly Ala Ser Thr Asp Ile Trp Glu Thr Glu Gly Gln Gln Phe Pro
 115 120 125

Thr Glu Val Gly Ser Gly Ala Gln Gly Ser Asn Gly Val Ala Ser Glu
 130 135 140

Ala Ser Asn Ile Glu Gly Ala Ile Thr Tyr Val Glu Ala Gly Phe Ala
 145 150 155 160

Asn Gln Ser Gly Leu Gly Val Ala Asn Ile Asp Phe Gly Ser Gly Pro
 165 170 175

Val Glu Leu Asn Ala Glu Ser Val Gly Val Ala Leu Gly Ala Leu Asp
 180 185 190

Phe Leu Thr Glu Gly His Asn Met Val Val Asp Thr Asp Ala Met Phe
 195 200 205

Ala Met Asn Glu Ala Gly Ala Tyr Pro Leu Ile Leu Thr Thr Tyr Glu
 210 215 220

Ile Val Cys Ser Ala Gly Tyr Asp Glu Thr Thr Arg Asp Gln Val Lys
 225 230 235 240

Asp Phe Leu Thr Val Ala Leu Asp Ser Gln Asp Asp Gln Leu Glu Ala
 245 250 255

Leu Gly Tyr Ile Pro Val Thr Gly Glu His Tyr Asp Arg Leu Val Ala
 260 265 270

Ala Val Glu Ala Ile Gln
 275

<210> 309

<211> 1050

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1027)

<223> RXA02497

<400> 309

tcgatgccgc cgctggcgaa gactcgggga aacctaataaa taccgaagaa gaatttgacc 60

gattcacact ttgccaccct agaccgtcta accttttaggt gtg aga tta ggt gta 115
 Val Arg Leu Gly Val
 1 5

tta gat gtg ggc agc aat act gtc cac cta gtt gca gta gac gcg cgt 163
 Leu Asp Val Gly Ser Asn Thr Val His Leu Val Ala Val Asp Ala Arg
 10 15 20

ccc ggt gga cac ccc acc ccg atg agc aat tgg cgt acc cca ctg cgc 211
 Pro Gly Gly His Pro Thr Pro Met Ser Asn Trp Arg Thr Pro Leu Arg
 25 30 35

ctt gtt gag ctt ctt gat gac tcc ggg gcg atc tcc gaa aag ggc atc 259
 Leu Val Glu Leu Leu Asp Asp Ser Gly Ala Ile Ser Glu Lys Gly Ile
 40 45 50

aac aaa ctc acc tca gca gtc ggg gaa gca gca gac cta gcg aaa acg 307
 Asn Lys Leu Thr Ser Ala Val Gly Glu Ala Ala Asp Leu Ala Lys Thr
 55 60 65

ctc ggc tgc gct gaa ctg atg cca ttt gct aca tcg gca gtc cgc tcc 355
 Leu Gly Cys Ala Glu Leu Met Pro Phe Ala Thr Ser Ala Val Arg Ser
 70 75 80 85

gcc acc aac agc gag gca gtg ctc gac cac gtg gag aag gaa acc ggc 403
 Ala Thr Asn Ser Glu Ala Val Leu Asp His Val Glu Lys Glu Thr Gly
 90 95 100

gtc cgc ctg tcc atc ctt tcc ggt gaa gac gaa gca cgc caa act ttc 451
 Val Arg Leu Ser Ile Leu Ser Gly Glu Asp Glu Ala Arg Gln Thr Phe
 105 110 115

ctc gca gtt cga cgt tgg tat gga tgg tcc gca ggg cgc ata act aac 499
 Leu Ala Val Arg Arg Trp Tyr Gly Trp Ser Ala Gly Arg Ile Thr Asn
 120 125 130

ctc gac atc ggt ggc ggc tcc ctg gaa cta tcc tcc gga acc gac gaa 547
 Leu Asp Ile Gly Gly Gly Ser Leu Glu Leu Ser Ser Gly Thr Asp Glu
 135 140 145

tcc cca gac ctc gcg ttc tca ctg gat ctg ggt gcg ggc cgc ttg acc 595
 Ser Pro Asp Leu Ala Phe Ser Leu Asp Leu Gly Ala Gly Arg Leu Thr
 150 155 160 165

 cac aac tgg ttc gac acc gat cca ccg gca cgt aag aaa atc aac ctc 643
 His Asn Trp Phe Asp Thr Asp Pro Pro Ala Arg Lys Lys Ile Asn Leu
 170 175 180

 ctg cgc gat tat atc gat gcg gaa ctt gca gaa ccc gcc cgc cag atg 691
 Leu Arg Asp Tyr Ile Asp Ala Glu Leu Ala Glu Pro Ala Arg Gln Met
 185 190 195

 cgc acc cta ggg ccc gcg cgc ctg gca gtg gga aca tcc aaa act ttc 739
 Arg Thr Leu Gly Pro Ala Arg Leu Ala Val Gly Thr Ser Lys Thr Phe
 200 205 210

 cgc acc ctg gca cga ctg act ggt gct gcg ccc tca tcc gca gga cca 787
 Arg Thr Leu Ala Arg Leu Thr Gly Ala Ala Pro Ser Ser Ala Gly Pro
 215 220 225

 cac gtc acc cga acc ctc acc gcg ccg ggt ctg cgc cag ctg atc gca 835
 His Val Thr Arg Thr Leu Thr Ala Pro Gly Leu Arg Gln Leu Ile Ala
 230 235 240 245

 ttt atc tca cga atg act gcg gcg gac cgc gct gag ctg gaa ggt atc 883
 Phe Ile Ser Arg Met Thr Ala Ala Asp Arg Ala Glu Leu Glu Gly Ile
 250 255 260

 agc tgc gat cgg tca cat cag atc gtg gca ggt gcg cta gtt gcg gaa 931
 Ser Ser Asp Arg Ser His Gln Ile Val Ala Gly Ala Leu Val Ala Glu
 265 270 275

 gct gcg atg cgt gcg ttg gat att gac aag gta gaa att tgt ccg tgg 979
 Ala Ala Met Arg Ala Leu Asp Ile Asp Lys Val Glu Ile Cys Pro Trp
 280 285 290

 gca ctt cgt gaa ggt gtg atc ctc acc agg atc gac aaa gga ctc gag 1027
 Ala Leu Arg Glu Gly Val Ile Leu Thr Arg Ile Asp Lys Gly Leu Glu
 295 300 305

 taacattttac ccggaagga gtt 1050

<210> 310

<211> 309

<212> PRT

<213> Corynebacterium glutamicum

<400> 310

Val Arg Leu Gly Val Leu Asp Val Gly Ser Asn Thr Val His Leu Val
 1 5 10 15

Ala Val Asp Ala Arg Pro Gly Gly His Pro Thr Pro Met Ser Asn Trp
 20 25 30

Arg Thr Pro Leu Arg Leu Val Glu Leu Leu Asp Asp Ser Gly Ala Ile
 35 40 45

Ser Glu Lys Gly Ile Asn Lys Leu Thr Ser Ala Val Gly Glu Ala Ala
 50 55 60

Asp Leu Ala Lys Thr Leu Gly Cys Ala Glu Leu Met Pro Phe Ala Thr
 65 70 75 80
 Ser Ala Val Arg Ser Ala Thr Asn Ser Glu Ala Val Leu Asp His Val
 85 90 95
 Glu Lys Glu Thr Gly Val Arg Leu Ser Ile Leu Ser Gly Glu Asp Glu
 100 105 110
 Ala Arg Gln Thr Phe Leu Ala Val Arg Arg Trp Tyr Gly Trp Ser Ala
 115 120 125
 Gly Arg Ile Thr Asn Leu Asp Ile Gly Gly Gly Ser Leu Glu Leu Ser
 130 135 140
 Ser Gly Thr Asp Glu Ser Pro Asp Leu Ala Phe Ser Leu Asp Leu Gly
 145 150 155 160
 Ala Gly Arg Leu Thr His Asn Trp Phe Asp Thr Asp Pro Pro Ala Arg
 165 170 175
 Lys Lys Ile Asn Leu Leu Arg Asp Tyr Ile Asp Ala Glu Leu Ala Glu
 180 185 190
 Pro Ala Arg Gln Met Arg Thr Leu Gly Pro Ala Arg Leu Ala Val Gly
 195 200 205
 Thr Ser Lys Thr Phe Arg Thr Leu Ala Arg Leu Thr Gly Ala Ala Pro
 210 215 220
 Ser Ser Ala Gly Pro His Val Thr Arg Thr Leu Thr Ala Pro Gly Leu
 225 230 235 240
 Arg Gln Leu Ile Ala Phe Ile Ser Arg Met Thr Ala Ala Asp Arg Ala
 245 250 255
 Glu Leu Glu Gly Ile Ser Ser Asp Arg Ser His Gln Ile Val Ala Gly
 260 265 270
 Ala Leu Val Ala Glu Ala Ala Met Arg Ala Leu Asp Ile Asp Lys Val
 275 280 285
 Glu Ile Cys Pro Trp Ala Leu Arg Glu Gly Val Ile Leu Thr Arg Ile
 290 295 300
 Asp Lys Gly Leu Glu
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<210> 311

<211> 1671

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1648)

<223> RXA01477

<400> 311

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cattattttaa	tgcatactcg	gcgctatttt	gaggagcctc	atg	cca	cag	tta	agc									115
				Met	Pro	Gln	Leu	Ser									
				1				5									
aga	cgc	cag	ttc	ttg	cag	aca	acc	gcc	gtt	act	gca	ggg	cta	gcc	act		163
Arg	Arg	Gln	Phe	Leu	Gln	Thr	Thr	Ala	Val	Thr	Ala	Gly	Leu	Ala	Thr		
				10					15					20			
ttt	gcg	ggc	aca	cct	gca	cgc	gct	gaa	gaa	cgc	caa	ttc	cag	cat	ggc		211
Phe	Ala	Gly	Thr	Pro	Ala	Arg	Ala	Glu	Glu	Arg	Gln	Phe	Gln	His	Gly		
			25					30					35				
gtg	gct	tcc	ggg	gac	ccc	acc	gca	acc	tct	gcc	att	ttg	tgg	act	cgg		259
Val	Ala	Ser	Gly	Asp	Pro	Thr	Ala	Thr	Ser	Ala	Ile	Leu	Trp	Thr	Arg		
		40					45					50					
ctg	acc	cca	att	ccc	gac	gcc	aca	cct	gga	agt	ggc	ctt	ggc	ccc	gac		307
Leu	Thr	Pro	Ile	Pro	Asp	Ala	Thr	Pro	Gly	Ser	Gly	Leu	Gly	Pro	Asp		
	55					60					65						
tct	cct	gtc	acc	tgg	gaa	gtc	tcc	ccc	act	cct	gat	ttc	gcc	agc	atc		355
Ser	Pro	Val	Thr	Trp	Glu	Val	Ser	Pro	Thr	Pro	Asp	Phe	Ala	Ser	Ile		
70					75				80						85		
acg	cgc	tcg	gga	acc	gta	atc	acc	tcc	gca	gca	agc	gat	cac	acc	gtc		403
Thr	Arg	Ser	Gly	Thr	Val	Ile	Thr	Ser	Ala	Ala	Ser	Asp	His	Thr	Val		
			90						95					100			
cac	gcg	cac	gcc	acg	ggg	ttg	agc	cca	tcc	acc	cgc	tat	ttc	tac	cgc		451
His	Ala	His	Ala	Thr	Gly	Leu	Ser	Pro	Ser	Thr	Arg	Tyr	Phe	Tyr	Arg		
			105					110					115				
ttc	atc	tcc	tcc	acc	ggc	gag	gtc	tcc	cct	gtg	ggg	cgc	acg	caa	aca		499
Phe	Ile	Ser	Ser	Thr	Gly	Glu	Val	Ser	Pro	Val	Gly	Arg	Thr	Gln	Thr		
		120					125					130					
aca	tcg	ctt	gtc	gac	gct	ccc	ctc	ccg	cac	ctt	cgc	ttt	gcc	ctt	gcg		547
Thr	Ser	Leu	Val	Asp	Ala	Pro	Leu	Pro	His	Leu	Arg	Phe	Ala	Leu	Ala		
	135					140					145						
tcg	tgt	gcc	aat	tgg	gag	gca	gga	ttt	ttt	gcc	gcc	tac	ggc	gac	atc		595
Ser	Cys	Ala	Asn	Trp	Glu	Ala	Gly	Phe	Phe	Ala	Ala	Tyr	Gly	Asp	Ile		
150					155				160						165		
gcc	cgg	cgc	gct	gac	gcc	ggc	gaa	ttg	gag	atg	ttg	att	ttt	ttg	ggg		643
Ala	Arg	Arg	Ala	Asp	Ala	Gly	Glu	Leu	Glu	Met	Leu	Ile	Phe	Leu	Gly		
			170					175						180			
gat	tac	atc	tac	gag	tac	gcc	acc	ggg	atg	ttc	gcc	gga	aag	gac	ggg		691
Asp	Tyr	Ile	Tyr	Glu	Tyr	Ala	Thr	Gly	Met	Phe	Ala	Gly	Lys	Asp	Gly		
		185						190					1				

gcg cat gcg gcg ttg ccg tgg att gtc atg tgg gat gac cat gag tcg Ala His Ala Ala Leu Pro Trp Ile Val Met Trp Asp Asp His Glu Ser 230 235 240 245	835
gcc aac aac tct aat cgt gag ggc gcg cag aat cat tcc gct gat gag Ala Asn Asn Ser Asn Arg Glu Gly Ala Gln Asn His Ser Ala Asp Glu 250 255 260	883
ggt tcg tgg gtg gat cgt caa aat gct gct cgg cag gtc ttt ttg gag Gly Ser Trp Val Asp Arg Gln Asn Ala Ala Arg Gln Val Phe Leu Glu 265 270 275	931
tgg atg ccg atc cgc cag gag gac acg ctc tat cgt tcc ttc act ttt Trp Met Pro Ile Arg Gln Glu Asp Thr Leu Tyr Arg Ser Phe Thr Phe 280 285 290	979
ggt gac ctc gcc acg ctg tca ctt ctt gat ctt cga agt ttc aga gat Gly Asp Leu Ala Thr Leu Ser Leu Leu Asp Leu Arg Ser Phe Arg Asp 295 300 305	1027
cca gca ccc tcc cag caa cag tgg ctg gag ggt caa cgt gcg gac acc Pro Ala Pro Ser Gln Gln Gln Trp Leu Glu Gly Gln Arg Ala Asp Thr 310 315 320 325	1075
atg atg ggg tcg cag cag ttt gag tgg ctg aaa tcc aac gtg gaa cac Met Met Gly Ser Gln Gln Phe Glu Trp Leu Lys Ser Asn Val Glu His 330 335 340	1123
acc acc acg acg tgg aat atc atc ggc agc tca gtg atg ttt gcc ccc Thr Thr Thr Thr Trp Asn Ile Ile Gly Ser Ser Val Met Phe Ala Pro 345 350 355	1171
atg gca att acc ggg cag cct ctt ttc cag atc cct gaa cct att ccc Met Ala Ile Thr Gly Gln Pro Leu Phe Gln Ile Pro Glu Pro Ile Pro 360 365 370	1219
gcc aat ttg gat cag tgg gac ggc tac tcc cgt gag cgc gac cga ctc Ala Asn Leu Asp Gln Trp Asp Gly Tyr Ser Arg Glu Arg Asp Arg Leu 375 380 385	1267
cta gct gta ctt gcc gat ttc gcc act cca acg ctt ttt cta tct ggc Leu Ala Val Leu Ala Asp Phe Ala Thr Pro Thr Leu Phe Leu Ser Gly 390 395 400 405	1315
gat atc cac tcc gaa tgg gca aac gcc atc cgg ttt aat ggt cga gaa Asp Ile His Ser Glu Trp Ala Asn Ala Ile Arg Phe Asn Gly Arg Glu 410 415 420	1363
atc ggt gtc gag gca gta tgc agc tcc atc acc tca gct aat gtc aac Ile Gly Val Glu Ala Val Cys Ser Ser Ile Thr Ser Ala Asn Val Asn 425 430 435	1411
gac ttc gcc aaa ctc cct gag gac aat ccg gtc tcc ctg caa gcg gaa Asp Phe Ala Lys Leu Pro Glu Asp Asn Pro Val Ser Leu Gln Ala Glu 440 445 450	1459
caa gta atc cga gcc aac agt tcg cat gtg cgc cac gtt gat ctt gac Gln Val Ile Arg Ala Asn Ser Ser His Val Arg His Val Asp Leu Asp 455 460 465	1507
gcc cac ggc tac gcc acg gtg aat ctc acc caa gat ggc gcg cac atg	1555

Ala His Gly Tyr Ala Thr Val Asn Leu Thr Gln Asp Gly Ala His Met
 470 475 480 485

gtc tgg cac cgc gtc gcc gat ctc tcc ctt ccg gac tca gaa gtt gct 1603
 Val Trp His Arg Val Ala Asp Leu Ser Leu Pro Asp Ser Glu Val Ala
 490 495 500

ccg gca att gca ctt gag tgg aaa cca ggc gtc gga ttc act act 1648
 Pro Ala Ile Ala Leu Glu Trp Lys Pro Gly Val Gly Phe Thr Thr
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tgagctgctg attttaggt ttt 1671

<210> 312

<211> 516

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 312

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 20 25 30

Gln Phe Gln His Gly Val Ala Ser Gly Asp Pro Thr Ala Thr Ser Ala
 35 40 45

Ile Leu Trp Thr Arg Leu Thr Pro Ile Pro Asp Ala Thr Pro Gly Ser
 50 55 60

Gly Leu Gly Pro Asp Ser Pro Val Thr Trp Glu Val Ser Pro Thr Pro
 65 70 75 80

Asp Phe Ala Ser Ile Thr Arg Ser Gly Thr Val Ile Thr Ser Ala Ala
 85 90 95

Ser Asp His Thr Val His Ala His Ala Thr Gly Leu Ser Pro Ser Thr
 100 105 110

Arg Tyr Phe Tyr Arg Phe Ile Ser Ser Thr Gly Glu Val Ser Pro Val
 115 120 125

Gly Arg Thr Gln Thr Thr Ser Leu Val Asp Ala Pro Leu Pro His Leu
 130 135 140

Arg Phe Ala Leu Ala Ser Cys Ala Asn Trp Glu Ala Gly Phe Phe Ala
 145 150 155 160

Ala Tyr Gly Asp Ile Ala Arg Arg Ala Asp Ala Gly Glu Leu Glu Met
 165 170 175

Leu Ile Phe Leu Gly Asp Tyr Ile Tyr Glu Tyr Ala Thr Gly Met Phe
 180 185 190

Ala Gly Lys Asp Gly Val Val Arg Pro His Gln Pro Leu His Glu Thr
 195 200 205

Ile Thr Leu Glu His Tyr Arg Thr Arg Tyr Gly His Tyr Arg Ser Asp
 210 215 220

Asn	His	Leu	Gln	Ala	Ala	His	Ala	Ala	Leu	Pro	Trp	Ile	Val	Met	Trp	
225					230					235					240	
Asp	Asp	His	Glu	Ser	Ala	Asn	Asn	Ser	Asn	Arg	Glu	Gly	Ala	Gln	Asn	
				245					250					255		
His	Ser	Ala	Asp	Glu	Gly	Ser	Trp	Val	Asp	Arg	Gln	Asn	Ala	Ala	Arg	
			260					265						270		
Gln	Val	Phe	Leu	Glu	Trp	Met	Pro	Ile	Arg	Gln	Glu	Asp	Thr	Leu	Tyr	
		275					280					285				
Arg	Ser	Phe	Thr	Phe	Gly	Asp	Leu	Ala	Thr	Leu	Ser	Leu	Leu	Asp	Leu	
	290					295					300					
Arg	Ser	Phe	Arg	Asp	Pro	Ala	Pro	Ser	Gln	Gln	Gln	Trp	Leu	Glu	Gly	
305					310					315					320	
Gln	Arg	Ala	Asp	Thr	Met	Met	Gly	Ser	Gln	Gln	Phe	Glu	Trp	Leu	Lys	
				325					330						335	
Ser	Asn	Val	Glu	His	Thr	Thr	Thr	Thr	Trp	Asn	Ile	Ile	Gly	Ser	Ser	
			340					345					350			
Val	Met	Phe	Ala	Pro	Met	Ala	Ile	Thr	Gly	Gln	Pro	Leu	Phe	Gln	Ile	
		355					360					365				
Pro	Glu	Pro	Ile	Pro	Ala	Asn	Leu	Asp	Gln	Trp	Asp	Gly	Tyr	Ser	Arg	
	370					375					380					
Glu	Arg	Asp	Arg	Leu	Leu	Ala	Val	Leu	Ala	Asp	Phe	Ala	Thr	Pro	Thr	
385					390					395					400	
Leu	Phe	Leu	Ser	Gly	Asp	Ile	His	Ser	Glu	Trp	Ala	Asn	Ala	Ile	Arg	
				405					410					415		
Phe	Asn	Gly	Arg	Glu	Ile	Gly	Val	Glu	Ala	Val	Cys	Ser	Ser	Ile	Thr	
			420					425						430		
Ser	Ala	Asn	Val	Asn	Asp	Phe	Ala	Lys	Leu	Pro	Glu	Asp	Asn	Pro	Val	
		435					440					445				
Ser	Leu	Gln	Ala	Glu	Gln	Val	Ile	Arg	Ala	Asn	Ser	Ser	His	Val	Arg	
	450					455					460					
His	Val	Asp	Leu	Asp	Ala	His	Gly	Tyr	Ala	Thr	Val	Asn	Leu	Thr	Gln	
465					470					475					480	
Asp	Gly	Ala	His	Met	Val	Trp	His	Arg	Val	Ala	Asp	Leu	Ser	Leu	Pro	
				485					490					495		
Asp	Ser	Glu	Val	Ala	Pro	Ala	Ile	Ala	Leu	Glu	Trp	Lys	Pro	Gly	Val	
			500					505						510		
Gly	Phe	Thr	Thr													

<210> 313

<211> 597

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(574)

<223> RXA01509

<400> 313

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                                         Met Ser Ile Glu Val
                                         1 5

acc gtc gaa atc cct aag gga tca cgc aac aag tac gaa atc gac cac 163
Thr Val Glu Ile Pro Lys Gly Ser Arg Asn Lys Tyr Glu Ile Asp His
                        10 15 20

gag acc gga aag gtc tac ctc gac cgc tac ctg ttc act cca atg gca 211
Glu Thr Gly Lys Val Tyr Leu Asp Arg Tyr Leu Phe Thr Pro Met Ala
                        25 30 35

tac cca ctg gac tac ggc tac atc gac cac acc ctc ggc gaa gac ggc 259
Tyr Pro Leu Asp Tyr Gly Tyr Ile Asp His Thr Leu Gly Glu Asp Gly
                        40 45 50

gac cca ttg gat gca ctg gtc atc ctc ccc gag tcc gtt ttt cca gca 307
Asp Pro Leu Asp Ala Leu Val Ile Leu Pro Glu Ser Val Phe Pro Ala
                        55 60 65

gtt gtg gtt aag tcc cga atc atc ggt gtt ttc aag atg acc gac gaa 355
Val Val Val Lys Ser Arg Ile Ile Gly Val Phe Lys Met Thr Asp Glu
                        70 75 80 85

gcc ggc ggc gac gac aag ctg ctc tcc gtt ctc gac gac cca cgc tac 403
Ala Gly Gly Asp Asp Lys Leu Leu Ser Val Leu Asp Asp Pro Arg Tyr
                        90 95 100

gac cac atc cag gac atc tcc gac gtg tcc gat ttc ctc aag gat gag 451
Asp His Ile Gln Asp Ile Ser Asp Val Ser Asp Phe Leu Lys Asp Glu
                        105 110 115

atc gag cac ttc ttc gtc cac tac aag gac ctg gaa aag ggc aag cac 499
Ile Glu His Phe Phe Val His Tyr Lys Asp Leu Glu Lys Gly Lys His
                        120 125 130

gtt gac ggt tcc ggc tgg ggc gac aag gct gag gct gaa aag atc cac 547
Val Asp Gly Ser Gly Trp Gly Asp Lys Ala Glu Ala Glu Lys Ile His
                        135 140 145

gct gag gca atc gac cgc tac aag gca taagtctttt gtaaattaag agc 597
Ala Glu Ala Ile Asp Arg Tyr Lys Ala
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<210> 314

<211> 158

<212> PRT

<213> Corynebacterium glutamicum

<400> 314

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Tyr Glu Ile Asp His Glu Thr Gly Lys Val Tyr Leu Asp Arg Tyr Leu
 20 25 30

Phe Thr Pro Met Ala Tyr Pro Leu Asp Tyr Gly Tyr Ile Asp His Thr
 35 40 45

Leu Gly Glu Asp Gly Asp Pro Leu Asp Ala Leu Val Ile Leu Pro Glu
 50 55 60

Ser Val Phe Pro Ala Val Val Val Lys Ser Arg Ile Ile Gly Val Phe
 65 70 75 80

Lys Met Thr Asp Glu Ala Gly Gly Asp Asp Lys Leu Leu Ser Val Leu
 85 90 95

Asp Asp Pro Arg Tyr Asp His Ile Gln Asp Ile Ser Asp Val Ser Asp
 100 105 110

Phe Leu Lys Asp Glu Ile Glu His Phe Phe Val His Tyr Lys Asp Leu
 115 120 125

Glu Lys Gly Lys His Val Asp Gly Ser Gly Trp Gly Asp Lys Ala Glu
 130 135 140

Ala Glu Lys Ile His Ala Glu Ala Ile Asp Arg Tyr Lys Ala
 145 150 155

<210> 315

<211> 723

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(700)

<223> RXA00100

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atccgcttgt ttcacatgcg gtgatcgcg ggagtaaacg atg att ttg gat tgg 115
 Met Ile Leu Asp Trp
 1 5

gtt atc tcc atc atg gag gca ctc ggc gcc gtt ggc gtg ggt gtc gcg 163
 Val Ile Ser Ile Met Glu Ala Leu Gly Ala Val Gly Val Gly Val Ala
 10 15 20

gtg ttt ttg gag aac gtt ttc ccg ccg att cca agt gag gtg gtg ctt 211
 Val Phe Leu Glu Asn Val Phe Pro Pro Ile Pro Ser Glu Val Val Leu
 25 30 35

ccg ctc gcg ggt ttc acc acc acg caa ggc gat ctc aat gtg tgg gcg 259
 Pro Leu Ala Gly Phe Thr Thr Thr Gln Gly Asp Leu Asn Val Trp Ala
 40 45 50

gcg ctt atg tgg tgc gtg atc ggg tgc gtt tcc gga gcg ttt ttg ctt 307
 Ala Leu Met Trp Ser Val Ile Gly Ser Val Ser Gly Ala Phe Leu Leu
 55 60 65

tac ggg ttg ggg cgc tca atc ggg gcg gca cgg ttg cgg cag gtc gcc 355
 Tyr Gly Leu Gly Arg Ser Ile Gly Ala Ala Arg Leu Arg Gln Val Ala
 70 75 80 85

gac tgg atg tgg ctt gtc gac gcg acc gac gtg gat aaa tcc cta tgc 403
 Asp Trp Met Trp Leu Val Asp Ala Thr Asp Val Asp Lys Ser Leu Ser
 90 95 100

tgg ttc gaa aag tac ggg aag tat tgc gtg ttt ttc ggt cgg ttg gtg 451
 Trp Phe Glu Lys Tyr Gly Lys Tyr Ser Val Phe Phe Gly Arg Leu Val
 105 110 115

ccg ggt gtc cga agt ttg att tgc att ccg gcg ggc gtc gac aag atg 499
 Pro Gly Val Arg Ser Leu Ile Ser Ile Pro Ala Gly Val Asp Lys Met
 120 125 130

aat ccg gtt ctc ttc ggt gtg ctc act gcg gtg ggc agc acc att tgg 547
 Asn Pro Val Leu Phe Gly Val Leu Thr Ala Val Gly Ser Thr Ile Trp
 135 140 145

aat gcg gtt ctg att tgg act ggt gtg tgg ttg ggg gcg gaa tgg gag 595
 Asn Ala Val Leu Ile Trp Thr Gly Val Trp Leu Gly Ala Glu Trp Glu
 150 155 160 165

acg gtg tgc atg tgg ttt gag agc tat tca acg atc att tac gta ggt 643
 Thr Val Ser Met Trp Phe Glu Ser Tyr Ser Thr Ile Ile Tyr Val Gly
 170 175 180

atc gcg ctc att gtn gct tac gtg ttg ttt ggt tta gtc cgt cgc cga 691
 Ile Ala Leu Ile Val Ala Tyr Val Leu Phe Gly Leu Val Arg Arg Arg
 185 190 195

att aaa act taaccatcgg ttcgtagccg aag 723
 Ile Lys Thr
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<210> 316

<211> 200

<212> PRT

<213> Corynebacterium glutamicum

<400> 316

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 20 25 30

Ser Glu Val Val Leu Pro Leu Ala Gly Phe Thr Thr Thr Gln Gly Asp
 35 40 45

Leu Asn Val Trp Ala Ala Leu Met Trp Ser Val Ile Gly Ser Val Ser
 50 55 60

Gly Ala Phe Leu Leu Tyr Gly Leu Gly Arg Ser Ile Gly Ala Ala Arg
 65 70 75 80

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<210> 317
<211> 705
<212> DNA
<213> Corynebacterium glutamicum
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<223> RXA00615
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Met Thr Ala Ser Val
1 5

ttt tat ccg gtg ctg tca gtt gtg gtg ctc atc gac tgc att ttg ccg 163
Phe Tyr Pro Val Leu Ser Val Val Val Leu Ile Asp Cys Ile Leu Pro
10 15 20

ctt atc ccc agt gag act gtt ctt gct ttg gca ggg gcg tgg tca gga 211
Leu Ile Pro Ser Glu Thr Val Leu Ala Leu Ala Gly Ala Trp Ser Gly

25 30 35

gct cgg gga act cca aac ttg tgg ttg gtt att tca gta gca acg ttg 259
Ala Arg Gly Thr Pro Asn Leu Trp Leu Val Ile Ser Val Ala Thr Leu
40 45 50

gcc gcg atc att ggt gac aac ctg tgt tat ttc ttt ggc acg cgg ttg 307
Ala Ala Ile Ile Gly Asp Asn Leu Cys Tyr Phe Phe Gly Thr Arg Leu
55 60 65

atc aat atg gtg aac agg att ccg gga gaa tcg agg cgc gga aaa gcg 355
Ile Asn Met Val Asn Arg Ile Pro Gly Glu Ser Arg Arg Gly Lys Ala

70	75	80	85	
ctg gag tgg gcg cgg aag aac ctt aat gaa cgg gat gtt tcg aca atc				403
Leu Glu Trp Ala Arg Lys Asn Leu Asn Glu Arg Asp Val Ser Thr Ile	90	95	100	
att atc gcc cgc ttt att ccg tgg gct agg tgg ttt gtc acc atc att				451
Ile Ile Ala Arg Phe Ile Pro Trp Ala Arg Trp Phe Val Thr Ile Ile	105	110	115	
ttg gga tct gtg gga tat tcc tgg tcg agg ttt atc gtg tgg gat tcc				499
Leu Gly Ser Val Gly Tyr Ser Trp Ser Arg Phe Ile Val Trp Asp Ser	120	125	130	
att gga gcg cta att tgg gca acc cag gca act ttg ttg ggt tat gtg				547
Ile Gly Ala Leu Ile Trp Ala Thr Gln Ala Thr Leu Leu Gly Tyr Val	135	140	145	
ggc gga tgg ctt ttc caa gaa caa ccg ttg atc ggc ctg gtt gca ggc				595
Gly Gly Trp Leu Phe Gln Glu Gln Pro Leu Ile Gly Leu Val Ala Gly	150	155	160	165
gca gct ttg gga atc ttc ttc ggg ttc ttt ttg cag tgg ctc aac aaa				643
Ala Ala Leu Gly Ile Phe Phe Gly Phe Phe Leu Gln Trp Leu Asn Lys	170	175	180	
atg tgg gag agg cgt cgt ctg gcg aaa gtg gct gca gaa tgaaaatcag				692
Met Trp Glu Arg Arg Arg Leu Ala Lys Val Ala Ala Glu	185	190		
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<210> 318				
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Gly Ala Trp Ser Gly Ala Arg Gly Thr Pro Asn Leu Trp Leu Val Ile				
35 40 45				
Ser Val Ala Thr Leu Ala Ala Ile Ile Gly Asp Asn Leu Cys Tyr Phe				
50 55 60				
Phe Gly Thr Arg Leu Ile Asn Met Val Asn Arg Ile Pro Gly Glu Ser				
65 70 75 80				
Arg Arg Gly Lys Ala Leu Glu Trp Ala Arg Lys Asn Leu Asn Glu Arg				
85 90 95				
Asp Val Ser Thr Ile Ile Ile Ala Arg Phe Ile Pro Trp Ala Arg Trp				
100 105 110				
Phe Val Thr Ile Ile Leu Gly Ser Val Gly Tyr Ser Trp Ser Arg Phe				

115	120	125
Ile Val Trp Asp Ser Ile Gly Ala Leu Ile Trp Ala Thr Gln Ala Thr		
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Leu Leu Gly Tyr Val Gly Gly Trp Leu Phe Gln Glu Gln Pro Leu Ile		
145	150	155
Gly Leu Val Ala Gly Ala Ala Leu Gly Ile Phe Phe Gly Phe Phe Leu		
165	170	175
Gln Trp Leu Asn Lys Met Trp Glu Arg Arg Arg Leu Ala Lys Val Ala		
180	185	190
Ala Glu		

<210> 319
 <211> 870
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(847)
 <223> RXN00250

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 Met Val Phe Thr Leu 5
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 gcg gac tcc gtc tcc cag gtt gcg cta ggt ccg tcc tgg ctg gac cct 163
 Ala Asp Ser Val Ser Gln Val Ala Leu Gly Pro Ser Trp Leu Asp Pro 20
 10 15
 atg gaa ctt ctt tcc ggc tcc ggc ccg ttc ggt agc ttc att ctt ccg 211
 Met Glu Leu Ser Gly Ser Gly Pro Phe Gly Ser Phe Ile Leu Pro 35
 25 30
 gcg atg ctt gcc att gtc ttt atc gaa tca ggc cta ctt ttc cca ctt 259
 Ala Met Leu Ala Ile Val Phe Ile Glu Ser Gly Leu Leu Phe Pro Leu 50
 40 45
 cta cca ggt gat tct ctc ctt ttc acc ggt ggt ctc cta gct aac cag 307
 Leu Pro Gly Asp Ser Leu Leu Phe Thr Gly Gly Leu Leu Ala Asn Gln 65
 55 60
 gct gac cct ttt gca ccg ctg tgg ctg gtg ctg atc ctc tgc cct atc 355
 Ala Asp Pro Phe Ala Pro Leu Trp Leu Val Leu Ile Leu Cys Pro Ile 85
 70 75 80
 gcc gca att ctt ggc gat cag gtg ggt tac tgg att ggc cac aag ttc 403
 Ala Ala Ile Leu Gly Asp Gln Val Gly Tyr Trp Ile Gly His Lys Phe 100
 90 95
 cac cct cgc ctg gtc aat cgt ccg gat ggc agg att ttc aag cag gaa 451
 His Pro Arg Leu Val Asn Arg Pro Asp Gly Arg Ile Phe Lys Gln Glu

105	110	115	
tac ctc aag cag act gag gat ttc ttt gag aag cat ggc ccc gtg acg			499
Tyr Leu Lys Gln Thr Glu Asp Phe Phe Glu Lys His Gly Pro Val Thr			
120	125	130	
atc att ttg tgc cgt ttc gtg ccc atc gtc cgt act tac gca cct ctg			547
Ile Ile Leu Cys Arg Phe Val Pro Ile Val Arg Thr Tyr Ala Pro Leu			
135	140	145	
gtc gca ggt atg gct ggc atg cgt tac cgc acg ttc att att tac aac			595
Val Ala Gly Met Ala Gly Met Arg Tyr Arg Thr Phe Ile Ile Tyr Asn			
150	155	160	165
atg atc ggt ggc att ttg tgg ggt tcc ggc gtg gtg gct ttg ggt gct			643
Met Ile Gly Gly Ile Leu Trp Gly Ser Gly Val Val Ala Leu Gly Ala			
170	175	180	
gcg ttg ggt cag ttc gat ttc gtc cgc aac aat att gat ctg att ttc			691
Ala Leu Gly Gln Phe Asp Phe Val Arg Asn Asn Ile Asp Leu Ile Phe			
185	190	195	
ttg ctg atc gtg ttc att tcg gtg gtt cct ggt ttg gtc ggc atg gcc			739
Leu Leu Ile Val Phe Ile Ser Val Val Pro Gly Leu Val Gly Met Ala			
200	205	210	
cgc aag ctg gct gac ggc cac aag caa gcc aac acc gag cca caa gaa			787
Arg Lys Leu Ala Asp Gly His Lys Gln Ala Asn Thr Glu Pro Gln Glu			
215	220	225	
aac ccc gca gtc cag aca gcc cca gta aaa acc cag gaa gcc cag gaa			835
Asn Pro Ala Val Gln Thr Ala Pro Val Lys Thr Gln Glu Ala Gln Glu			
230	235	240	245
gcc ccc cag aac taatctttcc ggtccgccag ttc			870
Ala Pro Gln Asn			

<210> 320

<211> 249

<212> PRT

<213> Corynebacterium glutamicum

<400> 320

Met Val Phe Thr Leu Ala Asp Ser Val Ser Gln Val Ala Leu Gly Pro			
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Ser Trp Leu Asp Pro Met Glu Leu Leu Ser Gly Ser Gly Pro Phe Gly			
20	25	30	
Ser Phe Ile Leu Pro Ala Met Leu Ala Ile Val Phe Ile Glu Ser Gly			
35	40	45	
Leu Leu Phe Pro Leu Leu Pro Gly Asp Ser Leu Leu Phe Thr Gly Gly			
50	55	60	
Leu Leu Ala Asn Gln Ala Asp Pro Phe Ala Pro Leu Trp Leu Val Leu			
65	70	75	80
Ile Leu Cys Pro Ile Ala Ala Ile Leu Gly Asp Gln Val Gly Tyr Trp			

	85		90		95
Ile Gly His Lys Phe His Pro Arg Leu Val Asn Arg Pro Asp Gly Arg	100		105		110
Ile Phe Lys Gln Glu Tyr Leu Lys Gln Thr Glu Asp Phe Phe Glu Lys	115		120		125
His Gly Pro Val Thr Ile Ile Leu Cys Arg Phe Val Pro Ile Val Arg	130		135		140
Thr Tyr Ala Pro Leu Val Ala Gly Met Ala Gly Met Arg Tyr Arg Thr	145		150		155
Phe Ile Ile Tyr Asn Met Ile Gly Gly Ile Leu Trp Gly Ser Gly Val	165		170		175
Val Ala Leu Gly Ala Ala Leu Gly Gln Phe Asp Phe Val Arg Asn Asn	180		185		190
Ile Asp Leu Ile Phe Leu Leu Ile Val Phe Ile Ser Val Val Pro Gly	195		200		205
Leu Val Gly Met Ala Arg Lys Leu Ala Asp Gly His Lys Gln Ala Asn	210		215		220
Thr Glu Pro Gln Glu Asn Pro Ala Val Gln Thr Ala Pro Val Lys Thr	225		230		235
Gln Glu Ala Gln Glu Ala Pro Gln Asn	245				

<210> 321
 <211> 525
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (79)..(525)
 <223> FRXA02010

<400> 321
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aagagtactc tgtccacc atg gtt ttt act ctt gcg gac tcc gtc tcc cag	111
Met Val Phe Thr Leu Ala Asp Ser Val Ser Gln	
1 5 10	

gtt gcg cta ggt ccg tcc tgg ctg gac cct atg gaa ctt ctt tcc ggc	159
Val Ala Leu Gly Pro Ser Trp Leu Asp Pro Met Glu Leu Leu Ser Gly	
15 20 25	

tcc ggc ccg ttc ggt agc ttc att ctt ccg gcg atg ctt gcc att gtc	207
Ser Gly Pro Phe Gly Ser Phe Ile Leu Pro Ala Met Leu Ala Ile Val	
30 35 40	

ttt atc gaa tca ggc cta ctt ttc cca ctt cta cca ggt gat tct ctc	255
Phe Ile Glu Ser Gly Leu Leu Phe Pro Leu Leu Pro Gly Asp Ser Leu	
45 50 55	

ctt ttc acc ggt ggt ctc cta gct aac cag gct gac cct ttt gca ccg 303
 Leu Phe Thr Gly Gly Leu Leu Ala Asn Gln Ala Asp Pro Phe Ala Pro
 60 65 70 75

ctg tgg ctg gtg ctg atc ctc tgc cct atc gcc gca att ctt ggc gat 351
 Leu Trp Leu Val Leu Ile Leu Cys Pro Ile Ala Ala Ile Leu Gly Asp
 80 85 90

cag gtg ggt tac tgg att ggc cac aag ttc cac cct cgc ctg gtc aat 399
 Gln Val Gly Tyr Trp Ile Gly His Lys Phe His Pro Arg Leu Val Asn
 95 100 105

cgt ccg gat ggc agg att ttc aag cag gaa tac ctc aag cag act gag 447
 Arg Pro Asp Gly Arg Ile Phe Lys Gln Glu Tyr Leu Lys Gln Thr Glu
 110 115 120

gat ttc ttt gag aag cat ggc ccc gtg acg atc att ttg tgc cgt ttc 495
 Asp Phe Phe Glu Lys His Gly Pro Val Thr Ile Ile Leu Cys Arg Phe
 125 130 135

gtg ccc atc gtc cgt act tac gca cct ctg 525
 Val Pro Ile Val Arg Thr Tyr Ala Pro Leu
 140 145

<210> 322

<211> 149

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 322

Met Val Phe Thr Leu Ala Asp Ser Val Ser Gln Val Ala Leu Gly Pro
 1 5 10 15

Ser Trp Leu Asp Pro Met Glu Leu Leu Ser Gly Ser Gly Pro Phe Gly
 20 25 30

Ser Phe Ile Leu Pro Ala Met Leu Ala Ile Val Phe Ile Glu Ser Gly
 35 40 45

Leu Leu Phe Pro Leu Leu Pro Gly Asp Ser Leu Leu Phe Thr Gly Gly
 50 55 60

Leu Leu Ala Asn Gln Ala Asp Pro Phe Ala Pro Leu Trp Leu Val Leu
 65 70 75 80

Ile Leu Cys Pro Ile Ala Ala Ile Leu Gly Asp Gln Val Gly Tyr Trp
 85 90 95

Ile Gly His Lys Phe His Pro Arg Leu Val Asn Arg Pro Asp Gly Arg
 100 105 110

Ile Phe Lys Gln Glu Tyr Leu Lys Gln Thr Glu Asp Phe Phe Glu Lys
 115 120 125

His Gly Pro Val Thr Ile Ile Leu Cys Arg Phe Val Pro Ile Val Arg
 130 135 140

Thr Tyr Ala Pro Leu
 145

<400> 323																
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gcaaattagc	acaacttcac	actttattta	ggagcatggt	atg	tct	gac	ctg	aag								115
				Met	Ser	Asp	Leu	Lys								5
				1												
tca	ctt	gcc	acg	aaa	ttt	gct	agc	gat	cat	gaa	tcc	gga	aag	ctg	ctg	163
Ser	Leu	Ala	Thr	Lys	Phe	Ala	Ser	Asp	His	Glu	Ser	Gly	Lys	Leu	Leu	
				10					15					20		
gtc	ctg	cct	acc	gtc	tgg	gat	acc	tgg	agc	gcg	ggg	ctc	gta	gaa	gaa	211
Val	Leu	Pro	Thr	Val	Trp	Asp	Thr	Trp	Ser	Ala	Gly	Leu	Val	Glu	Glu	
			25					30					35			
gca	gga	ttt	agt	ggc	ctg	acc	att	ggg	agc	cac	cca	gtc	gcg	gat	gcg	259
Ala	Gly	Phe	Ser	Gly	Leu	Thr	Ile	Gly	Ser	His	Pro	Val	Ala	Asp	Ala	
		40					45					50				
aca	gga	agc	tcc	gat	ggg	gaa	aac	atg	aat	ttt	gca	gat	tat	atg	gcg	307
Thr	Gly	Ser	Ser	Asp	Gly	Glu	Asn	Met	Asn	Phe	Ala	Asp	Tyr	Met	Ala	
	55					60					65					
gtg	gtc	aag	aag	atc	acc	tcg	gcg	gta	tcc	atc	ccc	gta	agc	gtt	gat	355
Val	Val	Lys	Lys	Ile	Thr	Ser	Ala	Val	Ser	Ile	Pro	Val	Ser	Val	Asp	
70				75						80					85	
gtg	gaa	tcc	ggg	tat	ggg	ctc	tcg	cct	gcg	gat	ttg	atc	gca	cag	att	403
Val	Glu	Ser	Gly	Tyr	Gly	Leu	Ser	Pro	Ala	Asp	Leu	Ile	Ala	Gln	Ile	
				90					95					100		
ttg	gaa	gct	ggc	gca	gtg	ggc	atc	aat	gtg	gaa	gat	gtt	gtg	cac	agc	451
Leu	Glu	Ala	Gly	Ala	Val	Gly	Ile	Asn	Val	Glu	Asp	Val	Val	His	Ser	
			105					110					115			
gag	ggg	aag	cgt	gtt	cgt	gag	gcg	cag	gag	cac	gct	gat	tac	atc	gct	499
Glu	Gly	Lys	Arg	Val	Arg	Glu	Ala	Gln	Glu	His	Ala	Asp	Tyr	Ile	Ala	
		120					125					130				
gcg	gca	cgt	caa	gct	gcc	gat	gtg	gca	ggg	gta	gat	gtg	gtg	atc	aac	547
Ala	Ala	Arg	Gln	Ala	Ala	Asp	Val	Ala	Gly	Val	Asp	Val	Val	Ile	Asn	
	135					140					145					
ggg	cgc	acg	gat	gcc	gtc	aaa	ctt	ggg	gca	gac	gtt	ttt	gaa	gat	ccg	595
Gly	Arg	Thr	Asp	Ala	Val	Lys	Leu	Gly	Ala	Asp	Val	Phe	Glu	Asp	Pro	
150					155					160					165	
atg	gtg	gag	gcc	atc	aag	gcg	atc	aag	ctc	atg	gaa	cag	gca	ggc	gcg	643
Met	Val	Glu	Ala	Ile	Lys	Arg	Ile	Lys	Leu	Met	Glu	Gln	Ala	Gly	Ala	

170										175					180					
cgt	tcg	gtg	tac	ccc	gtg	ggg	ctg	agc	acc	gcc	gag	cag	gtt	gag	cgc	691				
Arg	Ser	Val	Tyr	Pro	Val	Gly	Leu	Ser	Thr	Ala	Glu	Gln	Val	Glu	Arg					
			185					190					195							
ctg	gtg	gac	gct	gtg	tca	gtg	ccg	gtc	aac	atc	acc	gcg	cac	ccg	gtt	739				
Leu	Val	Asp	Ala	Val	Ser	Val	Pro	Val	Asn	Ile	Thr	Ala	His	Pro	Val					
		200					205					210								
gat	ggg	cac	ggc	gca	ggc	gat	ctg	gcc	acc	ctc	gca	ggc	ctt	ggc	gtg	787				
Asp	Gly	His	Gly	Ala	Gly	Asp	Leu	Ala	Thr	Leu	Ala	Gly	Leu	Gly	Val					
	215					220					225									
cgc	cgc	gtg	acc	ttc	ggg	ccg	ctc	tgg	caa	aaa	tgg	ctg	gct	gcc	acc	835				
Arg	Arg	Val	Thr	Phe	Gly	Pro	Leu	Trp	Gln	Lys	Trp	Leu	Ala	Ala	Thr					
230				235					240					245						
tcg	gcg	cag	cag	ctt	aag	ggc	tgg	gct	taaattgctt	gtcgacgcct	agt					885				
Ser	Ala	Gln	Gln	Leu	Lys	Gly	Trp	Ala												
				250																

<210> 324

<211> 254

<212> PRT

<213> Corynebacterium glutamicum

<400> 324

Met	Ser	Asp	Leu	Lys	Ser	Leu	Ala	Thr	Lys	Phe	Ala	Ser	Asp	His	Glu	
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Ser	Gly	Lys	Leu	Leu	Val	Leu	Pro	Thr	Val	Trp	Asp	Thr	Trp	Ser	Ala	
			20					25					30			
Gly	Leu	Val	Glu	Glu	Ala	Gly	Phe	Ser	Gly	Leu	Thr	Ile	Gly	Ser	His	
		35				40						45				
Pro	Val	Ala	Asp	Ala	Thr	Gly	Ser	Ser	Asp	Gly	Glu	Asn	Met	Asn	Phe	
	50					55					60					
Ala	Asp	Tyr	Met	Ala	Val	Val	Lys	Lys	Ile	Thr	Ser	Ala	Val	Ser	Ile	
65				70						75					80	
Pro	Val	Ser	Val	Asp	Val	Glu	Ser	Gly	Tyr	Gly	Leu	Ser	Pro	Ala	Asp	
			85					90					95			
Leu	Ile	Ala	Gln	Ile	Leu	Glu	Ala	Gly	Ala	Val	Gly	Ile	Asn	Val	Glu	
		100						105					110			
Asp	Val	Val	His	Ser	Glu	Gly	Lys	Arg	Val	Arg	Glu	Ala	Gln	Glu	His	
	115						120					125				
Ala	Asp	Tyr	Ile	Ala	Ala	Ala	Arg	Gln	Ala	Ala	Asp	Val	Ala	Gly	Val	
	130					135					140					
Asp	Val	Val	Ile	Asn	Gly	Arg	Thr	Asp	Ala	Val	Lys	Leu	Gly	Ala	Asp	
145					150					155					160	
Val	Phe	Glu	Asp	Pro	Met	Val	Glu	Ala	Ile	Lys	Arg	Ile	Lys	Leu	Met	
				165					170					175		

Glu Gln Ala Gly Ala Arg Ser Val Tyr Pro Val Gly Leu Ser Thr Ala
180 185 190

Glu Gln Val Glu Arg Leu Val Asp Ala Val Ser Val Pro Val Asn Ile
195 200 205

Thr Ala His Pro Val Asp Gly His Gly Ala Gly Asp Leu Ala Thr Leu
210 215 220

Ala Gly Leu Gly Val Arg Arg Val Thr Phe Gly Pro Leu Trp Gln Lys
225 230 235 240

Trp Leu Ala Ala Thr Ser Ala Gln Gln Leu Lys Gly Trp Ala
245 250

<210> 325

<211> 969

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(946)

<223> RXS01000

<400> 325

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tcattgaagt aatctccaac gcacttcgaa agaggctggt atg agc acc tta acc 115
Met Ser Thr Leu Thr
1 5

tct cac cgc aca gta ccg gcc ccc agc tct ccc ccg gcg cgc ccc aac 163
Ser His Arg Thr Val Pro Ala Pro Ser Ser Pro Pro Ala Arg Pro Asn
10 15 20

aaa ctg gcg cgc aat atc gtt gca att gtc gct gcg ctg att gtc ctt 211
Lys Leu Ala Arg Asn Ile Val Ala Ile Val Ala Ala Leu Ile Val Leu
25 30 35

ata gct acc ggc acg ctc aag atc gag tgg aat gag ctt ccg cag atg 259
Ile Ala Thr Gly Thr Leu Lys Ile Glu Trp Asn Glu Leu Pro Gln Met
40 45 50

ccc gcg cag gtg tgg cat tac tta gag ctg atg ttt agc gat ccc gat 307
Pro Ala Gln Val Trp His Tyr Leu Glu Leu Met Phe Ser Asp Pro Asp
55 60 65

tgg tcg aag ttt ggc cgc gcc gtc cag gaa atg tgg cgt tcc atc gcc 355
Trp Ser Lys Phe Gly Arg Ala Val Gln Glu Met Trp Arg Ser Ile Ala
70 75 80 85

atg gcg tgg ttg ggt gcc att tta tgc gtg gtg gtc tct gtc cct ctg 403
Met Ala Trp Leu Gly Ala Ile Leu Cys Val Val Val Ser Val Pro Leu
90 95 100

gga atg ttg gct gcc cgc ggg gtg gga cct tat tgg ctg cgt acc gtt 451
Gly Met Leu Ala Ala Arg Gly Val Gly Pro Tyr Trp Leu Arg Thr Val
105 110 115

tta cgg ttc gtg ttc gcg gtg att cgt gcg ttc ccc gaa gtg gtt atc 499
 Leu Arg Phe Val Phe Ala Val Ile Arg Ala Phe Pro Glu Val Val Ile
 120 125 130

 gca att att ttg cta act gtc acc ggc cta act cct ttt act ggt gcg 547
 Ala Ile Ile Leu Leu Thr Val Thr Gly Leu Thr Pro Phe Thr Gly Ala
 135 140 145

 ctc gca ttg ggt atc tcc ggt att gga caa cag gca aag tgg acc tat 595
 Leu Ala Leu Gly Ile Ser Gly Ile Gly Gln Gln Ala Lys Trp Thr Tyr
 150 155 160 165

 gaa gcc att gag tcc act ccc acc ggc ccg tca gag gca gtg cgt gca 643
 Glu Ala Ile Glu Ser Thr Pro Thr Gly Pro Ser Glu Ala Val Arg Ala
 170 175 180

 gcg ggt gga act acg ccg gag gtt ctg ccg tgg gcg ttg tgg cca cag 691
 Ala Gly Gly Thr Thr Pro Glu Val Leu Arg Trp Ala Leu Trp Pro Gln
 185 190 195

 gtt gcg cca tcc att gca tct ttt gcc ctg tac cgc ttt gag atc aac 739
 Val Ala Pro Ser Ile Ala Ser Phe Ala Leu Tyr Arg Phe Glu Ile Asn
 200 205 210

 atc cgt acc tct gcg gta ttg ggc atc gtt ggt gca ggt ggt atc ggt 787
 Ile Arg Thr Ser Ala Val Leu Gly Ile Val Gly Ala Gly Gly Ile Gly
 215 220 225

 agt atg ctt gcc aat tac acc aac tac agg cag tgg gac acc gtg ggc 835
 Ser Met Leu Ala Asn Tyr Thr Asn Tyr Arg Gln Trp Asp Thr Val Gly
 230 235 240 245

 atg ctg ctc atc gtc gtg gtt gtc gca acg atg atc gtc gat ctc atc 883
 Met Leu Leu Ile Val Val Val Val Ala Thr Met Ile Val Asp Leu Ile
 250 255 260

 tcc ggc acc atc cgc cgc cgc atc atg aag ggg gct agt gac cgt gtc 931
 Ser Gly Thr Ile Arg Arg Arg Ile Met Lys Gly Ala Ser Asp Arg Val
 265 270 275

 gtg gca cca agc aac tgacgctcca ccaagcatcc gca 969
 Val Ala Pro Ser Asn
 280

<210> 326

<211> 282

<212> PRT

<213> Corynebacterium glutamicum

<400> 326

Met Ser Thr Leu Thr Ser His Arg Thr Val Pro Ala Pro Ser Ser Pro
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Pro Ala Arg Pro Asn Lys Leu Ala Arg Asn Ile Val Ala Ile Val Ala
 20 25 30

Ala Leu Ile Val Leu Ile Ala Thr Gly Thr Leu Lys Ile Glu Trp Asn
 35 40 45

Glu Leu Pro Gln Met Pro Ala Gln Val Trp His Tyr Leu Glu Leu Met
 50 55 60
 Phe Ser Asp Pro Asp Trp Ser Lys Phe Gly Arg Ala Val Gln Glu Met
 65 70 75 80
 Trp Arg Ser Ile Ala Met Ala Trp Leu Gly Ala Ile Leu Cys Val Val
 85 90 95
 Val Ser Val Pro Leu Gly Met Leu Ala Ala Arg Gly Val Gly Pro Tyr
 100 105 110
 Trp Leu Arg Thr Val Leu Arg Phe Val Phe Ala Val Ile Arg Ala Phe
 115 120 125
 Pro Glu Val Val Ile Ala Ile Ile Leu Leu Thr Val Thr Gly Leu Thr
 130 135 140
 Pro Phe Thr Gly Ala Leu Ala Leu Gly Ile Ser Gly Ile Gly Gln Gln
 145 150 155 160
 Ala Lys Trp Thr Tyr Glu Ala Ile Glu Ser Thr Pro Thr Gly Pro Ser
 165 170 175
 Glu Ala Val Arg Ala Ala Gly Gly Thr Thr Pro Glu Val Leu Arg Trp
 180 185 190
 Ala Leu Trp Pro Gln Val Ala Pro Ser Ile Ala Ser Phe Ala Leu Tyr
 195 200 205
 Arg Phe Glu Ile Asn Ile Arg Thr Ser Ala Val Leu Gly Ile Val Gly
 210 215 220
 Ala Gly Gly Ile Gly Ser Met Leu Ala Asn Tyr Thr Asn Tyr Arg Gln
 225 230 235 240
 Trp Asp Thr Val Gly Met Leu Leu Ile Val Val Val Val Ala Thr Met
 245 250 255
 Ile Val Asp Leu Ile Ser Gly Thr Ile Arg Arg Arg Ile Met Lys Gly
 260 265 270
 Ala Ser Asp Arg Val Val Ala Pro Ser Asn
 275 280

<210> 327

<211> 927

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(904)

<223> RXS01002

<400> 327

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 caactaattt ccctgtttcc aataactcaag gtgtgcgc atg aat tct gat gct 115
 Met Asn Ser Asp Ala

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tcg	gct	acc	acc	aac	tcc	tgg	gct	atc	aac	ttc	gac	cat	gtg	tcg	gtg		163
Ser	Ala	Thr	Thr	Asn	Ser	Trp	Ala	Ile	Asn	Phe	Asp	His	Val	Ser	Val		
				10					15					20			
acg	tat	ccc	aat	ggg	acg	aaa	gcc	ctc	gat	gat	ggt	tcc	ctc	acc	atc		211
Thr	Tyr	Pro	Asn	Gly	Thr	Lys	Ala	Leu	Asp	Asp	Val	Ser	Leu	Thr	Ile		
			25					30					35				
aat	ccc	ggt	gag	atg	ggt	gcc	atc	gtg	ggt	ctg	tca	gga	tcg	ggt	aaa		259
Asn	Pro	Gly	Glu	Met	Val	Ala	Ile	Val	Gly	Leu	Ser	Gly	Ser	Gly	Lys		
		40					45					50					
tcc	acg	ctg	att	cgc	acg	atc	aac	ggt	ctt	gtc	cgc	gct	acg	gaa	ggc		307
Ser	Thr	Leu	Ile	Arg	Thr	Ile	Asn	Gly	Leu	Val	Arg	Ala	Thr	Glu	Gly		
	55					60					65						
acc	gtg	acg	gtg	ggg	ccg	cat	cag	atc	aac	acc	ttg	aag	ggg	aaa	gca		355
Thr	Val	Thr	Val	Gly	Pro	His	Gln	Ile	Asn	Thr	Leu	Lys	Gly	Lys	Ala		
	70					75				80					85		
ctg	cgt	gat	gcc	cgt	ggg	cag	atc	ggc	atg	att	ttc	cag	ggg	ttc	aac		403
Leu	Arg	Asp	Ala	Arg	Gly	Gln	Ile	Gly	Met	Ile	Phe	Gln	Gly	Phe	Asn		
				90				95						100			
ctg	tcg	gaa	cgc	agc	agt	gtg	ttc	cag	aat	ggt	ttg	gtg	ggc	cgc	ttc		451
Leu	Ser	Glu	Arg	Ser	Ser	Val	Phe	Gln	Asn	Val	Leu	Val	Gly	Arg	Phe		
			105					110					115				
gcg	cac	aca	gcg	tgg	tgg	cgt	aac	ctc	ctc	ggg	ttt	ccc	acg	gag	cac		499
Ala	His	Thr	Ala	Trp	Trp	Arg	Asn	Leu	Leu	Gly	Phe	Pro	Thr	Glu	His		
		120					125					130					
gac	aag	cag	att	gct	ttt	cac	gcg	ttg	gag	tcc	gtg	ggc	att	ttg	cac		547
Asp	Lys	Gln	Ile	Ala	Phe	His	Ala	Leu	Glu	Ser	Val	Gly	Ile	Leu	His		
	135					140					145						
aaa	gtg	tgg	acc	cga	gct	ggt	gct	ttg	tcg	ggt	gga	cag	aaa	cag	cgc		595
Lys	Val	Trp	Thr	Arg	Ala	Gly	Ala	Leu	Ser	Gly	Gly	Gln	Lys	Gln	Arg		
	150				155					160					165		
ggt	gct	att	gcg	cgc	gcc	tta	tcg	caa	gat	ccg	tct	gtc	atg	ctg	gca		643
Val	Ala	Ile	Ala	Arg	Ala	Leu	Ser	Gln	Asp	Pro	Ser	Val	Met	Leu	Ala		
				170					175					180			
gat	gag	cct	gtg	gca	agc	ctt	gat	ccg	cca	acc	gcg	cat	tcc	gtg	atg		691
Asp	Glu	Pro	Val	Ala	Ser	Leu	Asp	Pro	Pro	Thr	Ala	His	Ser	Val	Met		
			185					190					195				
cgc	gat	cta	gaa	aac	atc	aac	aac	gtg	gaa	ggc	ctc	acc	gtg	ttg	gtg		739
Arg	Asp	Leu	Glu	Asn	Ile	Asn	Asn	Val	Glu	Gly	Leu	Thr	Val	Leu	Val		
		200					205					210					
aac	ttg	cac	ttg	att	gat	ttg	gct	cgt	caa	tac	acc	aca	agg	ctt	gtg		787
Asn	Leu	His	Leu	Ile	Asp	Leu	Ala	Arg	Gln	Tyr	Thr	Thr	Arg	Leu	Val		
	215					220					225						
ggt	ttg	cgt	gcc	ggc	aag	ctg	gtc	tat	gac	ggt	cct	atc	tct	gag	gcc		835
Gly	Leu	Arg	Ala	Gly	Lys	Leu	Val	Tyr	Asp	Gly	Pro	Ile	Ser	Glu	Ala		
	230				235					240					245		

acc gat aaa gac ttt gaa gct atc tat ggt cgc ccc atc cag gct aaa 883
 Thr Asp Lys Asp Phe Glu Ala Ile Tyr Gly Arg Pro Ile Gln Ala Lys
 250 255 260

gac ctg cta ggt gat cgc gca tgaccacgcc ttcttctaca ctt 927
 Asp Leu Leu Gly Asp Arg Ala
 265

<210> 328

<211> 268

<212> PRT

<213> Corynebacterium glutamicum

<400> 328

Met Asn Ser Asp Ala Ser Ala Thr Thr Asn Ser Trp Ala Ile Asn Phe
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Asp His Val Ser Val Thr Tyr Pro Asn Gly Thr Lys Ala Leu Asp Asp
 20 25 30

Val Ser Leu Thr Ile Asn Pro Gly Glu Met Val Ala Ile Val Gly Leu
 35 40 45

Ser Gly Ser Gly Lys Ser Thr Leu Ile Arg Thr Ile Asn Gly Leu Val
 50 55 60

Arg Ala Thr Glu Gly Thr Val Thr Val Gly Pro His Gln Ile Asn Thr
 65 70 75 80

Leu Lys Gly Lys Ala Leu Arg Asp Ala Arg Gly Gln Ile Gly Met Ile
 85 90 95

Phe Gln Gly Phe Asn Leu Ser Glu Arg Ser Ser Val Phe Gln Asn Val
 100 105 110

Leu Val Gly Arg Phe Ala His Thr Ala Trp Trp Arg Asn Leu Leu Gly
 115 120 125

Phe Pro Thr Glu His Asp Lys Gln Ile Ala Phe His Ala Leu Glu Ser
 130 135 140

Val Gly Ile Leu His Lys Val Trp Thr Arg Ala Gly Ala Leu Ser Gly
 145 150 155 160

Gly Gln Lys Gln Arg Val Ala Ile Ala Arg Ala Leu Ser Gln Asp Pro
 165 170 175

Ser Val Met Leu Ala Asp Glu Pro Val Ala Ser Leu Asp Pro Pro Thr
 180 185 190

Ala His Ser Val Met Arg Asp Leu Glu Asn Ile Asn Asn Val Glu Gly
 195 200 205

Leu Thr Val Leu Val Asn Leu His Leu Ile Asp Leu Ala Arg Gln Tyr
 210 215 220

Thr Thr Arg Leu Val Gly Leu Arg Ala Gly Lys Leu Val Tyr Asp Gly
 225 230 235 240

Pro Ile Ser Glu Ala Thr Asp Lys Asp Phe Glu Ala Ile Tyr Gly Arg
 245 250 255

Pro Ile Gln Ala Lys Asp Leu Leu Gly Asp Arg Ala
 260 265

<210> 329

<211> 927

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(904)

<223> RXS01003

<400> 329

agctgggtcta tgacgggtcct atctctgagg ccaccgataa agactttgaa gctatctatg 60

gtcgcccat ccaggctaaa gacctgctag gtgatcgcg atg acc acg cct tct 115
 Met Thr Thr Pro Ser
 1 5

tct aca ctt atc cca caa aag cct cgg gct ggg gta aag acc tat ctc 163
 Ser Thr Leu Ile Pro Gln Lys Pro Arg Ala Gly Val Lys Thr Tyr Leu
 10 15 20

atc atc ggc gcc atc gtt gtc ttc acc gtg gca aca gca acc cca gcg 211
 Ile Ile Gly Ala Ile Val Val Phe Thr Val Ala Thr Ala Thr Pro Ala
 25 30 35

cta ggt ggc att gag ctt gat ttc gct tcc att gct gcg aat tgg cgc 259
 Leu Gly Gly Ile Glu Leu Asp Phe Ala Ser Ile Ala Ala Asn Trp Arg
 40 45 50

aat ggt gcc aac aaa ctc ctg caa atg ctg cag ccc aac ttt gcg ttc 307
 Asn Gly Ala Asn Lys Leu Leu Gln Met Leu Gln Pro Asn Phe Ala Phe
 55 60 65

ttg cct cgt acg tgg ctt ccc atg ttg gaa acc ctg cag atg gcg ctt 355
 Leu Pro Arg Thr Trp Leu Pro Met Leu Glu Thr Leu Gln Met Ala Leu
 70 75 80 85

gtt gga gct gtc ttg tct gct gcc gta tcg gtg cct ttg acg ttg tgg 403
 Val Gly Ala Val Leu Ser Ala Ala Val Ser Val Pro Leu Thr Leu Trp
 90 95 100

gca gcg cag gca acc aac acc agt gcg att ggt cgt ggc att gtc cgc 451
 Ala Ala Gln Ala Thr Asn Thr Ser Ala Ile Gly Arg Gly Ile Val Arg
 105 110 115

acc atc att aac gtg gtg cgc tct gtc ccc gac ttg gtg tat gcc acc 499
 Thr Ile Ile Asn Val Val Arg Ser Val Pro Asp Leu Val Tyr Ala Thr
 120 125 130

atc ttg gtc gcc atg gtt ggt gtc ggc gca tta cct ggc att ttg acg 547
 Ile Leu Val Ala Met Val Gly Val Gly Ala Leu Pro Gly Ile Leu Thr
 135 140 145

ctg ttt ctg ttc aac ctg ggc atc gtg gtc aag ctt gtc tct gag gcc 595

Leu Phe Leu Phe Asn Leu Gly Ile Val Val Lys Leu Val Ser Glu Ala
 150 155 160 165
 att gat tcc act gag cat ccc tat atg gaa gca gga cgc gca gca ggt 643
 Ile Asp Ser Thr Glu His Pro Tyr Met Glu Ala Gly Arg Ala Ala Gly
 170 175 180
 gga tca cag ttc caa atc aac cga gtc tcc gcg ctt cct gaa gtc atg 691
 Gly Ser Gln Phe Gln Ile Asn Arg Val Ser Ala Leu Pro Glu Val Met
 185 190 195
 ccg ctc ttt gcc aac caa tgg ctc tac acc cta gag ctg aat gta cgc 739
 Pro Leu Phe Ala Asn Gln Trp Leu Tyr Thr Leu Glu Leu Asn Val Arg
 200 205 210
 atc tcc gcc atc ctt ggc atc gtg ggc gca ggt ggc atc ggc agg ctg 787
 Ile Ser Ala Ile Leu Gly Ile Val Gly Ala Gly Gly Ile Gly Arg Leu
 215 220 225
 ctt gat gaa cgc cga gct ttc tat gcc tac gcg gat gtt tcc gtg atc 835
 Leu Asp Glu Arg Arg Ala Phe Tyr Ala Tyr Ala Asp Val Ser Val Ile
 230 235 240 245
 att ctg gaa atc ctc atc gtg gtg att gtc att gaa gta atc tcc aac 883
 Ile Leu Glu Ile Leu Ile Val Val Ile Val Ile Glu Val Ile Ser Asn
 250 255 260
 gca ctt cga aag agg ctg gta tgagcacctt aacctctcac cgc 927
 Ala Leu Arg Lys Arg Leu Val
 265

<210> 330

<211> 268

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 330

Met Thr Thr Pro Ser Ser Thr Leu Ile Pro Gln Lys Pro Arg Ala Gly
 1 5 10 15
 Val Lys Thr Tyr Leu Ile Ile Gly Ala Ile Val Val Phe Thr Val Ala
 20 25 30
 Thr Ala Thr Pro Ala Leu Gly Gly Ile Glu Leu Asp Phe Ala Ser Ile
 35 40 45
 Ala Ala Asn Trp Arg Asn Gly Ala Asn Lys Leu Leu Gln Met Leu Gln
 50 55 60
 Pro Asn Phe Ala Phe Leu Pro Arg Thr Trp Leu Pro Met Leu Glu Thr
 65 70 75 80
 Leu Gln Met Ala Leu Val Gly Ala Val Leu Ser Ala Ala Val Ser Val
 85 90 95
 Pro Leu Thr Leu Trp Ala Ala Gln Ala Thr Asn Thr Ser Ala Ile Gly
 100 105 110
 Arg Gly Ile Val Arg Thr Ile Ile Asn Val Val Arg Ser Val Pro Asp
 115 120 125

Leu Val Tyr Ala Thr Ile Leu Val Ala Met Val Gly Val Gly Ala Leu
 130 135 140
 Pro Gly Ile Leu Thr Leu Phe Leu Phe Asn Leu Gly Ile Val Val Lys
 145 150 155 160
 Leu Val Ser Glu Ala Ile Asp Ser Thr Glu His Pro Tyr Met Glu Ala
 165 170 175
 Gly Arg Ala Ala Gly Gly Ser Gln Phe Gln Ile Asn Arg Val Ser Ala
 180 185 190
 Leu Pro Glu Val Met Pro Leu Phe Ala Asn Gln Trp Leu Tyr Thr Leu
 195 200 205
 Glu Leu Asn Val Arg Ile Ser Ala Ile Leu Gly Ile Val Gly Ala Gly
 210 215 220
 Gly Ile Gly Arg Leu Leu Asp Glu Arg Arg Ala Phe Tyr Ala Tyr Ala
 225 230 235 240
 Asp Val Ser Val Ile Ile Leu Glu Ile Leu Ile Val Val Ile Val Ile
 245 250 255
 Glu Val Ile Ser Asn Ala Leu Arg Lys Arg Leu Val
 260 265

<210> 331
 <211> 1182
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1159)
 <223> RXS01902

<400> 331
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ttcttcggcg acaccagct gtacaacacc cactccaacc gtg cag aag aag tcc 115
 Val Gln Lys Lys Ser
 1 5

aga act ggg caa aca acc tgg aac ggc ggc cca cca atc gaa aac cca 163
 Arg Thr Gly Gln Thr Trp Asn Gly Gly Pro Pro Ile Glu Asn Pro
 10 15 20

gga acc tcc ttc atc ctc tcc gcg ggt gat cag gca aac cac tcc agc 211
 Gly Thr Ser Phe Ile Leu Ser Ala Gly Asp Gln Ala Asn His Ser Ser
 25 30 35

tgg gac gag cac tcc gca tac atc tcc cca gaa acc ctg cgc aac tac 259
 Trp Asp Glu His Ser Ala Tyr Ile Ser Pro Glu Thr Leu Arg Asn Tyr
 40 45 50

cgt ctg gcc gtg aac aat gga aac cac gac cag tac aac tac gac gcc 307
 Arg Leu Ala Val Asn Asn Gly Asn His Asp Gln Tyr Asn Tyr Asp Ala
 55 60 65

tac aac gcg atg tac cca cgc cct aac cag gtc gat gag aac tac ttc	355
Tyr Asn Ala Met Tyr Pro Arg Pro Asn Gln Val Asp Glu Asn Tyr Phe	
70 75 80 85	
ttc gag tac aac aat gca ctc ttc ctg tcc ctg gac tcc aac gac tac	403
Phe Glu Tyr Asn Asn Ala Leu Phe Leu Ser Leu Asp Ser Asn Asp Tyr	
90 95 100	
ttg gac atc gac gac gac atc gca ttc ctt cgc gac acc gtc gca gca	451
Leu Asp Ile Asp Asp Asp Ile Ala Phe Leu Arg Asp Thr Val Ala Ala	
105 110 115	
cac ggt gac gac aag gac tgg atc gtc ctg acc tac cac cat tcc act	499
His Gly Asp Asp Lys Asp Trp Ile Val Leu Thr Tyr His His Ser Thr	
120 125 130	
ttc tcc cag gcc tac cac atg gat gac gct cgc att aag tac cag cgc	547
Phe Ser Gln Ala Tyr His Met Asp Asp Ala Arg Ile Lys Tyr Gln Arg	
135 140 145	
gaa cgc ctc acc cca gtg atc tct gaa ctg aac gtt gac ttg gtt ctc	595
Glu Arg Leu Thr Pro Val Ile Ser Glu Leu Asn Val Asp Leu Val Leu	
150 155 160 165	
ggt gga cac gac cac atc tac acc cgc tcc cac ctg atg aac ggc ttc	643
Gly Gly His Asp His Ile Tyr Thr Arg Ser His Leu Met Asn Gly Phe	
170 175 180	
acc cca gtc gat gca ggc cgc gaa gca gtt gtc ggt gaa act ctg aac	691
Thr Pro Val Asp Ala Gly Arg Glu Ala Val Val Gly Glu Thr Leu Asn	
185 190 195	
cct aag gcc ggc gaa gtt gtt tac ctt gca acc aac tct tcc tca ggc	739
Pro Lys Ala Gly Glu Val Val Tyr Leu Ala Thr Asn Ser Ser Ser Gly	
200 205 210	
tcc aag ttc tac gac ttc tac gac ttc cag ctc ggc cag cgt tac gac	787
Ser Lys Phe Tyr Asp Phe Tyr Asp Phe Gln Leu Gly Gln Arg Tyr Asp	
215 220 225	
acc gga ctg gat ttc cag gaa acc gtc gat cag aag aag atc cgc acc	835
Thr Gly Leu Asp Phe Gln Glu Thr Val Asp Gln Lys Lys Ile Arg Thr	
230 235 240 245	
tac acc gca gtc tgg aac cag gac cag gtt cag gac tac acc aac gtt	883
Tyr Thr Ala Val Trp Asn Gln Asp Gln Val Gln Asp Tyr Thr Asn Val	
250 255 260	
gaa ctg acc cca gaa ggc ctg act gtg acc act aag gac gca gtc tcc	931
Glu Leu Thr Pro Glu Gly Leu Thr Val Thr Thr Lys Asp Ala Val Ser	
265 270 275	
ggc gag ctg gtt gac cag ttc acc ctg agc aag cag gac cgc gac gaa	979
Gly Glu Leu Val Asp Gln Phe Thr Leu Ser Lys Gln Asp Arg Asp Glu	
280 285 290	
gaa tct gaa gtc cca gtt gaa gat gac aag gac gga gac aac gcg acc	1027
Glu Ser Glu Val Pro Val Glu Asp Asp Lys Asp Gly Asp Asn Ala Thr	
295 300 305	

ggc tcc tcc aac ctt ggt cta gct gct atc ttg gct cca gtt ctg gcc 1075
 Gly Ser Ser Asn Leu Gly Leu Ala Ala Ile Leu Ala Pro Val Leu Ala
 310 315 320 325

atc ttc ggt ttc gtc ggt gga ctc ttt gtt ggc ggc ggc tcc ctc gct 1123
 Ile Phe Gly Phe Val Gly Gly Leu Phe Val Gly Gly Gly Ser Leu Ala
 330 335 340

gag ttc ttt gcc aac ctc ggc gtg aag atg cct ttc taatactgtc 1169
 Glu Phe Phe Ala Asn Leu Gly Val Lys Met Pro Phe
 345 350

tgagattcaa gca 1182

<210> 332

<211> 353

<212> PRT

<213> Corynebacterium glutamicum

<400> 332

Val Gln Lys Lys Ser Arg Thr Gly Gln Thr Thr Trp Asn Gly Gly Pro
 1 5 10 15

Pro Ile Glu Asn Pro Gly Thr Ser Phe Ile Leu Ser Ala Gly Asp Gln
 20 25 30

Ala Asn His Ser Ser Trp Asp Glu His Ser Ala Tyr Ile Ser Pro Glu
 35 40 45

Thr Leu Arg Asn Tyr Arg Leu Ala Val Asn Asn Gly Asn His Asp Gln
 50 55 60

Tyr Asn Tyr Asp Ala Tyr Asn Ala Met Tyr Pro Arg Pro Asn Gln Val
 65 70 75 80

Asp Glu Asn Tyr Phe Phe Glu Tyr Asn Asn Ala Leu Phe Leu Ser Leu
 85 90 95

Asp Ser Asn Asp Tyr Leu Asp Ile Asp Asp Asp Ile Ala Phe Leu Arg
 100 105 110

Asp Thr Val Ala Ala His Gly Asp Asp Lys Asp Trp Ile Val Leu Thr
 115 120 125

Tyr His His Ser Thr Phe Ser Gln Ala Tyr His Met Asp Asp Ala Arg
 130 135 140

Ile Lys Tyr Gln Arg Glu Arg Leu Thr Pro Val Ile Ser Glu Leu Asn
 145 150 155 160

Val Asp Leu Val Leu Gly Gly His Asp His Ile Tyr Thr Arg Ser His
 165 170 175

Leu Met Asn Gly Phe Thr Pro Val Asp Ala Gly Arg Glu Ala Val Val
 180 185 190

Gly Glu Thr Leu Asn Pro Lys Ala Gly Glu Val Val Tyr Leu Ala Thr
 195 200 205

Asn Ser Ser Ser Gly Ser Lys Phe Tyr Asp Phe Tyr Asp Phe Gln Leu

210	215	220
Gly Gln Arg Tyr Asp Thr	Gly Leu Asp Phe Gln Glu Thr Val Asp Gln	
225	230	235 240
Lys Lys Ile Arg Thr Tyr Thr Ala Val Trp Asn Gln Asp Gln Val Gln		
	245	250 255
Asp Tyr Thr Asn Val Glu Leu Thr Pro Glu Gly Leu Thr Val Thr Thr		
	260	265 270
Lys Asp Ala Val Ser Gly Glu Leu Val Asp Gln Phe Thr Leu Ser Lys		
	275	280 285
Gln Asp Arg Asp Glu Glu Ser Glu Val Pro Val Glu Asp Asp Lys Asp		
	290	295 300
Gly Asp Asn Ala Thr Gly Ser Ser Asn Leu Gly Leu Ala Ala Ile Leu		
	305	310 315 320
Ala Pro Val Leu Ala Ile Phe Gly Phe Val Gly Gly Leu Phe Val Gly		
	325	330 335
Gly Gly Ser Leu Ala Glu Phe Phe Ala Asn Leu Gly Val Lys Met Pro		
	340	345 350

Phe

<210> 333
 <211> 1266
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1243)
 <223> RXA01967

<400> 333
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gttgtcgcca accgtgccac cgcaaaccac caaacgtcac atg cgc atc caa agc 115
 Met Arg Ile Gln Ser
 1 5

ccc atg gaa att tcc tgg agt gaa gcg gtg cgc gaa ggc ggg gag cat 163
 Pro Met Glu Ile Ser Trp Ser Glu Ala Val Arg Glu Gly Gly Glu His
 10 15 20

tcc gct cgc cgc tgt ggt gac atg gct gtg tcc gcg ttg gct aag ccg 211
 Ser Ala Arg Arg Cys Gly Asp Met Ala Val Ser Ala Leu Ala Lys Pro
 25 30 35

aat ccc atc att gac gat gat ccg gaa ggc aac ccc gat gtt tgc atg 259
 Asn Pro Ile Ile Asp Asp Asp Pro Glu Gly Asn Pro Asp Val Cys Met
 40 45 50

tat acc tgg atc gtt gag tgt ccc ggc gct acc gca gtg ctg cta tgg 307
 Tyr Thr Trp Ile Val Glu Cys Pro Gly Ala Thr Ala Val Leu Leu Trp

55	60	65	
atc aat ggg gtt ttt gat cac gag cgc att gaa gaa tct gaa atg acc Ile Asn Gly Val Phe Asp His Glu Arg Ile Glu Glu Ser Glu Met Thr 70 75 80 85			355
cgc ctc gag ggc tct gat ctg tgg att ctc agc ttg cgt atg cct tcc Arg Leu Glu Gly Ser Asp Leu Trp Ile Leu Ser Leu Arg Met Pro Ser 90 95 100			403
gat tgg cga gcc agc tac acc gtc aac gcc tgg tct ggc gac ggg gtt Asp Trp Arg Ala Ser Tyr Thr Val Asn Ala Trp Ser Gly Asp Gly Val 105 110 115			451
gcg cca tgg cgt gag gcg ggc gat cgg atg cat atc cgc aaa gcc gcg Ala Pro Trp Arg Glu Ala Gly Asp Arg Met His Ile Arg Lys Ala Ala 120 125 130			499
atg tcg ggt ggg cgt ccg gat tcc cgc gcg atg ggt cat atc atg gat Met Ser Gly Gly Arg Pro Asp Ser Arg Ala Met Gly His Ile Met Asp 135 140 145			547
tcc tcg ctc gtt gaa ggc cct gat gcg ttg ccg gac tgc tgg gtt gcg Ser Ser Leu Val Glu Gly Pro Asp Ala Leu Pro Asp Cys Trp Val Ala 150 155 160 165			595
gcg tcg aca agc gta aaa gtc gtg gaa gaa acc gtc gcc ggc gag cat Ala Ser Thr Ser Val Lys Val Val Glu Glu Thr Val Ala Gly Glu His 170 175 180			643
ttc tgg ttc tat gag gcg ccg gtc aag gcg ccg ctg ctg gtg ctg ttt Phe Trp Phe Tyr Glu Ala Pro Val Lys Ala Pro Leu Leu Val Leu Phe 185 190 195			691
gat ggc caa cac tgg aac aac agc atg aat ctg cct gcg cag gtc gat Asp Gly Gln His Trp Asn Asn Ser Met Asn Leu Pro Ala Gln Val Asp 200 205 210			739
gcg gcc atc gcc atc ggc ttg ctg ccg ccg gtc agc ctg ctc atg atc Ala Ala Ile Ala Ile Gly Leu Leu Pro Pro Val Ser Leu Leu Met Ile 215 220 225			787
gat tcc gtc aac acc gaa cgc cgc tgg gat agt gtc ggc gtg cca ggt Asp Ser Val Asn Thr Glu Arg Arg Trp Asp Ser Val Gly Val Pro Gly 230 235 240 245			835
ggg cag gtt gat gtg ctt atc gac gcc ctc ctc ccg cac gtc cgc gaa Gly Gln Val Asp Val Leu Ile Asp Ala Leu Leu Pro His Val Arg Glu 250 255 260			883
acc tac aac gtt tcc gcg cgc ggc gaa gac acc att gtc acc ggt gca Thr Tyr Asn Val Ser Ala Arg Gly Glu Asp Thr Ile Val Thr Gly Ala 265 270 275			931
agc ttc ggc ggc ctg gcg tcc ctg tgg gct ctt gcg ctt tcc gac ggc Ser Phe Gly Gly Leu Ala Ser Leu Trp Ala Leu Ala Leu Ser Asp Gly 280 285 290			979
gaa gtc ggc cac gca atc gcg caa tcg cca agc ctg tgg cgc ttc aac Glu Val Gly His Ala Ile Ala Gln Ser Pro Ser Leu Trp Arg Phe Asn 295 300 305			1027

gtt gcc gac gcg ctt tct gca gca gag cag tgg agc tca atc cac ctg 1075
 Val Ala Asp Ala Leu Ser Ala Ala Glu Gln Trp Ser Ser Ile His Leu
 310 315 320 325

caa gct gga aaa tac gaa ggt gaa atg ctg cgc ctg tcg cat cag ctc 1123
 Gln Ala Gly Lys Tyr Glu Gly Glu Met Leu Arg Leu Ser His Gln Leu
 330 335 340

gcc gaa gat ctc tcc ggc gac atc cgc gag gtt cgt gtg cgc ggc gtg 1171
 Ala Glu Asp Leu Ser Gly Asp Ile Arg Glu Val Arg Val Arg Gly Val
 345 350 355

cat ggc ggc cac gat tgg gcc tgg tgg cgg gtg cat atg ctc acc gaa 1219
 His Gly Gly His Asp Trp Ala Trp Trp Arg Val His Met Leu Thr Glu
 360 365 370

ctc acc agg ctg ctt aaa acc ctc taatcaaagt aggggtgcaaa acg 1266
 Leu Thr Arg Leu Leu Lys Thr Leu
 375 380

<210> 334

<211> 381

<212> PRT

<213> Corynebacterium glutamicum

<400> 334

Met Arg Ile Gln Ser Pro Met Glu Ile Ser Trp Ser Glu Ala Val Arg
 1 5 10 15

Glu Gly Gly Glu His Ser Ala Arg Arg Cys Gly Asp Met Ala Val Ser
 20 25 30

Ala Leu Ala Lys Pro Asn Pro Ile Ile Asp Asp Asp Pro Glu Gly Asn
 35 40 45

Pro Asp Val Cys Met Tyr Thr Trp Ile Val Glu Cys Pro Gly Ala Thr
 50 55 60

Ala Val Leu Leu Trp Ile Asn Gly Val Phe Asp His Glu Arg Ile Glu
 65 70 75 80

Glu Ser Glu Met Thr Arg Leu Glu Gly Ser Asp Leu Trp Ile Leu Ser
 85 90 95

Leu Arg Met Pro Ser Asp Trp Arg Ala Ser Tyr Thr Val Asn Ala Trp
 100 105 110

Ser Gly Asp Gly Val Ala Pro Trp Arg Glu Ala Gly Asp Arg Met His
 115 120 125

Ile Arg Lys Ala Ala Met Ser Gly Gly Arg Pro Asp Ser Arg Ala Met
 130 135 140

Gly His Ile Met Asp Ser Ser Leu Val Glu Gly Pro Asp Ala Leu Pro
 145 150 155 160

Asp Cys Trp Val Ala Ala Ser Thr Ser Val Lys Val Val Glu Glu Thr
 165 170 175

Val Ala Gly Glu His Phe Trp Phe Tyr Glu Ala Pro Val Lys Ala Pro
 180 185 190
 Leu Leu Val Leu Phe Asp Gly Gln His Trp Asn Asn Ser Met Asn Leu
 195 200 205
 Pro Ala Gln Val Asp Ala Ala Ile Ala Ile Gly Leu Leu Pro Pro Val
 210 215 220
 Ser Leu Leu Met Ile Asp Ser Val Asn Thr Glu Arg Arg Trp Asp Ser
 225 230 235 240
 Val Gly Val Pro Gly Gly Gln Val Asp Val Leu Ile Asp Ala Leu Leu
 245 250 255
 Pro His Val Arg Glu Thr Tyr Asn Val Ser Ala Arg Gly Glu Asp Thr
 260 265 270
 Ile Val Thr Gly Ala Ser Phe Gly Gly Leu Ala Ser Leu Trp Ala Leu
 275 280 285
 Ala Leu Ser Asp Gly Glu Val Gly His Ala Ile Ala Gln Ser Pro Ser
 290 295 300
 Leu Trp Arg Phe Asn Val Ala Asp Ala Leu Ser Ala Ala Glu Gln Trp
 305 310 315 320
 Ser Ser Ile His Leu Gln Ala Gly Lys Tyr Glu Gly Glu Met Leu Arg
 325 330 335
 Leu Ser His Gln Leu Ala Glu Asp Leu Ser Gly Asp Ile Arg Glu Val
 340 345 350
 Arg Val Arg Gly Val His Gly Gly His Asp Trp Ala Trp Trp Arg Val
 355 360 365
 His Met Leu Thr Glu Leu Thr Arg Leu Leu Lys Thr Leu
 370 375 380

<210> 335

<211> 555

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(532)

<223> RXA00070

<400> 335

ccactcgtcc tcgacatact tctcctggca ctaaacgcag gggttgacac atctgggtag 60

actatcgaag tacattttgt gtcattgagg aggatcaacg gtg ggt atc aat cgc 115
 Val Gly Ile Asn Arg
 1 5

atc agc caa ggc tct gcc ccg aag ctg gga gtg cga agc acc aga cag 163
 Ile Ser Gln Gly Ser Ala Pro Lys Leu Gly Val Arg Ser Thr Arg Gln
 10 15 20

cga aaa gcc gta att gac gtt ctt gag gaa atc gat aac ttc gct tcc 211
 Arg Lys Ala Val Ile Asp Val Leu Glu Glu Ile Asp Asn Phe Ala Ser
 25 30 35

gcc aaa gaa atc cat cac gag cta tcc acc agg gaa cac aac gtc ggc 259
 Ala Lys Glu Ile His His Glu Leu Ser Thr Arg Glu His Asn Val Gly
 40 45 50

ctc aca acc gtc tac cga acc ctc caa tcc ctc gcc gac atc gga gca 307
 Leu Thr Thr Val Tyr Arg Thr Leu Gln Ser Leu Ala Asp Ile Gly Ala
 55 60 65

gtc gac gta ctt acc gtc acg ggt gga gaa act ctg tac cgc caa tgc 355
 Val Asp Val Leu Thr Val Thr Gly Gly Glu Thr Leu Tyr Arg Gln Cys
 70 75 80 85

cac gac gag gga cac cac cat cac ctg gtc tgc acc aat tgc ggt cgc 403
 His Asp Glu Gly His His His His Leu Val Cys Thr Asn Cys Gly Arg
 90 95 100

aca gtc gaa atc gat ggc ggt cca gta gag aca tgg gca cag gaa att 451
 Thr Val Glu Ile Asp Gly Gly Pro Val Glu Thr Trp Ala Gln Glu Ile
 105 110 115

gcc act aaa aac ggc ttt gct ctc agt agt cac gag gct gaa atc ttt 499
 Ala Thr Lys Asn Gly Phe Ala Leu Ser Ser His Glu Ala Glu Ile Phe
 120 125 130

gga ctt tgc gct gat tgt aag gaa aaa gtt acg tagttcaagg acatatgaag 552
 Gly Leu Cys Ala Asp Cys Lys Glu Lys Val Thr
 135 140

ctg 555

<210> 336

<211> 144

<212> PRT

<213> Corynebacterium glutamicum

<400> 336

Val Gly Ile Asn Arg Ile Ser Gln Gly Ser Ala Pro Lys Leu Gly Val
 1 5 10 15

Arg Ser Thr Arg Gln Arg Lys Ala Val Ile Asp Val Leu Glu Glu Ile
 20 25 30

Asp Asn Phe Ala Ser Ala Lys Glu Ile His His Glu Leu Ser Thr Arg
 35 40 45

Glu His Asn Val Gly Leu Thr Thr Val Tyr Arg Thr Leu Gln Ser Leu
 50 55 60

Ala Asp Ile Gly Ala Val Asp Val Leu Thr Val Thr Gly Gly Glu Thr
 65 70 75 80

Leu Tyr Arg Gln Cys His Asp Glu Gly His His His His Leu Val Cys
 85 90 95

Thr Asn Cys Gly Arg Thr Val Glu Ile Asp Gly Gly Pro Val Glu Thr
 100 105 110

Trp Ala Gln Glu Ile Ala Thr Lys Asn Gly Phe Ala Leu Ser Ser His
 115 120 125

Glu Ala Glu Ile Phe Gly Leu Cys Ala Asp Cys Lys Glu Lys Val Thr
 130 135 140

<210> 337

<211> 681

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(658)

<223> RXA01934

<400> 337

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acttcactgg cttagattcc ttaaaagaaa gcattcagga atg aca cct caa cca 115
 Met Thr Pro Gln Pro
 1 5

ctg att ttg cct ttc ggc gat aaa gtt ccg cgg atc cat gaa agc gca 163
 Leu Ile Leu Pro Phe Gly Asp Lys Val Pro Arg Ile His Glu Ser Ala
 10 15 20

tgg att gcc ccg aat gcc acg att atc ggg gat gtc gag att ggc ccg 211
 Trp Ile Ala Pro Asn Ala Thr Ile Ile Gly Asp Val Glu Ile Gly Pro
 25 30 35

gat gcg tcc att ttt tat ggc gtt gtc ctg cgc ggt gac gtc aac aaa 259
 Asp Ala Ser Ile Phe Tyr Gly Val Val Leu Arg Gly Asp Val Asn Lys
 40 45 50

atc acc atc ggc gcc cgc acc aac gtc cag gac aat tgt gtt ctc cac 307
 Ile Thr Ile Gly Ala Arg Thr Asn Val Gln Asp Asn Cys Val Leu His
 55 60 65

gtc gat ggc gat gcg ccg tgc acc ctc ggc gac gat gtc acg gtc ggc 355
 Val Asp Gly Asp Ala Pro Cys Thr Leu Gly Asp Asp Val Thr Val Gly
 70 75 80 85

cac atg gcg ctt gtt cac ggc gcg acg gtg ggc aac ggc acg ctt gtc 403
 His Met Ala Leu Val His Gly Ala Thr Val Gly Asn Gly Thr Leu Val
 90 95 100

ggc atg aaa tct gcg ctg ctt tcc ggc agc cac gtc ggc gcc ggc gca 451
 Gly Met Lys Ser Ala Leu Leu Ser Gly Ser His Val Gly Ala Gly Ala
 105 110 115

ctc att gcc gct ggt gcg gtg gtg ctg gag ggc cat gaa atc ccg gcg 499
 Leu Ile Ala Ala Gly Ala Val Val Leu Glu Gly His Glu Ile Pro Ala
 120 125 130

aaa gct tta gcg gcc ggg gtt ccg gcc aaa gtg cgc aga ttg ctt gac 547
 Lys Ala Leu Ala Ala Gly Val Pro Ala Lys Val Arg Arg Leu Leu Asp
 135 140 145

gac gcc cag tcc cag tca ttt atc ccc cac gcg ggc cgc tat gta gaa 595
 Asp Ala Gln Ser Gln Ser Phe Ile Pro His Ala Gly Arg Tyr Val Glu
 150 155 160 165

aca tca aaa gcc cag gct tcc atc gcg gaa gca ctg agc tta gat gag 643
 Thr Ser Lys Ala Gln Ala Ser Ile Ala Glu Ala Leu Ser Leu Asp Glu
 170 175 180

gtt agg gta cga gag taagtggctc gttgagtagt cga 681
 Val Arg Val Arg Glu
 185

<210> 338

<211> 186

<212> PRT

<213> Corynebacterium glutamicum

<400> 338

Met Thr Pro Gln Pro Leu Ile Leu Pro Phe Gly Asp Lys Val Pro Arg
 1 5 10 15

Ile His Glu Ser Ala Trp Ile Ala Pro Asn Ala Thr Ile Ile Gly Asp
 20 25 30

Val Glu Ile Gly Pro Asp Ala Ser Ile Phe Tyr Gly Val Val Leu Arg
 35 40 45

Gly Asp Val Asn Lys Ile Thr Ile Gly Ala Arg Thr Asn Val Gln Asp
 50 55 60

Asn Cys Val Leu His Val Asp Gly Asp Ala Pro Cys Thr Leu Gly Asp
 65 70 75 80

Asp Val Thr Val Gly His Met Ala Leu Val His Gly Ala Thr Val Gly
 85 90 95

Asn Gly Thr Leu Val Gly Met Lys Ser Ala Leu Leu Ser Gly Ser His
 100 105 110

Val Gly Ala Gly Ala Leu Ile Ala Ala Gly Ala Val Val Leu Glu Gly
 115 120 125

His Glu Ile Pro Ala Lys Ala Leu Ala Ala Gly Val Pro Ala Lys Val
 130 135 140

Arg Arg Leu Leu Asp Asp Ala Gln Ser Gln Ser Phe Ile Pro His Ala
 145 150 155 160

Gly Arg Tyr Val Glu Thr Ser Lys Ala Gln Ala Ser Ile Ala Glu Ala
 165 170 175

Leu Ser Leu Asp Glu Val Arg Val Arg Glu
 180 185

<210> 339

<211> 609

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(586)

<223> RXN01997

<400> 339

aaaaaggtgg gaaacttagc caatccaaag cccaaaaatg cgggttatgc tgcgctaacc 60

tatgctgaca	gccttgcgga	agttgtgtac	gtagggggcc	atg	aca	atc	aac	gag	115
				Met	Thr	Ile	Asn	Glu	
				1				5	

aag	atc	gca	tca	gct	ttc	aac	aac	caa	gtg	act	gca	gag	ctt	gaa	gct	163
Lys	Ile	Ala	Ser	Ala	Phe	Asn	Asn	Gln	Val	Thr	Ala	Glu	Leu	Glu	Ala	
				10				15						20		

tca	atg	gtg	tac	ctt	cag	ctc	tcc	tac	gtt	cta	gac	gat	ctg	ggc	ctc	211
Ser	Met	Val	Tyr	Leu	Gln	Leu	Ser	Tyr	Val	Leu	Asp	Asp	Leu	Gly	Leu	
			25				30						35			

acc	ggc	atg	cgc	gac	tgg	atg	aag	gca	cag	agc	aaa	gaa	gag	ctc	gaa	259
Thr	Gly	Met	Arg	Asp	Trp	Met	Lys	Ala	Gln	Ser	Lys	Glu	Glu	Leu	Glu	
		40					45					50				

cac	gca	cag	aag	ttc	gct	cag	cac	ctt	ctt	gac	cgt	gac	tac	acc	cca	307
His	Ala	Gln	Lys	Phe	Ala	Gln	His	Leu	Leu	Asp	Arg	Asp	Tyr	Thr	Pro	
	55					60				65						

cag	atc	ggt	gac	att	gca	cca	cca	aag	ctt	gat	gtc	acc	tcc	gct	atc	355
Gln	Ile	Gly	Asp	Ile	Ala	Pro	Pro	Lys	Leu	Asp	Val	Thr	Ser	Ala	Ile	
	70				75				80					85		

gag	gct	ttc	gag	gct	tcc	ctg	gca	cac	gag	cag	aag	atc	tcc	ggc	ctg	403
Glu	Ala	Phe	Glu	Ala	Ser	Leu	Ala	His	Glu	Gln	Lys	Ile	Ser	Gly	Leu	
				90				95						100		

atc	cgc	gag	ctc	gct	gcc	atc	cag	gac	gct	gag	aag	gac	tac	gat	tcc	451
Ile	Arg	Glu	Leu	Ala	Ala	Ile	Gln	Asp	Ala	Glu	Lys	Asp	Tyr	Asp	Ser	
			105				110						115			

cgc	gca	ctg	atc	gac	tgg	ttc	ctc	aac	gag	cag	atc	gaa	gaa	gaa	gca	499
Arg	Ala	Leu	Ile	Asp	Trp	Phe	Leu	Asn	Glu	Gln	Ile	Glu	Glu	Glu	Ala	
		120				125						130				

acc	gtc	ggc	gag	atc	atc	gac	cgc	ctc	cgt	atc	gct	ggt	gat	tcc	ggt	547
Thr	Val	Gly	Glu	Ile	Ile	Asp	Arg	Leu	Arg	Ile	Ala	Gly	Asp	Ser	Gly	
	135					140				145						

tcc	gga	atc	ctg	cgc	atc	gac	ggc	gaa	ctc	ggc	tcc	cgc	taaattcccc	596
Ser	Gly	Ile	Leu	Arg	Ile	Asp	Gly	Glu	Leu	Gly	Ser	Arg		
150					155					160				

gcagtttttta	atg	609
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<210> 340

<211> 162

<212> PRT

<213> Corynebacterium glutamicum

<400> 340

Met Thr Ile Asn Glu Lys Ile Ala Ser Ala Phe Asn Asn Gln Val Thr
 1 5 10 15
 Ala Glu Leu Glu Ala Ser Met Val Tyr Leu Gln Leu Ser Tyr Val Leu
 20 25 30
 Asp Asp Leu Gly Leu Thr Gly Met Arg Asp Trp Met Lys Ala Gln Ser
 35 40 45
 Lys Glu Glu Leu Glu His Ala Gln Lys Phe Ala Gln His Leu Leu Asp
 50 55 60
 Arg Asp Tyr Thr Pro Gln Ile Gly Asp Ile Ala Pro Pro Lys Leu Asp
 65 70 75 80
 Val Thr Ser Ala Ile Glu Ala Phe Glu Ala Ser Leu Ala His Glu Gln
 85 90 95
 Lys Ile Ser Gly Leu Ile Arg Glu Leu Ala Ala Ile Gln Asp Ala Glu
 100 105 110
 Lys Asp Tyr Asp Ser Arg Ala Leu Ile Asp Trp Phe Leu Asn Glu Gln
 115 120 125
 Ile Glu Glu Glu Ala Thr Val Gly Glu Ile Ile Asp Arg Leu Arg Ile
 130 135 140
 Ala Gly Asp Ser Gly Ser Gly Ile Leu Arg Ile Asp Gly Glu Leu Gly
 145 150 155 160
 Ser Arg

<210> 341
 <211> 490
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(490)
 <223> FRXA01997

<400> 341
 aaaaagggtgg gaaacttagc caatccaaag cccaaaaatg cgggttatgc tgcgctaacc 60

tatgctgaca gccttgcgga agttgtgtac gttaggggcc atg aca atc aac gag 115
 Met Thr Ile Asn Glu
 1 5

aag atc gca tca gct ttc aac aac caa gtg act gca gag ctt gaa gct 163
 Lys Ile Ala Ser Ala Phe Asn Asn Gln Val Thr Ala Glu Leu Glu Ala
 10 15 20

tca atg gtg tac ctt cag ctc tcc tac gtt cta gac gat ctg ggc ctc 211
 Ser Met Val Tyr Leu Gln Leu Ser Tyr Val Leu Asp Asp Leu Gly Leu
 25 30 35

acc ggc atg cgc gac tgg atg aag gca cag agc aaa gaa gag ctc gaa 259
 Thr Gly Met Arg Asp Trp Met Lys Ala Gln Ser Lys Glu Glu Leu Glu

40	45	50	
cac gca cag aag ttc gct cag cac ctt ctt gac cgt gac tac acc cca			307
His Ala Gln Lys Phe Ala Gln His Leu Leu Asp Arg Asp Tyr Thr Pro			
55	60	65	
cag atc ggt gac att gca cca cca aag ctt gat gtc acc tcc gct atc			355
Gln Ile Gly Asp Ile Ala Pro Pro Lys Leu Asp Val Thr Ser Ala Ile			
70	75	80	85
gag gct ttc gag gct tcc ctg gca cac gag cag aag atc tcc ggc ctg			403
Glu Ala Phe Glu Ala Ser Leu Ala His Glu Gln Lys Ile Ser Gly Leu			
90	95	100	
atc cgc gag ctc gct gcc atc cag gac gct gag aag gac tac gat tcc			451
Ile Arg Glu Leu Ala Ala Ile Gln Asp Ala Glu Lys Asp Tyr Asp Ser			
105	110	115	
cgc gca ctg atc gac tgg ttc ctc aac gag cag atc gaa			490
Arg Ala Leu Ile Asp Trp Phe Leu Asn Glu Gln Ile Glu			
120	125	130	

<210> 342

<211> 130

<212> PRT

<213> Corynebacterium glutamicum

<400> 342

Met Thr Ile Asn Glu Lys Ile Ala Ser Ala Phe Asn Asn Gln Val Thr	
1	15
Ala Glu Leu Glu Ala Ser Met Val Tyr Leu Gln Leu Ser Tyr Val Leu	
20	30
Asp Asp Leu Gly Leu Thr Gly Met Arg Asp Trp Met Lys Ala Gln Ser	
35	45
Lys Glu Glu Leu Glu His Ala Gln Lys Phe Ala Gln His Leu Leu Asp	
50	60
Arg Asp Tyr Thr Pro Gln Ile Gly Asp Ile Ala Pro Pro Lys Leu Asp	
65	80
Val Thr Ser Ala Ile Glu Ala Phe Glu Ala Ser Leu Ala His Glu Gln	
85	95
Lys Ile Ser Gly Leu Ile Arg Glu Leu Ala Ala Ile Gln Asp Ala Glu	
100	110
Lys Asp Tyr Asp Ser Arg Ala Leu Ile Asp Trp Phe Leu Asn Glu Gln	
115	125
Ile Glu	
130	

<210> 343

<211> 783

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(760)

<223> RXA01082

<400> 343

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ggccttgctt gcgttagttg cagtgcctcc tgaatatgct tctgaaacgg ttgtcgagca 60
cacttatcaa acatcggcgg cgaattaaga aggtgaacag ttg acg cag tgg ggt 115
Leu Thr Gln Trp Gly
1 5

aat tcg aat gtt gtg gag gac tat ctc aca gca ctt ttc cgt gca gaa 163
Asn Ser Asn Val Val Glu Asp Tyr Leu Thr Ala Leu Phe Arg Ala Glu
10 15 20

gaa tgg gat gag gaa cca aca aca gga aaa ctc gct gaa gta att gga 211
Glu Trp Asp Glu Glu Pro Thr Thr Gly Lys Leu Ala Glu Val Ile Gly
25 30 35

gtt acc gca tca acg gtg tcg gcg acg ctc aaa aaa ctc aac cct gag 259
Val Thr Ala Ser Thr Val Ser Ala Thr Leu Lys Lys Leu Asn Pro Glu
40 45 50

ggc ttc gtc aat tac cgt ccc tac ggg gac atc gag ctg acg ccc gca 307
Gly Phe Val Asn Tyr Arg Pro Tyr Gly Asp Ile Glu Leu Thr Pro Ala
55 60 65

ggg cga gac atc gcc atc aac gtg atc agg cgg cgc cgg atc att gag 355
Gly Arg Asp Ile Ala Ile Asn Val Ile Arg Arg Arg Arg Ile Ile Glu
70 75 80 85

acc tat ctg tct gag aag ctt gga tta ggc gct cat gaa cta cac ggc 403
Thr Tyr Leu Ser Glu Lys Leu Gly Leu Gly Ala His Glu Leu His Gly
90 95 100

gag gca gat tta tta gag cac gca gtg tct cca ctg gtg ttg gag aag 451
Glu Ala Asp Leu Leu Glu His Ala Val Ser Pro Leu Val Leu Glu Lys
105 110 115

atg ttt cag gca gtg ggc tat cca acg ttg gat cct cac ggg gat ccc 499
Met Phe Gln Ala Val Gly Tyr Pro Thr Leu Asp Pro His Gly Asp Pro
120 125 130

atc ccc acc gaa tct ggg gag atg acc atc aat gat gga ctc atg ctt 547
Ile Pro Thr Glu Ser Gly Glu Met Thr Ile Asn Asp Gly Leu Met Leu
135 140 145

ttg gga cta aaa gct ggc gca tct gcc acg gtt aca cgt gtt agg gac 595
Leu Gly Leu Lys Ala Gly Ala Ser Ala Thr Val Thr Arg Val Arg Asp
150 155 160 165

gga aac cca tca gtg gtt cgg tac ctc act gga gtg gga att acc gtg 643
Gly Asn Pro Ser Val Val Arg Tyr Leu Thr Gly Val Gly Ile Thr Val
170 175 180

ggc aca acg gtc acg gtc gtt gaa gct ctt agc gat att gcc aca ctg 691
Gly Thr Thr Val Thr Val Val Glu Ala Leu Ser Asp Ile Ala Thr Leu
185 190 195

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cgc ctg cag atc ggg gaa atg ttt caa gac att ccc ctt gca gtg gca 739
 Arg Leu Gln Ile Gly Glu Met Phe Gln Asp Ile Pro Leu Ala Val Ala
 200 205 210

aac gca gtg cgc gta tca cgt tagttcagcg tgcccagcgc gct 783
 Asn Ala Val Arg Val Ser Arg
 215 220

<210> 344

<211> 220

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 344

Leu Thr Gln Trp Gly Asn Ser Asn Val Val Glu Asp Tyr Leu Thr Ala
 1 5 10 15

Leu Phe Arg Ala Glu Glu Trp Asp Glu Glu Pro Thr Thr Gly Lys Leu
 20 25 30

Ala Glu Val Ile Gly Val Thr Ala Ser Thr Val Ser Ala Thr Leu Lys
 35 40 45

Lys Leu Asn Pro Glu Gly Phe Val Asn Tyr Arg Pro Tyr Gly Asp Ile
 50 55 60

Glu Leu Thr Pro Ala Gly Arg Asp Ile Ala Ile Asn Val Ile Arg Arg
 65 70 75 80

Arg Arg Ile Ile Glu Thr Tyr Leu Ser Glu Lys Leu Gly Leu Gly Ala
 85 90 95

His Glu Leu His Gly Glu Ala Asp Leu Leu Glu His Ala Val Ser Pro
 100 105 110

Leu Val Leu Glu Lys Met Phe Gln Ala Val Gly Tyr Pro Thr Leu Asp
 115 120 125

Pro His Gly Asp Pro Ile Pro Thr Glu Ser Gly Glu Met Thr Ile Asn
 130 135 140

Asp Gly Leu Met Leu Leu Gly Leu Lys Ala Gly Ala Ser Ala Thr Val
 145 150 155 160

Thr Arg Val Arg Asp Gly Asn Pro Ser Val Val Arg Tyr Leu Thr Gly
 165 170 175

Val Gly Ile Thr Val Gly Thr Thr Val Thr Val Val Glu Ala Leu Ser
 180 185 190

Asp Ile Ala Thr Leu Arg Leu Gln Ile Gly Glu Met Phe Gln Asp Ile
 195 200 205

Pro Leu Ala Val Ala Asn Ala Val Arg Val Ser Arg
 210 215 220

<210> 345

<211> 1068

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1045)

<223> RXA01236

<400> 345

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ggtttcaacc acaacatctc gctcaatcgc tggactgtca gtg ctt gtg gca aca 115
                                   Val Leu Val Ala Thr
                                   1 5
gca cta atc gct ggc tgt agt tcc gca gag gat ggg acg gtt gac tcg 163
Ala Leu Ile Ala Gly Cys Ser Ser Ala Glu Asp Gly Thr Val Asp Ser
                                   10 15 20
ggg agc agc aca gag gtc acc aca acc caa agc aag gaa ggt ttt cct 211
Gly Ser Ser Thr Glu Val Thr Thr Thr Gln Ser Lys Glu Gly Phe Pro
                                   25 30 35
gtc acc gtc acg ttt gcc cca gaa gca cct gtg acc att gag gat caa 259
Val Thr Val Thr Phe Ala Pro Glu Ala Pro Val Thr Ile Glu Asp Gln
                                   40 45 50
cca gag cgc atc gtc agt ttg tcc cca gcg att aca gaa acc ttg ttc 307
Pro Glu Arg Ile Val Ser Leu Ser Pro Ala Ile Thr Glu Thr Leu Phe
                                   55 60 65
gct gtc ggg gca ggg gat cat gtc gtc gca gtg gat gaa tac tca aac 355
Ala Val Gly Ala Gly Asp His Val Val Ala Val Asp Glu Tyr Ser Asn
                                   70 75 80 85
tac cca gag gac gca ccg ctg gtg cag ggt ctg tct ggt ttt act ccc 403
Tyr Pro Glu Asp Ala Pro Leu Val Gln Gly Leu Ser Gly Phe Thr Pro
                                   90 95 100
aat gtg gag tcc atc ttg gat tac gat cct gac ctg gtc gtg ttg atg 451
Asn Val Glu Ser Ile Leu Asp Tyr Asp Pro Asp Leu Val Val Leu Met
                                   105 110 115
tct gca gat gat tcc att ttg acc ggc ctg gat gct gca gga gtg gat 499
Ser Ala Asp Asp Ser Ile Leu Thr Gly Leu Asp Ala Ala Gly Val Asp
                                   120 125 130
act tta gtg atc ccc gca gca gag aac ttg gat gag acc tac tcc cag 547
Thr Leu Val Ile Pro Ala Ala Glu Asn Leu Asp Glu Thr Tyr Ser Gln
                                   135 140 145
att gaa caa gta ggt cga gcc acc gga ttt gaa gat caa gca aca acg 595
Ile Glu Gln Val Gly Arg Ala Thr Gly Phe Glu Asp Gln Ala Thr Thr
150 155 160 165
gtt gtt gat cag atg aaa acc gcc att gat gct gca gtt gcc aca gtt 643
Val Val Asp Gln Met Lys Thr Ala Ile Asp Ala Ala Val Ala Thr Val
170 175 180
cct gaa gag gta aaa gag cag ggc tta acc tac ttc cac gag ctg ggc 691
Pro Glu Glu Val Lys Glu Gln Gly Leu Thr Tyr Phe His Glu Leu Gly
185 190 195

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agt gat ttg ttc act gtg tca gag caa acc tac atc ggt cag att tac 739
Ser Asp Leu Phe Thr Val Ser Glu Gln Thr Tyr Ile Gly Gln Ile Tyr
200 205 210

gac atg ttt ggt ctc acc tct att gct gac ggt ggc gac gct tac tcg 787
Asp Met Phe Gly Leu Thr Ser Ile Ala Asp Gly Gly Asp Ala Tyr Ser
215 220 225

cag cta tcc aac gaa gca atc att gcg gca aac cct gat ctg att ttc 835
Gln Leu Ser Asn Glu Ala Ile Ile Ala Ala Asn Pro Asp Leu Ile Phe
230 235 240 245

ctc agc gat gcc aag gcc gaa aac ctc act gca gaa gat att gcg gcg 883
Leu Ser Asp Ala Lys Ala Glu Asn Leu Thr Ala Glu Asp Ile Ala Ala
250 255 260

cgt cca ggc tgg gac acc att gat gca gta gcc aat gga cgt atc tac 931
Arg Pro Gly Trp Asp Thr Ile Asp Ala Val Ala Asn Gly Arg Ile Tyr
265 270 275

att ttg gac gat gat att gct tcc agg tgg gga cct cgc gta tcc cag 979
Ile Leu Asp Asp Asp Ile Ala Ser Arg Trp Gly Pro Arg Val Ser Gln
280 285 290

ctg gtg gaa gaa atc gca gcg cag ttg aat cag ctt gct tct tct gaa 1027
Leu Val Glu Glu Ile Ala Ala Gln Leu Asn Gln Leu Ala Ser Ser Glu
295 300 305

gct gtg ccg gcc gct gct taagttttcg tgctgaagag aat 1068
Ala Val Pro Ala Ala Ala
310 315

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<210> 346

<211> 315

<212> PRT

<213> Corynebacterium glutamicum

<400> 346

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Val Leu Val Ala Thr Ala Leu Ile Ala Gly Cys Ser Ser Ala Glu Asp
1 5 10 15

Gly Thr Val Asp Ser Gly Ser Ser Thr Glu Val Thr Thr Thr Gln Ser
20 25 30

Lys Glu Gly Phe Pro Val Thr Val Thr Phe Ala Pro Glu Ala Pro Val
35 40 45

Thr Ile Glu Asp Gln Pro Glu Arg Ile Val Ser Leu Ser Pro Ala Ile
50 55 60

Thr Glu Thr Leu Phe Ala Val Gly Ala Gly Asp His Val Val Ala Val
65 70 75 80

Asp Glu Tyr Ser Asn Tyr Pro Glu Asp Ala Pro Leu Val Gln Gly Leu
85 90 95

Ser Gly Phe Thr Pro Asn Val Glu Ser Ile Leu Asp Tyr Asp Pro Asp
100 105 110

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Leu Val Val Leu Met Ser Ala Asp Asp Ser Ile Leu Thr Gly Leu Asp
 115 120 125
 Ala Ala Gly Val Asp Thr Leu Val Ile Pro Ala Ala Glu Asn Leu Asp
 130 135 140
 Glu Thr Tyr Ser Gln Ile Glu Gln Val Gly Arg Ala Thr Gly Phe Glu
 145 150 155 160
 Asp Gln Ala Thr Thr Val Val Asp Gln Met Lys Thr Ala Ile Asp Ala
 165 170 175
 Ala Val Ala Thr Val Pro Glu Glu Val Lys Glu Gln Gly Leu Thr Tyr
 180 185 190
 Phe His Glu Leu Gly Ser Asp Leu Phe Thr Val Ser Glu Gln Thr Tyr
 195 200 205
 Ile Gly Gln Ile Tyr Asp Met Phe Gly Leu Thr Ser Ile Ala Asp Gly
 210 215 220
 Gly Asp Ala Tyr Ser Gln Leu Ser Asn Glu Ala Ile Ile Ala Ala Asn
 225 230 235 240
 Pro Asp Leu Ile Phe Leu Ser Asp Ala Lys Ala Glu Asn Leu Thr Ala
 245 250 255
 Glu Asp Ile Ala Ala Arg Pro Gly Trp Asp Thr Ile Asp Ala Val Ala
 260 265 270
 Asn Gly Arg Ile Tyr Ile Leu Asp Asp Asp Ile Ala Ser Arg Trp Gly
 275 280 285
 Pro Arg Val Ser Gln Leu Val Glu Glu Ile Ala Ala Gln Leu Asn Gln
 290 295 300
 Leu Ala Ser Ser Glu Ala Val Pro Ala Ala Ala
 305 310 315

<210> 347
 <211> 1059
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1036)
 <223> RXA01354

<400> 347
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 tgcaaaatta tttaggcaag gctacctttt gcctatgcat atg aag att agc cgg 115
 Met Lys Ile Ser Arg
 1 5

cgc gca ttc ctc ggc aca ctg ctc ggc gcc acc acc ctt gct gta act 163
 Arg Ala Phe Leu Gly Thr Leu Leu Gly Ala Thr Thr Leu Ala Val Thr
 10 15 20

gcc tgc gcg caa tcc tct caa aac caa aac tcc tcc gct tcc tca tct	211
Ala Cys Ala Gln Ser Ser Gln Asn Gln Asn Ser Ser Ala Ser Ser Ser	
25 30 35	
tct tca tcc tca gcg gaa tca agc acc tct tca tcc tcc tcc gat gaa	259
Ser Ser Ser Ser Ala Glu Ser Ser Thr Ser Ser Ser Ser Ser Asp Glu	
40 45 50	
cag cgc atc gtc gcc ctc aac acc ggt cag ttg gac aac ctc ctc ctt	307
Gln Arg Ile Val Ala Leu Asn Thr Gly Gln Leu Asp Asn Leu Leu Leu	
55 60 65	
ctc ggc atc acc cca gtg ggc gtc gcc gct gca aaa aac tct gac ctg	355
Leu Gly Ile Thr Pro Val Gly Val Ala Ala Lys Asn Ser Asp Leu	
70 75 80 85	
atc cca cag ttc ctc aag gat cgc ttc ggt gca gac atg gac ttg gac	403
Ile Pro Gln Phe Leu Lys Asp Arg Phe Gly Ala Asp Met Asp Leu Asp	
90 95 100	
agc atc gcc gac tgc ggt ctc cgc caa tct cca gac atc gaa gcc atc	451
Ser Ile Ala Asp Cys Gly Leu Arg Gln Ser Pro Asp Ile Glu Ala Ile	
105 110 115	
gcg aac ctc aac ccc acc ctg atc tgc gca aac tcc cgc gcc gac gaa	499
Ala Asn Leu Asn Pro Thr Leu Ile Cys Ala Asn Ser Arg Ala Asp Glu	
120 125 130	
gag gtc ctc aac aaa ctc cgc acg atc gcc ccc gtg gtc acc ggc gaa	547
Glu Val Leu Asn Lys Leu Arg Thr Ile Ala Pro Val Val Thr Gly Glu	
135 140 145	
ggt ggc ggt gaa aac tgg aag caa gac ctc ctc acc atc gca gag gca	595
Gly Gly Gly Glu Asn Trp Lys Gln Asp Leu Leu Thr Ile Ala Glu Ala	
150 155 160 165	
gca ggc cag aag gaa aag gct gaa acc ctc ctg aaa tca tac gag gac	643
Ala Gly Gln Lys Glu Lys Ala Glu Thr Leu Leu Lys Ser Tyr Glu Asp	
170 175 180	
tca gca gcc gaa atc gcc gca aac cag cct gcg aac cca cca acc gtt	691
Ser Ala Ala Glu Ile Ala Ala Asn Gln Pro Ala Asn Pro Pro Thr Val	
185 190 195	
tcc ttc ctg cgc acc aaa gat cag gaa ttc cag atg tac ggc gca caa	739
Ser Phe Leu Arg Thr Lys Asp Gln Glu Phe Gln Met Tyr Gly Ala Gln	
200 205 210	
tcc atg gcc gga acg gtt gct gcc gat tgc ggt tac gcc cgc cca gaa	787
Ser Met Ala Gly Thr Val Ala Ala Asp Cys Gly Tyr Ala Arg Pro Glu	
215 220 225	
aac cag cag ttc acc gac acg gca ggt caa gac ctc tcc gct gag ctc	835
Asn Gln Gln Phe Thr Asp Thr Ala Gly Gln Asp Leu Ser Ala Glu Leu	
230 235 240 245	
att gcc caa gct gat gcc gac tgg ctt ttc tac ggc atc aaa gaa ggc	883
Ile Ala Gln Ala Asp Ala Asp Trp Leu Phe Tyr Gly Ile Lys Glu Gly	
250 255 260	
aac atc aac cct gaa gac acc cca ttg tgg act tca ctc aaa gcg gtt	931

Asn Ile Asn Pro Glu Asp Thr Pro Leu Trp Thr Ser Leu Lys Ala Val
 265 270 275

 cag tcc aac caa gca atc cca gtt gac ggc gat tcc tgg tac ctc aac 979
 Gln Ser Asn Gln Ala Ile Pro Val Asp Gly Asp Ser Trp Tyr Leu Asn
 280 285 290

 gca tcc ctc gtg tcg gct gaa atc atc ctc caa ggc ctc aaa gac aac 1027
 Ala Ser Leu Val Ser Ala Glu Ile Ile Leu Gln Gly Leu Lys Asp Asn
 295 300 305

 gtc acc gtc taagccgatt taagggcctc aaa 1059
 Val Thr Val
 310

<210> 348

<211> 312

<212> PRT

<213> Corynebacterium glutamicum

<400> 348

Met Lys Ile Ser Arg Arg Ala Phe Leu Gly Thr Leu Leu Gly Ala Thr
 1 5 10 15

 Thr Leu Ala Val Thr Ala Cys Ala Gln Ser Ser Gln Asn Gln Asn Ser
 20 25 30

 Ser Ala Ser Ser Ser Ser Ser Ser Ser Ala Glu Ser Ser Thr Ser Ser
 35 40 45

 Ser Ser Ser Asp Glu Gln Arg Ile Val Ala Leu Asn Thr Gly Gln Leu
 50 55 60

 Asp Asn Leu Leu Leu Leu Gly Ile Thr Pro Val Gly Val Ala Ala Ala
 65 70 75 80

 Lys Asn Ser Asp Leu Ile Pro Gln Phe Leu Lys Asp Arg Phe Gly Ala
 85 90 95

 Asp Met Asp Leu Asp Ser Ile Ala Asp Cys Gly Leu Arg Gln Ser Pro
 100 105 110

 Asp Ile Glu Ala Ile Ala Asn Leu Asn Pro Thr Leu Ile Cys Ala Asn
 115 120 125

 Ser Arg Ala Asp Glu Glu Val Leu Asn Lys Leu Arg Thr Ile Ala Pro
 130 135 140

 Val Val Thr Gly Glu Gly Gly Gly Glu Asn Trp Lys Gln Asp Leu Leu
 145 150 155 160

 Thr Ile Ala Glu Ala Ala Gly Gln Lys Glu Lys Ala Glu Thr Leu Leu
 165 170 175

 Lys Ser Tyr Glu Asp Ser Ala Ala Glu Ile Ala Ala Asn Gln Pro Ala
 180 185 190

 Asn Pro Pro Thr Val Ser Phe Leu Arg Thr Lys Asp Gln Glu Phe Gln
 195 200 205

```

Met Tyr Gly Ala Gln Ser Met Ala Gly Thr Val Ala Ala Asp Cys Gly
 210                      215                      220

Tyr Ala Arg Pro Glu Asn Gln Gln Phe Thr Asp Thr Ala Gly Gln Asp
225                      230                      235                      240

Leu Ser Ala Glu Leu Ile Ala Gln Ala Asp Ala Asp Trp Leu Phe Tyr
                245                      250                      255

Gly Ile Lys Glu Gly Asn Ile Asn Pro Glu Asp Thr Pro Leu Trp Thr
                260                      265                      270

Ser Leu Lys Ala Val Gln Ser Asn Gln Ala Ile Pro Val Asp Gly Asp
                275                      280                      285

Ser Trp Tyr Leu Asn Ala Ser Leu Val Ser Ala Glu Ile Ile Leu Gln
290                      295                      300

Gly Leu Lys Asp Asn Val Thr Val
305                      310

```

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<210> 349
<211> 1071
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(1048)
<223> RXA01620

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<400> 349
cggccgagca gtaaacttgc aggtcaatgc aacttttttaa ccgtagaaag ttatggccaa 60

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```

agactggcaa taggttaaga acttgcgtta ggatagccta atg caa tct att cga      115
                               Met Gln Ser Ile Arg
                               1                      5

```

```

acg acc ttc agg tgc ctt tca cgc agc gca gtt atc gtg ggt acc gtt      163
Thr Thr Phe Arg Ser Leu Ser Arg Ser Ala Val Ile Val Gly Thr Val
                10                      15                      20

```

```

ttg gct ttg ggt atc gca gga tgt tcc acg gcc agt gat gaa gcc aca      211
Leu Ala Leu Gly Ile Ala Gly Cys Ser Thr Ala Ser Asp Glu Ala Thr
                25                      30                      35

```

```

agc acc agc gac gat gta gct gtc ggc ggc cgc cta ttt tct aca gcg      259
Ser Thr Ser Asp Asp Val Ala Val Gly Gly Arg Leu Phe Ser Thr Ala
                40                      45                      50

```

```

gat tcc gcc acc gcc gct ctg gga agc gac gcc gaa cca ggc caa ttc      307
Asp Ser Ala Thr Ala Ala Leu Gly Ser Asp Ala Glu Pro Gly Gln Phe
                55                      60                      65

```

```

ccc cgc acc gtt gtg cat tca cgc ggc gaa act acc ctt gag cag cag      355
Pro Arg Thr Val Val His Ser Arg Gly Glu Thr Thr Leu Glu Gln Gln
                70                      75                      80                      85

```

```

cca caa cga gtc gtg gtt ctc gac agc ggt gaa atc gac cag gtt ttg      403
Pro Gln Arg Val Val Val Leu Asp Ser Gly Glu Ile Asp Gln Val Leu

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90										95					100					
agc	ctc	ggc	gtg	act	ccc	gtc	ggc	atc	gcc	agc	ccg	aaa	gac	gcc	tcc	451				
Ser	Leu	Gly	Val	Thr	Pro	Val	Gly	Ile	Ala	Ser	Pro	Lys	Asp	Ala	Ser					
			105					110					115							
agc	cag	ccc	gct	tac	ctc	gaa	aat	cag	ctg	gca	gat	gta	caa	act	gtg	499				
Ser	Gln	Pro	Ala	Tyr	Leu	Glu	Asn	Gln	Leu	Ala	Asp	Val	Gln	Thr	Val					
		120					125					130								
ggc	acc	acg	agt	gag	ctc	aat	ttc	gaa	gcc	atc	gcc	gcc	ctc	aag	cct	547				
Gly	Thr	Thr	Ser	Glu	Leu	Asn	Phe	Glu	Ala	Ile	Ala	Ala	Leu	Lys	Pro					
		135				140					145									
gac	ctg	att	ctg	ggc	agc	aag	ctg	cgc	gtc	gac	gaa	tcc	tac	gat	cag	595				
Asp	Leu	Ile	Leu	Gly	Ser	Lys	Leu	Arg	Val	Asp	Glu	Ser	Tyr	Asp	Gln					
150					155				160						165					
ctc	tcc	caa	atc	gca	cca	acc	gtg	ctg	agt	att	cgc	ccc	gga	ttc	ccc	643				
Leu	Ser	Gln	Ile	Ala	Pro	Thr	Val	Leu	Ser	Ile	Arg	Pro	Gly	Phe	Pro					
			170					175						180						
tgg	aag	gaa	aac	ttc	ctc	ctc	acc	gcc	gac	gcg	ctc	ggg	ctc	gag	ggc	691				
Trp	Lys	Glu	Asn	Phe	Leu	Leu	Thr	Ala	Asp	Ala	Leu	Gly	Leu	Glu	Gly					
			185					190					195							
aaa	gcc	gtc	gag	gtt	ctc	aac	gag	tac	caa	acc	cat	gtc	gat	gca	gtc	739				
Lys	Ala	Val	Glu	Val	Leu	Asn	Glu	Tyr	Gln	Thr	His	Val	Asp	Ala	Val					
		200					205					210								
cgc	gag	acc	atc	gac	ggc	agc	cca	gaa	atc	tca	ctc	gtc	cgc	ttc	atg	787				
Arg	Glu	Thr	Ile	Asp	Gly	Ser	Pro	Glu	Ile	Ser	Leu	Val	Arg	Phe	Met					
	215					220				225										
cct	ggt	cgc	acc	cgc	ctg	tac	gga	aac	ctc	tct	ttc	atc	ggt	gca	atc	835				
Pro	Gly	Arg	Thr	Arg	Leu	Tyr	Gly	Asn	Leu	Ser	Phe	Ile	Gly	Ala	Ile					
230					235					240					245					
ctt	aag	gac	ctg	ggg	ctt	tct	cgc	cca	gag	atc	caa	aat	atc	gac	gat	883				
Leu	Lys	Asp	Leu	Gly	Leu	Ser	Arg	Pro	Glu	Ile	Gln	Asn	Ile	Asp	Asp					
			250					255					260							
ctt	gcc	gtg	gag	atc	tcc	ccc	gaa	aac	atc	acc	gat	gcc	aac	ggc	gac	931				
Leu	Ala	Val	Glu	Ile	Ser	Pro	Glu	Asn	Ile	Thr	Asp	Ala	Asn	Gly	Asp					
			265				270						275							
tgg	att	ttc	tac	tcc	acc	tac	ggc	aag	ccc	gag	gcc	acc	gag	cag	gac	979				
Trp	Ile	Phe	Tyr	Ser	Thr	Tyr	Gly	Lys	Pro	Glu	Ala	Thr	Glu	Gln	Asp					
		280					285					290								
aac	att	ttg	tcc	aac	gag	ctg	tgg	cac	aac	ctt	ccc	cgc	cgt	cca	aga	1027				
Asn	Ile	Leu	Ser	Asn	Glu	Leu	Trp	His	Asn	Leu	Pro	Arg	Arg	Pro	Arg					
	295				300					305										
agg	tca	tgc	cct	gga	ggg	caa	tgacgagagc	tggttc	catgg	ggg						1071				
Arg	Ser	Cys	Pro	Gly	Gly	Gln														
310					315															

<210> 350

<211> 316

<212> PRT

<213> Corynebacterium glutamicum

<400> 350

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Met Gln Ser Ile Arg Thr Thr Phe Arg Ser Leu Ser Arg Ser Ala Val
 1             5             10             15

Ile Val Gly Thr Val Leu Ala Leu Gly Ile Ala Gly Cys Ser Thr Ala
      20             25             30

Ser Asp Glu Ala Thr Ser Thr Ser Asp Asp Val Ala Val Gly Gly Arg
      35             40             45

Leu Phe Ser Thr Ala Asp Ser Ala Thr Ala Ala Leu Gly Ser Asp Ala
 50             55             60

Glu Pro Gly Gln Phe Pro Arg Thr Val Val His Ser Arg Gly Glu Thr
 65             70             75             80

Thr Leu Glu Gln Gln Pro Gln Arg Val Val Val Leu Asp Ser Gly Glu
      85             90             95

Ile Asp Gln Val Leu Ser Leu Gly Val Thr Pro Val Gly Ile Ala Ser
      100             105             110

Pro Lys Asp Ala Ser Ser Gln Pro Ala Tyr Leu Glu Asn Gln Leu Ala
      115             120             125

Asp Val Gln Thr Val Gly Thr Thr Ser Glu Leu Asn Phe Glu Ala Ile
      130             135             140

Ala Ala Leu Lys Pro Asp Leu Ile Leu Gly Ser Lys Leu Arg Val Asp
 145             150             155             160

Glu Ser Tyr Asp Gln Leu Ser Gln Ile Ala Pro Thr Val Leu Ser Ile
      165             170             175

Arg Pro Gly Phe Pro Trp Lys Glu Asn Phe Leu Leu Thr Ala Asp Ala
      180             185             190

Leu Gly Leu Glu Gly Lys Ala Val Glu Val Leu Asn Glu Tyr Gln Thr
      195             200             205

His Val Asp Ala Val Arg Glu Thr Ile Asp Gly Ser Pro Glu Ile Ser
      210             215             220

Leu Val Arg Phe Met Pro Gly Arg Thr Arg Leu Tyr Gly Asn Leu Ser
 225             230             235             240

Phe Ile Gly Ala Ile Leu Lys Asp Leu Gly Leu Ser Arg Pro Glu Ile
      245             250             255

Gln Asn Ile Asp Asp Leu Ala Val Glu Ile Ser Pro Glu Asn Ile Thr
      260             265             270

Asp Ala Asn Gly Asp Trp Ile Phe Tyr Ser Thr Tyr Gly Lys Pro Glu
      275             280             285

Ala Thr Glu Gln Asp Asn Ile Leu Ser Asn Glu Leu Trp His Asn Leu
      290             295             300

```

Pro Arg Arg Pro Arg Arg Ser Cys Pro Gly Gly Gln
 305 310 315

<210> 351
 <211> 915
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(892)
 <223> RXA02052

<400> 351
 cctcggcgtc gcactccttc taagctcctg ttcttcaaca tcttccgatg aatcaatcca 60
 acctgaagtt gccagcactg gatattcagt ggagcacgca atg ggc acc acc gaa 115
 Met Gly Thr Thr Glu
 1 5
 atc cct gaa acc cca acg cgt gtg gtc gtc att gat tcc cca cac ctc 163
 Ile Pro Glu Thr Pro Thr Arg Val Val Val Ile Asp Ser Pro His Leu
 10 15 20
 gac gca ctt ttg gct ttg gga att act cca gtc gga gct acg gaa tct 211
 Asp Ala Leu Leu Ala Leu Gly Ile Thr Pro Val Gly Ala Thr Glu Ser
 25 30 35
 gga tcc gaa aat ggt ttc ccc gcc tac ttg gct gac gag cta aaa gac 259
 Gly Ser Glu Asn Gly Phe Pro Ala Tyr Leu Ala Asp Glu Leu Lys Asp
 40 45 50
 acc gaa tct gtt ggg ctg aca tct gag cca aat ttg gaa aag atc gcc 307
 Thr Glu Ser Val Gly Leu Thr Ser Glu Pro Asn Leu Glu Lys Ile Ala
 55 60 65
 gca ctg gat ccg gat ttg atc att ggc gca aag gtc cgc cac gag gct 355
 Ala Leu Asp Pro Asp Leu Ile Ile Gly Ala Lys Val Arg His Glu Ala
 70 75 80 85
 att tat gat cag ctt tca gac atc gca cca acc gtg atg tcc gaa ggt 403
 Ile Tyr Asp Gln Leu Ser Asp Ile Ala Pro Thr Val Met Ser Glu Gly
 90 95 100
 tcc ggc aca aac tgg aat gaa cag gca gaa atc act gcg gca gca gta 451
 Ser Gly Thr Asn Trp Asn Glu Gln Ala Glu Ile Thr Ala Ala Ala Val
 105 110 115
 aac aag tct gat gag atg gac aaa ctg atc tca gac ttg gac acc cgt 499
 Asn Lys Ser Asp Glu Met Asp Lys Leu Ile Ser Asp Leu Asp Thr Arg
 120 125 130
 gcc aca gag ctt ggt gaa gag atc ggt gct gac gga caa acc gct tca 547
 Ala Thr Glu Leu Gly Glu Glu Ile Gly Ala Asp Gly Gln Thr Ala Ser
 135 140 145
 atg gtt cga ttc cgc acg gac aac ttc agg ctc tat ggt ccc gag acc 595
 Met Val Arg Phe Arg Thr Asp Asn Phe Arg Leu Tyr Gly Pro Glu Thr
 150 155 160 165

ttc tct ggt tca gtt ctg gaa caa gtt gga ttt gac ctg ggg gaa cgt 643
 Phe Ser Gly Ser Val Leu Glu Gln Val Gly Phe Asp Leu Gly Glu Arg
 170 175 180

 gat tgg aat gag tac tcc atg atg gag cta tcc tca gaa aac ttt ggg 691
 Asp Trp Asn Glu Tyr Ser Met Met Glu Leu Ser Ser Glu Asn Phe Gly
 185 190 195

 cag atc gat gga gac ctt att ttc tac acc atc cca gga tcc cct gaa 739
 Gln Ile Asp Gly Asp Leu Ile Phe Tyr Thr Ile Pro Gly Ser Pro Glu
 200 205 210

 gca acc act tat cca aag att tcc gaa ctg tgg gtt gat tca cca gca 787
 Ala Thr Thr Tyr Pro Lys Ile Ser Glu Leu Trp Val Asp Ser Pro Ala
 215 220 225

 gtt cgg caa ggt aga act tac gag ttt gaa gac gaa acc tgg atg gtc 835
 Val Arg Gln Gly Arg Thr Tyr Glu Phe Glu Asp Glu Thr Trp Met Val
 230 235 240 245

 ggc atc ggt gta tta ggt gcc aat gaa atc ttg gat gac ctg gaa gaa 883
 Gly Ile Gly Val Leu Gly Ala Asn Glu Ile Leu Asp Asp Leu Glu Glu
 250 255 260

 act ctg agc tagtttcctt taggccaagc aac 915
 Thr Leu Ser

<210> 352

<211> 264

<212> PRT

<213> Corynebacterium glutamicum

<400> 352

Met Gly Thr Thr Glu Ile Pro Glu Thr Pro Thr Arg Val Val Val Ile
 1 5 10 15

 Asp Ser Pro His Leu Asp Ala Leu Leu Ala Leu Gly Ile Thr Pro Val
 20 25 30

 Gly Ala Thr Glu Ser Gly Ser Glu Asn Gly Phe Pro Ala Tyr Leu Ala
 35 40 45

 Asp Glu Leu Lys Asp Thr Glu Ser Val Gly Leu Thr Ser Glu Pro Asn
 50 55 60

 Leu Glu Lys Ile Ala Ala Leu Asp Pro Asp Leu Ile Ile Gly Ala Lys
 65 70 75 80

 Val Arg His Glu Ala Ile Tyr Asp Gln Leu Ser Asp Ile Ala Pro Thr
 85 90 95

 Val Met Ser Glu Gly Ser Gly Thr Asn Trp Asn Glu Gln Ala Glu Ile
 100 105 110

 Thr Ala Ala Ala Val Asn Lys Ser Asp Glu Met Asp Lys Leu Ile Ser
 115 120 125

 Asp Leu Asp Thr Arg Ala Thr Glu Leu Gly Glu Glu Ile Gly Ala Asp
 130 135 140

Gly Gln Thr Ala Ser Met Val Arg Phe Arg Thr Asp Asn Phe Arg Leu
 145 150 155 160
 Tyr Gly Pro Glu Thr Phe Ser Gly Ser Val Leu Glu Gln Val Gly Phe
 165 170 175
 Asp Leu Gly Glu Arg Asp Trp Asn Glu Tyr Ser Met Met Glu Leu Ser
 180 185 190
 Ser Glu Asn Phe Gly Gln Ile Asp Gly Asp Leu Ile Phe Tyr Thr Ile
 195 200 205
 Pro Gly Ser Pro Glu Ala Thr Thr Tyr Pro Lys Ile Ser Glu Leu Trp
 210 215 220
 Val Asp Ser Pro Ala Val Arg Gln Gly Arg Thr Tyr Glu Phe Glu Asp
 225 230 235 240
 Glu Thr Trp Met Val Gly Ile Gly Val Leu Gly Ala Asn Glu Ile Leu
 245 250 255
 Asp Asp Leu Glu Glu Thr Leu Ser
 260

<210> 353
 <211> 1200
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1177)
 <223> RXA00372

<400> 353
 gcagacattt ccataagtcc tgcgaaatgc gccattcat gtaaagatgt tatttcctcc 60

cccaaacact ccttaaaatt tcaagaaggg cottattttc atg tct tcg aag cac 115
 Met Ser Ser Lys His
 1 5

cct ttg aag cgc act gcc gtt act gtt ttt gca ctc ggc gct tcc gct 163
 Pro Leu Lys Arg Thr Ala Val Thr Val Phe Ala Leu Gly Ala Ser Ala
 10 15 20

gct ctc ctc gtg gct tgc tct gaa cct tct gag gac gtt tcc acc gca 211
 Ala Leu Leu Val Ala Cys Ser Glu Pro Ser Glu Asp Val Ser Thr Ala
 25 30 35

gag acc acc act gca agc tct tcc gct aac gca tcc gat gca gcc ggt 259
 Glu Thr Thr Thr Ala Ser Ser Ser Ala Asn Ala Ser Asp Ala Ala Gly
 40 45 50

gaa aaa gta acc atc acc gtc tac acc tct gag cct gag gaa aag gtc 307
 Glu Lys Val Thr Ile Thr Val Tyr Thr Ser Glu Pro Glu Glu Lys Val
 55 60 65

gat gag atc aac aag gcg ttc atg gaa gcc aac cca gat att gag gtt 355
 Asp Glu Ile Asn Lys Ala Phe Met Glu Ala Asn Pro Asp Ile Glu Val

70	75	80	85	
gag gtg tac cgc gct ggt act ggc gat ctg act gct cgc att gaa gct	403			
Glu Val Tyr Arg Ala Gly Thr Gly Asp Leu Thr Ala Arg Ile Glu Ala				
90 95 100				
gaa aag gca tcc ggt tct atc gag gct gat gtg ttg tgg gct gcg gat	451			
Glu Lys Ala Ser Gly Ser Ile Glu Ala Asp Val Leu Trp Ala Ala Asp				
105 110 115				
gct gca acc ttt gaa act tat gca gca cag ggc gac ctt gca gag ctg	499			
Ala Ala Thr Phe Glu Thr Tyr Ala Ala Gln Gly Asp Leu Ala Glu Leu				
120 125 130				
gaa gat gtt gag act tcc gac atc att gaa gag gct ctg gat gct gag	547			
Glu Asp Val Glu Thr Ser Asp Ile Ile Glu Glu Ala Leu Asp Ala Glu				
135 140 145				
aac ttt tat gta ggc acc cgc atc atc cca acc gtg att gca tac aac	595			
Asn Phe Tyr Val Gly Thr Arg Ile Ile Pro Thr Val Ile Ala Tyr Asn				
150 155 160 165				
act gaa gtt gtt gat cag gct gag ctt cct acg tct tgg gct gat ctg	643			
Thr Glu Val Val Asp Gln Ala Glu Leu Pro Thr Ser Trp Ala Asp Leu				
170 175 180				
act gat cct aag tat gca ggc caa ctg gtc atg ccg gat cca gct gtg	691			
Thr Asp Pro Lys Tyr Ala Gly Gln Leu Val Met Pro Asp Pro Ala Val				
185 190 195				
tct ggt gct gca gcc ttc aat gct tct gtg tgg aag aac gac cct gcg	739			
Ser Gly Ala Ala Ala Phe Asn Ala Ser Val Trp Lys Asn Asp Pro Ala				
200 205 210				
ctt ggc gaa gcc tgg atc acc gcc ttg ggt gaa aac caa cca atg atc	787			
Leu Gly Glu Ala Trp Ile Thr Ala Leu Gly Glu Asn Gln Pro Met Ile				
215 220 225				
gct cag tcc aac ggc cca acc tcc cag gag atc gct ggc ggt ggc cac	835			
Ala Gln Ser Asn Gly Pro Thr Ser Gln Glu Ile Ala Gly Gly Gly His				
230 235 240 245				
cca gtg ggc atc gtg gtg gac tac ttg gtg cgc gac ttg gct gct gct	883			
Pro Val Gly Ile Val Val Asp Tyr Leu Val Arg Asp Leu Ala Ala Ala				
250 255 260				
gga tct cca atc gac acc atc tac gca tcg gag ggt tct cct tac atc	931			
Gly Ser Pro Ile Asp Thr Ile Tyr Ala Ser Glu Gly Ser Pro Tyr Ile				
265 270 275				
act gag cct gca ggt gtg ttc gct gat tct gaa aag aag gaa gca gcc	979			
Thr Glu Pro Ala Gly Val Phe Ala Asp Ser Glu Lys Lys Glu Ala Ala				
280 285 290				
gag cgc tac atc aac ttc ctg ctg tct gtt gaa ggc cag gaa atc gca	1027			
Glu Arg Tyr Ile Asn Phe Leu Leu Ser Val Glu Gly Gln Glu Ile Ala				
295 300 305				
gtt gag cag gca tac ctg cca gtg cgt gaa gat gtc gga act cca gag	1075			
Val Glu Gln Ala Tyr Leu Pro Val Arg Glu Asp Val Gly Thr Pro Glu				
310 315 320 325				

ggc acc ccc gag ttg gct gac atc gag ctc atg acc cct gac ctg gag 1123
 Gly Thr Pro Glu Leu Ala Asp Ile Glu Leu Met Thr Pro Asp Leu Glu
 330 335 340

gtt gta acc gct gat aag gcg gct gct gtt gag ttc ttc caa aac gca 1171
 Val Val Thr Ala Asp Lys Ala Ala Val Glu Phe Phe Gln Asn Ala
 345 350 355

atg aac tagttttcct atgcagttat ctc 1200
 Met Asn

<210> 354

<211> 359

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 354

Met Ser Ser Lys His Pro Leu Lys Arg Thr Ala Val Thr Val Phe Ala
 1 5 10 15

Leu Gly Ala Ser Ala Ala Leu Leu Val Ala Cys Ser Glu Pro Ser Glu
 20 25 30

Asp Val Ser Thr Ala Glu Thr Thr Thr Ala Ser Ser Ser Ala Asn Ala
 35 40 45

Ser Asp Ala Ala Gly Glu Lys Val Thr Ile Thr Val Tyr Thr Ser Glu
 50 55 60

Pro Glu Glu Lys Val Asp Glu Ile Asn Lys Ala Phe Met Glu Ala Asn
 65 70 75 80

Pro Asp Ile Glu Val Glu Val Tyr Arg Ala Gly Thr Gly Asp Leu Thr
 85 90 95

Ala Arg Ile Glu Ala Glu Lys Ala Ser Gly Ser Ile Glu Ala Asp Val
 100 105 110

Leu Trp Ala Ala Asp Ala Ala Thr Phe Glu Thr Tyr Ala Ala Gln Gly
 115 120 125

Asp Leu Ala Glu Leu Glu Asp Val Glu Thr Ser Asp Ile Ile Glu Glu
 130 135 140

Ala Leu Asp Ala Glu Asn Phe Tyr Val Gly Thr Arg Ile Ile Pro Thr
 145 150 155 160

Val Ile Ala Tyr Asn Thr Glu Val Val Asp Gln Ala Glu Leu Pro Thr
 165 170 175

Ser Trp Ala Asp Leu Thr Asp Pro Lys Tyr Ala Gly Gln Leu Val Met
 180 185 190

Pro Asp Pro Ala Val Ser Gly Ala Ala Ala Phe Asn Ala Ser Val Trp
 195 200 205

Lys Asn Asp Pro Ala Leu Gly Glu Ala Trp Ile Thr Ala Leu Gly Glu
 210 215 220

Asn Gln Pro Met Ile Ala Gln Ser Asn Gly Pro Thr Ser Gln Glu Ile
 225 230 235 240
 Ala Gly Gly Gly His Pro Val Gly Ile Val Val Asp Tyr Leu Val Arg
 245 250 255
 Asp Leu Ala Ala Ala Gly Ser Pro Ile Asp Thr Ile Tyr Ala Ser Glu
 260 265 270
 Gly Ser Pro Tyr Ile Thr Glu Pro Ala Gly Val Phe Ala Asp Ser Glu
 275 280 285
 Lys Lys Glu Ala Ala Glu Arg Tyr Ile Asn Phe Leu Leu Ser Val Glu
 290 295 300
 Gly Gln Glu Ile Ala Val Glu Gln Ala Tyr Leu Pro Val Arg Glu Asp
 305 310 315 320
 Val Gly Thr Pro Glu Gly Thr Pro Glu Leu Ala Asp Ile Glu Leu Met
 325 330 335
 Thr Pro Asp Leu Glu Val Val Thr Ala Asp Lys Ala Ala Ala Val Glu
 340 345 350
 Phe Phe Gln Asn Ala Met Asn
 355

<210> 355
 <211> 1137
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1114)
 <223> RXA00088

<400> 355
 gctgtgttac tttcatcttt aggtaaccta cctcactaa agctctggga atactctggc 60

agttttggtg gattatcttt atagactttc aaaggacgac atg gtg aaa aac cga 115
 Met Val Lys Asn Arg
 1 5

ttc aag cta gtt tca atc gca act gtt gcg gcc ctg gcg ctc gtt ggc 163
 Phe Lys Leu Val Ser Ile Ala Thr Val Ala Ala Leu Ala Leu Val Gly
 10 15 20

tgc tct tcc acc gac agc acc tct tcc gag tct tct tcc gct gca gag 211
 Cys Ser Ser Thr Asp Ser Thr Ser Ser Glu Ser Ser Ser Ala Ala Glu
 25 30 35

tca acc gct gca gct agc acc ctg act atc gaa gac aac cac ggc acc 259
 Ser Thr Ala Ala Ala Ser Thr Leu Thr Ile Glu Asp Asn His Gly Thr
 40 45 50

gaa ggg atc tcc ctg cca atc gag ggc gtc gct gcg acc gac aac cgc 307
 Glu Gly Ile Ser Leu Pro Ile Glu Gly Val Ala Thr Asp Asn Arg
 55 60 65

gca ttc gaa ctg ctt gat cgc tgg ggt gta gag ctc gtt gca gct cca	355
Ala Phe Glu Leu Leu Asp Arg Trp Gly Val Glu Leu Val Ala Ala Pro	
70 75 80 85	
ctt cag ctg gtt cca ttt acc gtt acg ggc tac acc gaa gag ggc ggc	403
Leu Gln Leu Val Pro Phe Thr Val Thr Gly Tyr Thr Glu Glu Gly Gly	
90 95 100	
gtc gct aac ctt ggc tcc cac cgc gag cca gac ctg gaa gca ctt gct	451
Val Ala Asn Leu Gly Ser His Arg Glu Pro Asp Leu Glu Ala Leu Ala	
105 110 115	
gct gca cag cct tcc ctg atc atc aac ggc cag cgc ttc gct cag tac	499
Ala Ala Gln Pro Ser Leu Ile Ile Asn Gly Gln Arg Phe Ala Gln Tyr	
120 125 130	
tac gat gac atc att gcc ctg aac cct gac gca acc gtt gtt gag cta	547
Tyr Asp Asp Ile Ile Ala Leu Asn Pro Asp Ala Thr Val Val Glu Leu	
135 140 145	
gac cca cgc gat ggc gag cca ctt gac cag gag ctt atc cgc cag gct	595
Asp Pro Arg Asp Gly Glu Pro Leu Asp Gln Glu Leu Ile Arg Gln Ala	
150 155 160 165	
gaa acc ctc ggt gag atc ttc ggc gaa gaa gaa gat gct gca aag atc	643
Glu Thr Leu Gly Glu Ile Phe Gly Glu Glu Glu Asp Ala Ala Lys Ile	
170 175 180	
gtt gct gat ttc gag tcc gca ctt gag cgc gct aag acc gca tac gca	691
Val Ala Asp Phe Glu Ser Ala Leu Glu Arg Ala Lys Thr Ala Tyr Ala	
185 190 195	
gca atc tcc gac cag acc gtc atg gca gtt aac gtt tcc ggc gga aac	739
Ala Ile Ser Asp Gln Thr Val Met Ala Val Asn Val Ser Gly Gly Asn	
200 205 210	
att ggc tac atc gct cct tcc gtt gga cgc acc tac ggt cca atc ttc	787
Ile Gly Tyr Ile Ala Pro Ser Val Gly Arg Thr Tyr Gly Pro Ile Phe	
215 220 225	
gac ctg gtt gga ctc acc cca gca ctc gag gtt ggc aac gcg tcc tcc	835
Asp Leu Val Gly Leu Thr Pro Ala Leu Glu Val Gly Asn Ala Ser Ser	
230 235 240 245	
gac cac gag ggc gac gac att aac gtc gaa gca atc gca gct gca aac	883
Asp His Glu Gly Asp Asp Ile Asn Val Glu Ala Ile Ala Ala Ala Asn	
250 255 260	
cca gac ctg atc ctg gtc atg gac cgc gat ggt ggc acc agc acc cgc	931
Pro Asp Leu Ile Leu Val Met Asp Arg Asp Gly Gly Thr Ser Thr Arg	
265 270 275	
aac gaa gct gat tac gtt cca gca gag cag atc gtc tcc gac aat gaa	979
Asn Glu Ala Asp Tyr Val Pro Ala Glu Gln Ile Val Ser Asp Asn Glu	
280 285 290	
gca ctg gca aac gtc aag gct gtc acc gac gga tac gtt tac tac gca	1027
Ala Leu Ala Asn Val Lys Ala Val Thr Asp Gly Tyr Val Tyr Tyr Ala	
295 300 305	

cct gca gat acc tac acc aac gaa aac atc atc acc tac acc gag atc 1075
 Pro Ala Asp Thr Tyr Thr Asn Glu Asn Ile Ile Thr Tyr Thr Glu Ile
 310 315 320 325

ctc aac ggc atg gca gat atg ttc gag aag gca gct cag taggggatcg 1124
 Leu Asn Gly Met Ala Asp Met Phe Glu Lys Ala Ala Gln
 330 335

atccacact gac 1137

<210> 356

<211> 338

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 356

Met Val Lys Asn Arg Phe Lys Leu Val Ser Ile Ala Thr Val Ala Ala
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Leu Ala Leu Val Gly Cys Ser Ser Thr Asp Ser Thr Ser Ser Glu Ser
 20 25 30

Ser Ser Ala Ala Glu Ser Thr Ala Ala Ala Ser Thr Leu Thr Ile Glu
 35 40 45

Asp Asn His Gly Thr Glu Gly Ile Ser Leu Pro Ile Glu Gly Val Ala
 50 55 60

Ala Thr Asp Asn Arg Ala Phe Glu Leu Leu Asp Arg Trp Gly Val Glu
 65 70 75 80

Leu Val Ala Ala Pro Leu Gln Leu Val Pro Phe Thr Val Thr Gly Tyr
 85 90 95

Thr Glu Glu Gly Gly Val Ala Asn Leu Gly Ser His Arg Glu Pro Asp
 100 105 110

Leu Glu Ala Leu Ala Ala Ala Gln Pro Ser Leu Ile Ile Asn Gly Gln
 115 120 125

Arg Phe Ala Gln Tyr Tyr Asp Asp Ile Ile Ala Leu Asn Pro Asp Ala
 130 135 140

Thr Val Val Glu Leu Asp Pro Arg Asp Gly Glu Pro Leu Asp Gln Glu
 145 150 155 160

Leu Ile Arg Gln Ala Glu Thr Leu Gly Glu Ile Phe Gly Glu Glu Glu
 165 170 175

Asp Ala Ala Lys Ile Val Ala Asp Phe Glu Ser Ala Leu Glu Arg Ala
 180 185 190

Lys Thr Ala Tyr Ala Ala Ile Ser Asp Gln Thr Val Met Ala Val Asn
 195 200 205

Val Ser Gly Gly Asn Ile Gly Tyr Ile Ala Pro Ser Val Gly Arg Thr
 210 215 220

Tyr Gly Pro Ile Phe Asp Leu Val Gly Leu Thr Pro Ala Leu Glu Val
 225 230 235 240

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<210> 357
<211> 1233
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
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<222> (101)..(1210)  
<223> RXS00156
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<400> 357
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tttttatgca atatcaacca aaagttaggta cgatcctcat atg aat gaa cgc aca 115
Met Asn Glu Arg Thr
1 5

tcg	gat	gca	ttt	gac	gcc	ctc	ctt	gtg	ctc	tcc	ttc	ggg	ggg	ccc	gaa	163
Ser	Asp	Ala	Phe	Asp	Ala	Leu	Leu	Val	Leu	Ser	Phe	Gly	Gly	Pro	Glu	
				10					15					20		

ggg cac gag gag gtt cgt ccg ttt ttg gag aat gtc act cac gga agg 211
Gly His Glu Glu Val Arg Pro Phe Leu Glu Asn Val Thr His Gly Arg
25 30 35

ggg att ccg ccg gaa cgt cta gat gaa gtg gcg gtt cat tac cac cac 259
Gly Ile Pro Pro Glu Arg Leu Asp Glu Val Ala Val His Tyr His His
40 45 50

ttc ggt ggt atc agc ccc atc aat gcg ctg aac agg gaa att atc gcc 307
Phe Gly Gly Ile Ser Pro Ile Asn Ala Leu Asn Arg Glu Ile Ile Ala
55 60 65

aat	gtg	gaa	aaa	gaa	ttg	gcg	tct	cgc	gat	cac	aag	ctg	cct	gtt	tat	355
Asn	Val	Glu	Lys	Glu	Leu	Ala	Ser	Arg	Asp	His	Lys	Leu	Pro	Val	Tyr	
70					75					80					85	

ttt ggt aac cgc aac tgg aag ccg ttt gat aat gag gcc gct gaa caa 403

Phe	Gly	Asn	Arg	Asn	Trp	Lys	Pro	Phe	Asp	Asn	Glu	Ala	Ala	Glu	Gln	
				90					95					100		
atg	gct	gat	gac	ggc	gtg	aaa	aac	gcg	ctg	gtg	ttg	gca	act	tcc	gct	451
Met	Ala	Asp	Asp	Gly	Val	Lys	Asn	Ala	Leu	Val	Leu	Ala	Thr	Ser	Ala	
			105					110					115			
tgg	ggt	ggc	tac	tcc	ggt	tgt	cgg	cag	tac	cag	gaa	gat	att	cag	ggc	499
Trp	Gly	Gly	Tyr	Ser	Gly	Cys	Arg	Gln	Tyr	Gln	Glu	Asp	Ile	Gln	Gly	
		120					125					130				
atg	atc	aag	cac	ctg	gag	tct	cag	ggg	cag	tcg	atc	acg	ttc	acc	aag	547
Met	Ile	Lys	His	Leu	Glu	Ser	Gln	Gly	Gln	Ser	Ile	Thr	Phe	Thr	Lys	
	135					140					145					
ctg	cgt	cag	ttc	tac	gat	cac	cct	cgt	ttt	gtc	tcc	acc	atg	gct	caa	595
Leu	Arg	Gln	Phe	Tyr	Asp	His	Pro	Arg	Phe	Val	Ser	Thr	Met	Ala	Gln	
150					155					160					165	
ttg	gtt	cag	gat	tcc	tac	gcg	aag	ctt	ccc	gat	gag	ctg	cga	gat	gag	643
Leu	Val	Gln	Asp	Ser	Tyr	Ala	Lys	Leu	Pro	Asp	Glu	Leu	Arg	Asp	Glu	
				170					175					180		
gcg	cgt	ctg	gtc	ttc	acc	gcg	cac	tcc	att	cca	ctg	act	gcg	gac	aat	691
Ala	Arg	Leu	Val	Phe	Thr	Ala	His	Ser	Ile	Pro	Leu	Thr	Ala	Asp	Asn	
			185					190					195			
gct	gcg	gga	acc	cct	gag	gat	ggc	tcc	ttg	tat	tcc	aca	cag	gtc	aag	739
Ala	Ala	Gly	Thr	Pro	Glu	Asp	Gly	Ser	Leu	Tyr	Ser	Thr	Gln	Val	Lys	
		200					205					210				
gaa	gcg	tca	gca	ctg	att	gct	gag	gct	gtt	ggt	gtg	tca	gat	ttt	gat	787
Glu	Ala	Ser	Ala	Leu	Ile	Ala	Glu	Ala	Val	Gly	Val	Ser	Asp	Phe	Asp	
	215					220					225					
gtg	gtg	tgg	cag	tcc	cgc	tcg	ggt	agc	ccg	cac	act	ccg	tgg	ctg	gag	835
Val	Val	Trp	Gln	Ser	Arg	Ser	Gly	Ser	Pro	His	Thr	Pro	Trp	Leu	Glu	
230					235					240				245		
cct	gac	atc	gtg	gat	cac	gca	gtg	gag	ctc	aac	gag	aag	ggt	caa	aaa	883
Pro	Asp	Ile	Val	Asp	His	Ala	Val	Glu	Leu	Asn	Glu	Lys	Gly	Gln	Lys	
				250				255						260		
gcg	ctc	gtt	gtc	tgc	cct	gta	ggc	ttt	att	tct	gat	cat	atg	gaa	gtc	931
Ala	Leu	Val	Val	Cys	Pro	Val	Gly	Phe	Ile	Ser	Asp	His	Met	Glu	Val	
			265					270					275			
att	tgg	gat	ctt	gat	tcc	gag	ctg	atg	gaa	gaa	gcc	gag	aag	cgc	aac	979
Ile	Trp	Asp	Leu	Asp	Ser	Glu	Leu	Met	Glu	Glu	Ala	Glu	Lys	Arg	Asn	
		280					285					290				
atg	gtg	gtc	gag	cgt	gtc	gct	acc	gtt	ggc	ccc	acc	gat	gaa	ttc	gca	1027
Met	Val	Val	Glu	Arg	Val	Ala	Thr	Val	Gly	Pro	Thr	Asp	Glu	Phe	Ala	
	295					300					305					
gcc	ctt	gtg	gtt	gat	ctc	atc	gag	gag	gca	gag	ctc	aag	cgc	gtt	atc	1075
Ala	Leu	Val	Val	Asp	Leu	Ile	Glu	Glu	Ala	Glu	Leu	Lys	Arg	Val	Ile	
310					315					320					325	
gag	cgc	ctt	gga	aag	ctg	cca	gca	cgc	gga	agt	tcc	gtc	aac	ggc	gca	1123
Glu	Arg	Leu	Gly	Lys	Leu	Pro	Ala	Arg	Gly	Ser	Ser	Val	Asn	Gly	Ala	

	330	335	340	
ccg tgt ggc gac ggc tgc tgt ggt acc gcc aag cat aaa acc gcg cgg				1171
Pro Cys Gly Asp Gly Cys Cys Gly Thr Ala Lys His Lys Thr Ala Arg				
	345	350	355	
gtg aac ccc aac gct cgc tca gcg gcg cca gct gcc aac taggagtgat				1220
Val Asn Pro Asn Ala Arg Ser Ala Ala Pro Ala Ala Asn				
	360	365	370	
agtccctcgc aaa				1233

<210> 358

<211> 370

<212> PRT

<213> Corynebacterium glutamicum

<400> 358

Met Asn Glu Arg Thr Ser Asp Ala Phe Asp Ala Leu Leu Val Leu Ser	
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Phe Gly Gly Pro Glu Gly His Glu Glu Val Arg Pro Phe Leu Glu Asn	
20 25 30	

Val Thr His Gly Arg Gly Ile Pro Pro Glu Arg Leu Asp Glu Val Ala	
35 40 45	

Val His Tyr His His Phe Gly Gly Ile Ser Pro Ile Asn Ala Leu Asn	
50 55 60	

Arg Glu Ile Ile Ala Asn Val Glu Lys Glu Leu Ala Ser Arg Asp His	
65 70 75 80	

Lys Leu Pro Val Tyr Phe Gly Asn Arg Asn Trp Lys Pro Phe Asp Asn	
85 90 95	

Glu Ala Ala Glu Gln Met Ala Asp Asp Gly Val Lys Asn Ala Leu Val	
100 105 110	

Leu Ala Thr Ser Ala Trp Gly Gly Tyr Ser Gly Cys Arg Gln Tyr Gln	
115 120 125	

Glu Asp Ile Gln Gly Met Ile Lys His Leu Glu Ser Gln Gly Gln Ser	
130 135 140	

Ile Thr Phe Thr Lys Leu Arg Gln Phe Tyr Asp His Pro Arg Phe Val	
145 150 155 160	

Ser Thr Met Ala Gln Leu Val Gln Asp Ser Tyr Ala Lys Leu Pro Asp	
165 170 175	

Glu Leu Arg Asp Glu Ala Arg Leu Val Phe Thr Ala His Ser Ile Pro	
180 185 190	

Leu Thr Ala Asp Asn Ala Ala Gly Thr Pro Glu Asp Gly Ser Leu Tyr	
195 200 205	

Ser Thr Gln Val Lys Glu Ala Ser Ala Leu Ile Ala Glu Ala Val Gly	
210 215 220	

Val Ser Asp Phe Asp Val Val Trp Gln Ser Arg Ser Gly Ser Pro His
 225 230 235 240

Thr Pro Trp Leu Glu Pro Asp Ile Val Asp His Ala Val Glu Leu Asn
 245 250 255

Glu Lys Gly Gln Lys Ala Leu Val Val Cys Pro Val Gly Phe Ile Ser
 260 265 270

Asp His Met Glu Val Ile Trp Asp Leu Asp Ser Glu Leu Met Glu Glu
 275 280 285

Ala Glu Lys Arg Asn Met Val Val Glu Arg Val Ala Thr Val Gly Pro
 290 295 300

Thr Asp Glu Phe Ala Ala Leu Val Val Asp Leu Ile Glu Glu Ala Glu
 305 310 315 320

Leu Lys Arg Val Ile Glu Arg Leu Gly Lys Leu Pro Ala Arg Gly Ser
 325 330 335

Ser Val Asn Gly Ala Pro Cys Gly Asp Gly Cys Cys Gly Thr Ala Lys
 340 345 350

His Lys Thr Ala Arg Val Asn Pro Asn Ala Arg Ser Ala Ala Pro Ala
 355 360 365

Ala Asn
 370

<210> 359

<211> 810

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(787)

<223> RXS00624

<400> 359

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caacaggacg acaacggccg gacatgagac aatacaatgc atg tcc ggc cgt ctt 115
 Met Ser Gly Arg Leu
 1 5

ctt gtt tca gtt tct agt att ttc gac cag acc cga tcg gcg gct gac 163
 Leu Val Ser Val Ser Ser Ile Phe Asp Gln Thr Arg Ser Ala Ala Asp
 10 15 20

agg ctc att tca gac ctg cga gcc gac ggc atc gag gtc tca tta ctt 211
 Arg Leu Ile Ser Asp Leu Arg Ala Asp Gly Ile Glu Val Ser Leu Leu
 25 30 35

gtc gca ccc cgc atc gat ggg gac tgg cgt ctc gcc aaa gac aaa ggg 259
 Val Ala Pro Arg Ile Asp Gly Asp Trp Arg Leu Ala Lys Asp Lys Gly
 40 45 50

acc ctc gcg tgg atg gaa caa caa cgc gaa cgc ggc cac gaa ctc atc 307

Thr Leu Ala Trp Met Glu Gln Gln Arg Glu Arg Gly His Glu Leu Ile
 55 60 65
 ctc aac ggt ttc gac caa gca gtt cag gga cgt cgc tca gaa ttc gcc 355
 Leu Asn Gly Phe Asp Gln Ala Val Gln Gly Arg Arg Ser Glu Phe Ala
 70 75 80 85
 aac ctt gaa cgg cac gaa gca cgt ctt cgc ctt acc ggt gcc att agg 403
 Asn Leu Glu Arg His Glu Ala Arg Leu Arg Leu Thr Gly Ala Ile Arg
 90 95 100
 caa atg cag aaa att ggc ttc gaa ttc caa atc ttt gcc cca cct cgt 451
 Gln Met Gln Lys Ile Gly Phe Glu Phe Gln Ile Phe Ala Pro Pro Arg
 105 110 115
 tgg aga atg tca gaa ggc acc ttc gcg gta ctc cca gaa ttt gat ttc 499
 Trp Arg Met Ser Glu Gly Thr Phe Ala Val Leu Pro Glu Phe Asp Phe
 120 125 130
 aac gtc gcc gcc tcg acc agg gga tta cat aac ctc gac acc ggc gaa 547
 Asn Val Ala Ala Ser Thr Arg Gly Leu His Asn Leu Asp Thr Gly Glu
 135 140 145
 ttc ttg gcg tgt aga aac ctc tcc gtg ggt gaa ggt ttt ggt gct gca 595
 Phe Leu Ala Cys Arg Asn Leu Ser Val Gly Glu Gly Phe Gly Ala Ala
 150 155 160 165
 aaa tgg tgg cgc aag aat gtc atc aag gct gtc act cgt gga gcg gaa 643
 Lys Trp Trp Arg Lys Asn Val Ile Lys Ala Val Thr Arg Gly Ala Glu
 170 175 180
 aaa gga aat aca gtg cgc ttg tcc gca tcg gcg cga aat ctc acc aac 691
 Lys Gly Asn Thr Val Arg Leu Ser Ala Ser Ala Arg Asn Leu Thr Asn
 185 190 195
 cct aaa gtc gca gct gac ttc cgg gaa gct gca tta gct gcc ttg gat 739
 Pro Lys Val Ala Ala Asp Phe Arg Glu Ala Ala Leu Ala Ala Leu Asp
 200 205 210
 ttg ggt gct cag gtg caa acc tat tct cag gcg gcc gca caa ctg gcc 787
 Leu Gly Ala Gln Val Gln Thr Tyr Ser Gln Ala Ala Ala Gln Leu Ala
 215 220 225
 tagttgggga ggttcggggc acc 810

<210> 360

<211> 229

<212> PRT

<213> Corynebacterium glutamicum

<400> 360

Met Ser Gly Arg Leu Leu Val Ser Val Ser Ser Ile Phe Asp Gln Thr
 1 5 10 15

Arg Ser Ala Ala Asp Arg Leu Ile Ser Asp Leu Arg Ala Asp Gly Ile
 20 25 30

Glu Val Ser Leu Leu Val Ala Pro Arg Ile Asp Gly Asp Trp Arg Leu
 35 40 45

Ala Lys Asp Lys Gly Thr Leu Ala Trp Met Glu Gln Gln Arg Glu Arg
 50 55 60

Gly His Glu Leu Ile Leu Asn Gly Phe Asp Gln Ala Val Gln Gly Arg
 65 70 75 80

Arg Ser Glu Phe Ala Asn Leu Glu Arg His Glu Ala Arg Leu Arg Leu
 85 90 95

Thr Gly Ala Ile Arg Gln Met Gln Lys Ile Gly Phe Glu Phe Gln Ile
 100 105 110

Phe Ala Pro Pro Arg Trp Arg Met Ser Glu Gly Thr Phe Ala Val Leu
 115 120 125

Pro Glu Phe Asp Phe Asn Val Ala Ala Ser Thr Arg Gly Leu His Asn
 130 135 140

Leu Asp Thr Gly Glu Phe Leu Ala Cys Arg Asn Leu Ser Val Gly Glu
 145 150 155 160

Gly Phe Gly Ala Ala Lys Trp Trp Arg Lys Asn Val Ile Lys Ala Val
 165 170 175

Thr Arg Gly Ala Glu Lys Gly Asn Thr Val Arg Leu Ser Ala Ser Ala
 180 185 190

Arg Asn Leu Thr Asn Pro Lys Val Ala Ala Asp Phe Arg Glu Ala Ala
 195 200 205

Leu Ala Ala Leu Asp Leu Gly Ala Gln Val Gln Thr Tyr Ser Gln Ala
 210 215 220

Ala Ala Gln Leu Ala
 225

<210> 361
 <211> 1068
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1045)
 <223> RXA00024

<400> 361
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acgctcctat gctcggggca gtaagttgtg agcataggaa atg gag cac ggc gtg 115
 Met Glu His Gly Val
 1 5

acc gtt att aaa ggc act gaa ttt gat gtt ttc cca cta aac ctc ggt 163
 Thr Val Ile Lys Gly Thr Glu Phe Asp Val Phe Pro Leu Asn Leu Gly
 10 15 20

gga aat acc ttt ggc tgg acc tcg aat agg gaa cag acc ttc gcg gtt 211
 Gly Asn Thr Phe Gly Trp Thr Ser Asn Arg Glu Gln Thr Phe Ala Val
 25 30 35

ttg gat gca ttc gtg gca gcg gga gga aac ttt gtt gac acc gcc gat	259
Leu Asp Ala Phe Val Ala Ala Gly Gly Asn Phe Val Asp Thr Ala Asp	
40 45 50	
tct tat tct gca tgg gtt gaa ggc aat gag ggt ggc gag tcg gag cgg	307
Ser Tyr Ser Ser Ala Trp Val Glu Gly Asn Glu Gly Glu Ser Glu Arg	
55 60 65	
gag ctc ggc gcg tgg att aag gaa cgt ggc gca gac aag ctg atc att	355
Glu Leu Gly Ala Trp Ile Lys Glu Arg Gly Ala Asp Lys Leu Ile Ile	
70 75 80 85	
gct acc aag tct ggt gcg ttg gag cct gtt gct ggt cgt tcc cgt gag	403
Ala Thr Lys Ser Gly Ala Leu Glu Pro Val Ala Gly Arg Ser Arg Glu	
90 95 100	
gca act ttc aag gct gtc gag ggt tcc ctg gag cgt ttg ggc gtg gaa	451
Ala Thr Phe Lys Ala Val Glu Gly Ser Leu Glu Arg Leu Gly Val Glu	
105 110 115	
tcg atc gat att ttt tac tac cac tac gac gat gag gca gtc agc att	499
Ser Ile Asp Ile Phe Tyr Tyr His Tyr Asp Asp Glu Ala Val Ser Ile	
120 125 130	
gat gag cag gtt gct atc gct aat gat ctg att gca cag ggc aag att	547
Asp Glu Gln Val Ala Ile Ala Asn Asp Leu Ile Ala Gln Gly Lys Ile	
135 140 145	
aag cac ctc gca ttg tct aac tac agc gcg gag cgt tta gct gag ttc	595
Lys His Leu Ala Leu Ser Asn Tyr Ser Ala Glu Arg Leu Ala Glu Phe	
150 155 160 165	
ttt gag aag tct gta ggc act cca gcg cag ccg gtt gct ctg caa ccg	643
Phe Glu Lys Ser Val Gly Thr Pro Ala Gln Pro Val Ala Leu Gln Pro	
170 175 180	
cac tac aac ctg gtg tcg agg aag gat tat gag gag aac gtg cag cca	691
His Tyr Asn Leu Val Ser Arg Lys Asp Tyr Glu Glu Asn Val Gln Pro	
185 190 195	
ctc gcc gag aag cat ggc gtt gca gtc ttc cct tat ttc gcg ctt gcc	739
Leu Ala Glu Lys His Gly Val Ala Val Phe Pro Tyr Phe Ala Leu Ala	
200 205 210	
gcg ggt ctt ttg acc gga aag tac acc tcc aag gag gat att tcg ggt	787
Ala Gly Leu Leu Thr Gly Lys Tyr Thr Ser Lys Glu Asp Ile Ser Gly	
215 220 225	
aaa gcg cgt gcg ggg cag ttg gat cgt tac gcc agc gat gag gcg ttt	835
Lys Ala Arg Ala Gly Gln Leu Asp Arg Tyr Ala Ser Asp Glu Ala Phe	
230 235 240 245	
gcc gtg gtg aca gag ttg cgt gct gtt gcc gat gag ttg ggt gtt gcg	883
Ala Val Val Thr Glu Leu Arg Ala Val Ala Asp Glu Leu Gly Val Ala	
250 255 260	
cca acg act gtg gcg ctt gcg tgg ttg gtt gcg cat ggt gtg acc gca	931
Pro Thr Thr Val Ala Leu Ala Trp Leu Val Ala His Gly Val Thr Ala	
265 270 275	

Tyr Phe Ala Leu Ala Ala Gly Leu Leu Thr Gly Lys Tyr Thr Ser Lys
210 215 220

Glu Asp Ile Ser Gly Lys Ala Arg Ala Gly Gln Leu Asp Arg Tyr Ala
225 230 235 240

Ser Asp Glu Ala Phe Ala Val Val Thr Glu Leu Arg Ala Val Ala Asp
245 250 255

Glu Leu Gly Val Ala Pro Thr Thr Val Ala Leu Ala Trp Leu Val Ala
260 265 270

His Gly Val Thr Ala Pro Ile Ala Ser Val Ser Lys Val Glu Gln Leu
275 280 285

Lys Asp Leu Met Ala Val Lys Asp Val Glu Leu Ser Ala Glu Gln Leu
290 295 300

Ala Arg Leu Asp Lys Val Ser Glu Pro Phe Ala
305 310 315

<210> 363

<211> 1329

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1306)

<223> RXA02526

<400> 363

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tgcgagagaga gcactctcaa ctgctcaagc ccgccatggt gtg atc act gaa gac 115
Val Ile Thr Glu Asp
1 5

gat gct gca cag atc aac cag gcg gca gtc ctt tcc aac att gac cgc 163
Asp Ala Ala Gln Ile Asn Gln Ala Ala Val Leu Ser Asn Ile Asp Arg
10 15 20

gag aag ctg tgg gaa gat gcc aaa aat gtc ggc tac ccc atc ctt ggc 211
Glu Lys Leu Trp Glu Asp Ala Lys Asn Val Gly Tyr Pro Ile Leu Gly
25 30 35

ttg gta aga caa atc gcc agt cac ctt cca gaa ggc ccc aac ggg cga 259
Leu Val Arg Gln Ile Ala Ser His Leu Pro Glu Gly Pro Asn Gly Arg
40 45 50

gtc cac tac ggc gcc acg acc caa gtc atc atg gac act gga ctg gtg 307
Val His Tyr Gly Ala Thr Thr Gln Val Ile Met Asp Thr Gly Leu Val
55 60 65

ttg caa atg act gcc tct ttg aac gcc ctt gat aaa cag atc gtg cgt 355
Leu Gln Met Thr Ala Ser Leu Asn Ala Leu Asp Lys Gln Ile Val Arg
70 75 80 85

ctg ggg aat gca ctg gca gca cgg gct gaa gag cac aaa gac acc gtg 403
Leu Gly Asn Ala Leu Ala Ala Arg Ala Glu Glu His Lys Asp Thr Val
90 95 100

atg ccg gga cgc acc cat gct cag cag gca att ccc act aca ttt gga 451

Met	Pro	Gly	Arg	Thr	His	Ala	Gln	Gln	Ala	Ile	Pro	Thr	Thr	Phe	Gly		
			105					110					115				
gca	acc	ctc	gct	acc	ttt	ttg	gat	caa	atc	cgc	agg	cag	agg	gaa	cga	499	
Ala	Thr	Leu	Ala	Thr	Phe	Leu	Asp	Gln	Ile	Arg	Arg	Gln	Arg	Glu	Arg		
		120					125					130					
ctt	gag	gaa	gca	ctc	gag	cgc	gtg	cga	gtc	att	tcg	ctg	ttt	ggt	gct	547	
Leu	Glu	Glu	Ala	Leu	Glu	Arg	Val	Arg	Val	Ile	Ser	Leu	Phe	Gly	Ala		
	135					140					145						
ggt	gga	aac	aac	gca	gca	caa	ggc	gaa	caa	gcg	gca	acg	gtt	cgt	gca	595	
Gly	Gly	Asn	Asn	Ala	Ala	Gln	Gly	Glu	Gln	Ala	Ala	Thr	Val	Arg	Ala		
150					155					160					165		
gag	atg	gcc	cgc	ctg	ttg	gat	ctg	aag	gac	ccg	gtg	gtg	tca	tgg	cat	643	
Glu	Met	Ala	Arg	Leu	Leu	Asp	Leu	Lys	Asp	Pro	Val	Val	Ser	Trp	His		
				170					175					180			
gtg	gaa	cgc	gat	gtg	ctt	ggg	gac	ttc	gga	tgg	gtg	tgc	tca	acg	ctg	691	
Val	Glu	Arg	Asp	Val	Leu	Gly	Asp	Phe	Gly	Trp	Val	Cys	Ser	Thr	Leu		
			185					190					195				
tgt	gga	tcg	atg	gca	aaa	ttt	ggc	cga	aac	atc	gtg	gat	ctt	tcc	cga	739	
Cys	Gly	Ser	Met	Ala	Lys	Phe	Gly	Arg	Asn	Ile	Val	Asp	Leu	Ser	Arg		
		200					205					210					
act	gaa	atc	gga	gaa	gtt	ttt	gag	cct	tac	aac	tcc	cat	cgg	ggt	gca	787	
Thr	Glu	Ile	Gly	Glu	Val	Phe	Glu	Pro	Tyr	Asn	Ser	His	Arg	Gly	Ala		
	215					220					225						
tct	tcc	atg	atg	cct	cag	aaa	gtc	aac	ccg	att	tct	tcc	gag	ctc	atg	835	
Ser	Ser	Met	Met	Pro	Gln	Lys	Val	Asn	Pro	Ile	Ser	Ser	Glu	Leu	Met		
230					235					240					245		
att	ggt	att	tca	gtg	gtg	gcg	ggt	gcc	ttg	acc	tcg	act	ttg	cca	cgg	883	
Ile	Gly	Ile	Ser	Val	Val	Ala	Gly	Ala	Leu	Thr	Ser	Thr	Leu	Pro	Arg		
				250					255					260			
ctt	cag	gaa	tcg	gga	cat	gaa	cga	gca	gca	gga	gag	tgg	cag	gga	gaa	931	
Leu	Gln	Glu	Ser	Gly	His	Glu	Arg	Ala	Ala	Gly	Glu	Trp	Gln	Gly	Glu		
			265					270					275				
tgg	ctt	gtc	att	cca	acg	ttg	gcc	aat	cta	gct	ggc	gct	gca	ctc	gat	979	
Trp	Leu	Val	Ile	Pro	Thr	Leu	Ala	Asn	Leu	Ala	Gly	Ala	Ala	Leu	Asp		
		280					285					290					
gaa	gcc	att	gtg	gtg	gct	gaa	gga	atg	cga	gtg	gat	aca	gat	cgt	atg	1027	
Glu	Ala	Ile	Val	Val	Ala	Glu	Gly	Met	Arg	Val	Asp	Thr	Asp	Arg	Met		
	295					300					305						
tcc	tcg	aac	ttg	gct	ttt	gct	ggt	gga	ttg	atc	atg	gcg	gaa	gct	cag	1075	
Ser	Ser	Asn	Leu	Ala	Phe	Ala	Gly	Gly	Leu	Ile	Met	Ala	Glu	Ala	Gln		
310					315					320					325		
atg	att	caa	cta	gct	cca	gct	ctg	ggg	cgt	gag	aaa	gct	cat	gac	ttg	1123	
Met	Ile	Gln	Leu	Ala	Pro	Ala	Leu	Gly	Arg	Glu	Lys	Ala	His	Asp	Leu		
				330					335					340			
gtt	tat	gaa	gca	tcc	aca	aag	act	cgt	gaa	gag	cac	acc	acg	ctg	gca	1171	
Val	Tyr	Glu	Ala	Ser	Thr	Lys	Thr	Arg	Glu	Glu	His	Thr	Thr	Leu	Ala		

345	350	355	
gaa gaa ctg ccg ata att gca gtt caa cat ggg gtc gaa gac ctg ttg			1219
Glu Glu Leu Pro Ile Ile Ala Val Gln His Gly Val Glu Asp Leu Leu			
360	365	370	
cct aag aat ttt gcg cag cct gca gac tac gtc ggc gaa gca caa tcc			1267
Pro Lys Asn Phe Ala Gln Pro Ala Asp Tyr Val Gly Glu Ala Gln Ser			
375	380	385	
atg gtg aat gca gct gtc gcc gcc tgg aat gcc caa ctt taacaaccca			1316
Met Val Asn Ala Ala Val Ala Ala Trp Asn Ala Gln Leu			
390	395	400	
aaactttaac aac			1329

<210> 364

<211> 402

<212> PRT

<213> Corynebacterium glutamicum

<400> 364

Val Ile Thr Glu Asp Asp Ala Ala Gln Ile Asn Gln Ala Ala Val Leu			
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Ser Asn Ile Asp Arg Glu Lys Leu Trp Glu Asp Ala Lys Asn Val Gly			
20	25	30	
Tyr Pro Ile Leu Gly Leu Val Arg Gln Ile Ala Ser His Leu Pro Glu			
35	40	45	
Gly Pro Asn Gly Arg Val His Tyr Gly Ala Thr Thr Gln Val Ile Met			
50	55	60	
Asp Thr Gly Leu Val Leu Gln Met Thr Ala Ser Leu Asn Ala Leu Asp			
65	70	75	80
Lys Gln Ile Val Arg Leu Gly Asn Ala Leu Ala Ala Arg Ala Glu Glu			
85	90	95	
His Lys Asp Thr Val Met Pro Gly Arg Thr His Ala Gln Gln Ala Ile			
100	105	110	
Pro Thr Thr Phe Gly Ala Thr Leu Ala Thr Phe Leu Asp Gln Ile Arg			
115	120	125	
Arg Gln Arg Glu Arg Leu Glu Glu Ala Leu Glu Arg Val Arg Val Ile			
130	135	140	
Ser Leu Phe Gly Ala Gly Gly Asn Asn Ala Ala Gln Gly Glu Gln Ala			
145	150	155	160
Ala Thr Val Arg Ala Glu Met Ala Arg Leu Leu Asp Leu Lys Asp Pro			
165	170	175	
Val Val Ser Trp His Val Glu Arg Asp Val Leu Gly Asp Phe Gly Trp			
180	185	190	
Val Cys Ser Thr Leu Cys Gly Ser Met Ala Lys Phe Gly Arg Asn Ile			
195	200	205	

Val Asp Leu Ser Arg Thr Glu Ile Gly Glu Val Phe Glu Pro Tyr Asn
 210 215 220
 Ser His Arg Gly Ala Ser Ser Met Met Pro Gln Lys Val Asn Pro Ile
 225 230 235 240
 Ser Ser Glu Leu Met Ile Gly Ile Ser Val Val Ala Gly Ala Leu Thr
 245 250 255
 Ser Thr Leu Pro Arg Leu Gln Glu Ser Gly His Glu Arg Ala Ala Gly
 260 265 270
 Glu Trp Gln Gly Glu Trp Leu Val Ile Pro Thr Leu Ala Asn Leu Ala
 275 280 285
 Gly Ala Ala Leu Asp Glu Ala Ile Val Val Ala Glu Gly Met Arg Val
 290 295 300
 Asp Thr Asp Arg Met Ser Ser Asn Leu Ala Phe Ala Gly Gly Leu Ile
 305 310 315 320
 Met Ala Glu Ala Gln Met Ile Gln Leu Ala Pro Ala Leu Gly Arg Glu
 325 330 335
 Lys Ala His Asp Leu Val Tyr Glu Ala Ser Thr Lys Thr Arg Glu Glu
 340 345 350
 His Thr Thr Leu Ala Glu Glu Leu Pro Ile Ile Ala Val Gln His Gly
 355 360 365
 Val Glu Asp Leu Leu Pro Lys Asn Phe Ala Gln Pro Ala Asp Tyr Val
 370 375 380
 Gly Glu Ala Gln Ser Met Val Asn Ala Ala Val Ala Ala Trp Asn Ala
 385 390 395 400
 Gln Leu

<210> 365
 <211> 1108
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1099)
 <223> RXN02813

<400> 365
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 cagcctttcc gacgagactt tcctaaagaa tcttcttgct gtg gag gcc gct ttg 115
 Val Glu Ala Ala Leu

1

5

gcg gtt gca gct gcc ccc gag cac gca gca atg gcg aag gcc acc att 163
 Ala Val Ala Ala Ala Pro Glu His Ala Ala Met Ala Lys Ala Thr Ile
 10 15 20

gat tct tat cag ttg gat gtg gag gag ctt tcc cgt cgc gca gcc gag	211
Asp Ser Tyr Gln Leu Asp Val Glu Glu Leu Ser Arg Arg Ala Ala Glu	
25 30 35	
ggc ggt aat ccg ctc att ccg ctg gtc act gac ctc aag gcc atc aat	259
Gly Gly Asn Pro Leu Ile Pro Leu Val Thr Asp Leu Lys Ala Ile Asn	
40 45 50	
ccg gca ggc atc cac att ggc gca acg agc cag gac atc att gat tct	307
Pro Ala Gly Ile His Ile Gly Ala Thr Ser Gln Asp Ile Ile Asp Ser	
55 60 65	
gcg tta atg ctg tgc atg aag gaa ggg gtg ggg gag gtc gtc gac aag	355
Ala Leu Met Leu Cys Met Lys Glu Gly Val Gly Glu Val Val Asp Lys	
70 75 80 85	
ctt aaa aag ctt gcg cga gat ttg gcc gag ctc acc gcg gag cat aaa	403
Leu Lys Lys Leu Ala Arg Asp Leu Ala Glu Leu Thr Ala Glu His Lys	
90 95 100	
gca acc ccg atc atg ggg cgc acg ttg ggg cag atc gcg acg ccg acg	451
Ala Thr Pro Ile Met Gly Arg Thr Leu Gly Gln Ile Ala Thr Pro Thr	
105 110 115	
acg ttc ggc gcg ctg acc ggc ggc tgg ctg gtt gcg gtg gac aat gcg	499
Thr Phe Gly Ala Leu Thr Gly Gly Trp Leu Val Ala Val Asp Asn Ala	
120 125 130	
gca cgc gcc ctg gag gcg ctg gag ttt ccg gtg tcg tat ggc ggt gcc	547
Ala Arg Ala Leu Glu Ala Leu Glu Phe Pro Val Ser Tyr Gly Gly Ala	
135 140 145	
agc gga aat atg acg gcg gtg cac ccg cgt ggc ttc gag att cag gcg	595
Ser Gly Asn Met Thr Ala Val His Pro Arg Gly Phe Glu Ile Gln Ala	
150 155 160 165	
aag ctg gcc gag gag ttg ggc ctt ttt gat ccg cag tgg gtg tgg cat	643
Lys Leu Ala Glu Glu Leu Gly Leu Phe Asp Pro Gln Trp Val Trp His	
170 175 180	
tcc gat cgc acg ccg atc act gcg atc gcg tcg gcg ctg gca acg gcc	691
Ser Asp Arg Thr Pro Ile Thr Ala Ile Ala Ser Ala Leu Ala Thr Ala	
185 190 195	
gct ggt gtg gta cgc aaa att gct ggt gac gtg gtg ttt tac tca caa	739
Ala Gly Val Val Arg Lys Ile Ala Gly Asp Val Val Phe Tyr Ser Gln	
200 205 210	
acc gag gtc ggc gag ttg cgg gag aaa tcc ccc ggc ggc agc tcc gcg	787
Thr Glu Val Gly Glu Leu Arg Glu Lys Ser Pro Gly Gly Ser Ser Ala	
215 220 225	
atg ccc cac aaa gcc aat ccg gcc gct gcg att gcg tgc gac ggt tac	835
Met Pro His Lys Ala Asn Pro Ala Ala Ala Ile Ala Cys Asp Gly Tyr	
230 235 240 245	
gcg cgc cgg gca cct ggc ctt ctt gca acg ctt ttc gac gcc ctc gac	883
Ala Arg Arg Ala Pro Gly Leu Leu Ala Thr Leu Phe Asp Ala Leu Asp	
250 255 260	

Gln Trp Val Trp His Ser Asp Arg Thr Pro Ile Thr Ala Ile Ala Ser


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<210> 367
<211> 651
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (1)..(642)
<223> FRXA02813
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Gly	Ala	Leu	Thr	Gly	Gly	Trp	Leu	Val	Ala	Val	Asp	Asn	Ala	Ala	Arg	
1				5					10					15		
gcc	ctg	gag	gcg	ctg	gag	ttt	ccg	gtg	tgc	tat	ggc	ggt	gcc	agc	gga	96
Ala	Leu	Glu	Ala	Leu	Glu	Phe	Pro	Val	Ser	Tyr	Gly	Gly	Ala	Ser	Gly	
			20					25					30			
aat	atg	acg	gcg	gtg	cac	ccg	cgt	ggc	ttc	gag	att	cag	gcg	aag	ctg	144
Asn	Met	Thr	Ala	Val	His	Pro	Arg	Gly	Phe	Glu	Ile	Gln	Ala	Lys	Leu	
		35					40					45				
gcc	gag	gag	ttg	ggc	ctt	ttt	gat	ccg	cag	tgg	gtg	tgg	cat	tcc	gat	192
Ala	Glu	Glu	Leu	Gly	Leu	Phe	Asp	Pro	Gln	Trp	Val	Trp	His	Ser	Asp	
	50					55					60					
cgc	acg	ccg	atc	act	gcg	atc	gcg	tgc	gcg	ctg	gca	acg	gcc	gct	ggt	240
Arg	Thr	Pro	Ile	Thr	Ala	Ile	Ala	Ser	Ala	Leu	Ala	Thr	Ala	Ala	Gly	
65					70					75				80		

gtg gta cgc aaa att gct ggt gac gtg gtg ttt tac tca caa acc gag 288
 Val Val Arg Lys Ile Ala Gly Asp Val Val Phe Tyr Ser Gln Thr Glu
 85 90 95

gtc ggc gag ttg cgg gag aaa tcc ccc ggc ggc agc tcc gcg atg ccc 336
 Val Gly Glu Leu Arg Glu Lys Ser Pro Gly Gly Ser Ser Ala Met Pro
 100 105 110

cac aaa gcc aat ccg gcc gct gcg att gcg tgc gac ggt tac gcg cgc 384
 His Lys Ala Asn Pro Ala Ala Ala Ile Ala Cys Asp Gly Tyr Ala Arg
 115 120 125

cgg gca cct ggc ctt ctt gca acg ctt ttc gac gcc ctc gac tgc cgt 432
 Arg Ala Pro Gly Leu Leu Ala Thr Leu Phe Asp Ala Leu Asp Cys Arg
 130 135 140

ttg cag cgc ggc acc ggc agc tgg cac gcg gag tgg gca acg ctg cgc 480
 Leu Gln Arg Gly Thr Gly Ser Trp His Ala Glu Trp Ala Thr Leu Arg
 145 150 155 160

gag ttg gct gct gtc act cac tca gca gtg agc agg gct gca acc agc 528
 Glu Leu Ala Ala Val Thr His Ser Ala Val Ser Arg Ala Ala Thr Ser
 165 170 175

atc gat ggc atc acc gtc aac gtt gat gtg atg gca agt cgc gtc aat 576
 Ile Asp Gly Ile Thr Val Asn Val Asp Val Met Ala Ser Arg Val Asn
 180 185 190

gga cca acc ggg cac gcc gaa gat ttg gcg gag cgg gca cta gaa att 624
 Gly Pro Thr Gly His Ala Glu Asp Leu Ala Glu Arg Ala Leu Glu Ile
 195 200 205

tat gga aaa gga cgc agt taatggatc 651
 Tyr Gly Lys Gly Arg Ser
 210

<210> 368
 <211> 214
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 368
 Gly Ala Leu Thr Gly Gly Trp Leu Val Ala Val Asp Asn Ala Ala Arg
 1 5 10 15

Ala Leu Glu Ala Leu Glu Phe Pro Val Ser Tyr Gly Gly Ala Ser Gly
 20 25 30

Asn Met Thr Ala Val His Pro Arg Gly Phe Glu Ile Gln Ala Lys Leu
 35 40 45

Ala Glu Glu Leu Gly Leu Phe Asp Pro Gln Trp Val Trp His Ser Asp
 50 55 60

Arg Thr Pro Ile Thr Ala Ile Ala Ser Ala Leu Ala Thr Ala Ala Gly
 65 70 75 80

Val Val Arg Lys Ile Ala Gly Asp Val Val Phe Tyr Ser Gln Thr Glu
 85 90 95

Val Gly Glu Leu Arg Glu Lys Ser Pro Gly Gly Ser Ser Ala Met Pro
 100 105 110

His Lys Ala Asn Pro Ala Ala Ala Ile Ala Cys Asp Gly Tyr Ala Arg
 115 120 125

Arg Ala Pro Gly Leu Leu Ala Thr Leu Phe Asp Ala Leu Asp Cys Arg
 130 135 140

Leu Gln Arg Gly Thr Gly Ser Trp His Ala Glu Trp Ala Thr Leu Arg
 145 150 155 160

Glu Leu Ala Ala Val Thr His Ser Ala Val Ser Arg Ala Ala Thr Ser
 165 170 175

Ile Asp Gly Ile Thr Val Asn Val Asp Val Met Ala Ser Arg Val Asn
 180 185 190

Gly Pro Thr Gly His Ala Glu Asp Leu Ala Glu Arg Ala Leu Glu Ile
 195 200 205

Tyr Gly Lys Gly Arg Ser
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<210> 369

<211> 260

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(237)

<223> RXA01113

<400> 369

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 Gly Asp Ile Trp Glu Arg Pro Gly Leu Asp His Thr Gln Arg Arg Leu
 1 5 10 15

ctc acc atc gcg att ttg acc gcg gtg ggc aat gac ggc gag ttg gac 96
 Leu Thr Ile Ala Ile Leu Thr Ala Val Gly Asn Asp Gly Glu Leu Asp
 20 25 30

atg cac att cgt gct gct ctg cgc gct ggc gtg gat cag gaa acc atc 144
 Met His Ile Arg Ala Ala Leu Arg Ala Gly Val Asp Gln Glu Thr Ile
 35 40 45

ggc gag gtc atc ctg cac act gcg gtg tat gcg ggt gtg ccg aac tcc 192
 Gly Glu Val Ile Leu His Thr Ala Val Tyr Ala Gly Val Pro Asn Ser
 50 55 60

aac cat ggt ttc aag ctg ctg aac aac gct gtg tca gac ctt cag 237
 Asn His Gly Phe Lys Leu Leu Asn Asn Ala Val Ser Asp Leu Gln
 65 70 75

taattctcga agctctccac ggg

260

<210> 370

<211> 79

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 370

Gly	Asp	Ile	Trp	Glu	Arg	Pro	Gly	Leu	Asp	His	Thr	Gln	Arg	Arg	Leu
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Leu	Thr	Ile	Ala	Ile	Leu	Thr	Ala	Val	Gly	Asn	Asp	Gly	Glu	Leu	Asp
			20					25					30		

Met	His	Ile	Arg	Ala	Ala	Leu	Arg	Ala	Gly	Val	Asp	Gln	Glu	Thr	Ile
		35					40					45			

Gly	Glu	Val	Ile	Leu	His	Thr	Ala	Val	Tyr	Ala	Gly	Val	Pro	Asn	Ser
	50					55					60				

Asn	His	Gly	Phe	Lys	Leu	Leu	Asn	Asn	Ala	Val	Ser	Asp	Leu	Gln	
65					70					75					

<210> 371

<211> 444

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(421)

<223> RXA02126

<400> 371

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ggttttcctg	tgtattccgg	caagtagaaa	gattttttatc	atg	gga	caa	aaa	gta	115
				Met	Gly	Gln	Lys	Val	
				1				5	

acc	gca	ggt	cgt	gac	atc	cta	gga	gag	ttt	gca	cct	aag	tcc	gct	gaa	163
Thr	Ala	Gly	Arg	Asp	Ile	Leu	Gly	Glu	Phe	Ala	Pro	Lys	Ser	Ala	Glu	
			10					15						20		

ctc	aac	gat	gat	gtc	ctc	ttt	ggc	cag	gtg	tgg	tcg	agg	gaa	tca	gag	211
Leu	Asn	Asp	Asp	Val	Leu	Phe	Gly	Gln	Val	Trp	Ser	Arg	Glu	Ser	Glu	
			25					30					35			

ctt	tcc	cca	cgt	gac	cga	agc	atc	gtg	atc	gtg	aca	atg	ttg	atg	gca	259
Leu	Ser	Pro	Arg	Asp	Arg	Ser	Ile	Val	Ile	Val	Thr	Met	Leu	Met	Ala	
		40					45					50				

agt	ggc	gtg	ctg	gat	agt	gct	ttt	gaa	agc	cac	gtt	cag	cga	gcc	aaa	307
Ser	Gly	Val	Leu	Asp	Ser	Ala	Phe	Glu	Ser	His	Val	Gln	Arg	Ala	Lys	
	55					60					65					

gac	aac	ggt	gtc	act	gct	gaa	gaa	atc	gca	gag	atc	atc	acc	cac	gtg	355
Asp	Asn	Gly	Val	Thr	Ala	Glu	Glu	Ile	Ala	Glu	Ile	Ile	Thr	His	Val	
	70				75					80					85	

gcc	ttt	tat	gca	ggt	tgg	cca	aag	gct	tgg	gct	gcg	ttc	cgc	atc	gca	403
Ala	Phe	Tyr	Ala	Gly	Trp	Pro	Lys	Ala	Trp	Ala	Ala	Phe	Arg	Ile	Ala	
				90					95						100	

aag gac att tac acc aag taatagcgag gcagaaaaca cat
 Lys Asp Ile Tyr Thr Lys
 105

444

<210> 372
 <211> 107
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 372
 Met Gly Gln Lys Val Thr Ala Gly Arg Asp Ile Leu Gly Glu Phe Ala
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 Pro Lys Ser Ala Glu Leu Asn Asp Asp Val Leu Phe Gly Gln Val Trp
 20 25 30
 Ser Arg Glu Ser Glu Leu Ser Pro Arg Asp Arg Ser Ile Val Ile Val
 35 40 45
 Thr Met Leu Met Ala Ser Gly Val Leu Asp Ser Ala Phe Glu Ser His
 50 55 60
 Val Gln Arg Ala Lys Asp Asn Gly Val Thr Ala Glu Glu Ile Ala Glu
 65 70 75 80
 Ile Ile Thr His Val Ala Phe Tyr Ala Gly Trp Pro Lys Ala Trp Ala
 85 90 95
 Ala Phe Arg Ile Ala Lys Asp Ile Tyr Thr Lys
 100 105

<210> 373
 <211> 1284
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1261)
 <223> RXA01465

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 Val Ala Gly Leu Phe
 1 5
 cca ctt aac cag aaa gcc ata gaa aaa ttg tct gat tta acc atc caa 163
 Pro Leu Asn Gln Lys Ala Ile Glu Lys Leu Ser Asp Leu Thr Ile Gln
 10 15 20
 aaa gtc gaa tcc cgt atc ctc gac gtt ccc ctc att cgc cca cac ggc 211
 Lys Val Glu Ser Arg Ile Leu Asp Val Pro Leu Ile Arg Pro His Gly
 25 30 35
 ttc gca act acc acc tcc act gag cag cac att ctg ctg gtc agc gtg 259
 Phe Ala Thr Thr Ser Thr Glu Gln His Ile Leu Leu Val Ser Val
 40 45 50

cac tta gaa aac ggt gtc atc ggc tac ggt gag ggc gtt gtg ccc ggc	307
His Leu Glu Asn Gly Val Ile Gly Tyr Gly Glu Gly Val Val Pro Gly	
55 60 65	
ggt cca tgg tgg ggc ggc gag tcg gtt gag acc atg aag gcg ctt gtc	355
Gly Pro Trp Trp Gly Gly Glu Ser Val Glu Thr Met Lys Ala Leu Val	
70 75 80 85	
gac ggc tac ctc gcc cca gtg ctc atc ggc cgt gct gtc tcc gag ctt	403
Asp Gly Tyr Leu Ala Pro Val Leu Ile Gly Arg Ala Val Ser Glu Leu	
90 95 100	
gca gga att atg gca gac ctt gag cgt gtt gtt gca cgt gcg cgt tat	451
Ala Gly Ile Met Ala Asp Leu Glu Arg Val Val Ala Arg Ala Arg Tyr	
105 110 115	
gcc aag gcg gct gtt gac gtc gca atg cat gat gcc tgg gca cgc agc	499
Ala Lys Ala Ala Val Asp Val Ala Met His Asp Ala Trp Ala Arg Ser	
120 125 130	
ctc aat gtg ccc gtc cgc gac ctg ctt ggt ggc acc gtg cgc gac aag	547
Leu Asn Val Pro Val Arg Asp Leu Leu Gly Gly Thr Val Arg Asp Lys	
135 140 145	
gtg gat gtc acc tgg gcg ctg ggc gtt ttg ccg ctt gat gtt gcg gtg	595
Val Asp Val Thr Trp Ala Leu Gly Val Leu Pro Leu Asp Val Ala Val	
150 155 160 165	
gcg gaa att gaa gag cgc atc gag gag ttt ggt aac cgt tcc ttc aag	643
Ala Glu Ile Glu Glu Arg Ile Glu Glu Phe Gly Asn Arg Ser Phe Lys	
170 175 180	
ttg aag atg ggt gct ggc gat cct gcg gaa gat act cgc cgt gta gca	691
Leu Lys Met Gly Ala Gly Asp Pro Ala Glu Asp Thr Arg Arg Val Ala	
185 190 195	
gaa ttg gcg cgc gaa gtt ggc gac cgc gtt tct ctg cgc att gat att	739
Glu Leu Ala Arg Glu Val Gly Asp Arg Val Ser Leu Arg Ile Asp Ile	
200 205 210	
aac gca cgt tgg gat cgc cgc acc gct ctg cat tac ttg ccg att ctc	787
Asn Ala Arg Trp Asp Arg Arg Thr Ala Leu His Tyr Leu Pro Ile Leu	
215 220 225	
gcg gag gct ggc gtc gag ctg ttc gag cag ccc acc ccg gcc gac gac	835
Ala Glu Ala Gly Val Glu Leu Phe Glu Gln Pro Thr Pro Ala Asp Asp	
230 235 240 245	
ctg gaa acc ctg cgc gaa atc acc cgc cgc acc aac gtt tcg gtc atg	883
Leu Glu Thr Leu Arg Glu Ile Thr Arg Arg Thr Asn Val Ser Val Met	
250 255 260	
gca gat gaa tcc gtg tgg acc cca gct gaa gct ctc gcg gtg gtg aaa	931
Ala Asp Glu Ser Val Trp Thr Pro Ala Glu Ala Leu Ala Val Val Lys	
265 270 275	
gcc cag gct gcg gat gtt atc gca ctg aaa acc act aag cac ggt ggt	979
Ala Gln Ala Ala Asp Val Ile Ala Leu Lys Thr Thr Lys His Gly Gly	
280 285 290	

ctg ctg gaa tcc aag aag atc gcc gct atc gcc gaa gcc ggc ggg ctg 1027
 Leu Leu Glu Ser Lys Lys Ile Ala Ala Ile Ala Glu Ala Gly Gly Leu
 295 300 305

gcc tgc cat ggt gca acc agt ctg gaa ggt cca atc ggc acc gca gca 1075
 Ala Cys His Gly Ala Thr Ser Leu Glu Gly Pro Ile Gly Thr Ala Ala
 310 315 320 325

tcc ctg cag ttt gcg gca tcc acc aag gcg atc tcc tac ggt aca gaa 1123
 Ser Leu Gln Phe Ala Ala Ser Thr Lys Ala Ile Ser Tyr Gly Thr Glu
 330 335 340

ctg ttc gga ccg cag ttg ctc aaa gat acc tat att gtc caa gaa ttt 1171
 Leu Phe Gly Pro Gln Leu Leu Lys Asp Thr Tyr Ile Val Gln Glu Phe
 345 350 355

gag tac aag gac ggc cag gtt gct att cca caa ggc cca ggt ttg ggc 1219
 Glu Tyr Lys Asp Gly Gln Val Ala Ile Pro Gln Gly Pro Gly Leu Gly
 360 365 370

gtc gat gtg gac atg gac aaa gtc aac ttc tac acc cgt aaa 1261
 Val Asp Val Asp Met Asp Lys Val Asn Phe Tyr Thr Arg Lys
 375 380 385

taaggagaat tatcgatgct gtt 1284

<210> 374

<211> 387

<212> PRT

<213> Corynebacterium glutamicum

<400> 374

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Asp Leu Thr Ile Gln Lys Val Glu Ser Arg Ile Leu Asp Val Pro Leu
 20 25 30

Ile Arg Pro His Gly Phe Ala Thr Thr Thr Ser Thr Glu Gln His Ile
 35 40 45

Leu Leu Val Ser Val His Leu Glu Asn Gly Val Ile Gly Tyr Gly Glu
 50 55 60

Gly Val Val Pro Gly Gly Pro Trp Trp Gly Gly Glu Ser Val Glu Thr
 65 70 75 80

Met Lys Ala Leu Val Asp Gly Tyr Leu Ala Pro Val Leu Ile Gly Arg
 85 90 95

Ala Val Ser Glu Leu Ala Gly Ile Met Ala Asp Leu Glu Arg Val Val
 100 105 110

Ala Arg Ala Arg Tyr Ala Lys Ala Ala Val Asp Val Ala Met His Asp
 115 120 125

Ala Trp Ala Arg Ser Leu Asn Val Pro Val Arg Asp Leu Leu Gly Gly
 130 135 140

Thr Val Arg Asp Lys Val Asp Val Thr Trp Ala Leu Gly Val Leu Pro

145 150 155 160
 Leu Asp Val Ala Val Ala Glu Ile Glu Glu Arg Ile Glu Glu Phe Gly
 165 170 175
 Asn Arg Ser Phe Lys Leu Lys Met Gly Ala Gly Asp Pro Ala Glu Asp
 180 185 190
 Thr Arg Arg Val Ala Glu Leu Ala Arg Glu Val Gly Asp Arg Val Ser
 195 200 205
 Leu Arg Ile Asp Ile Asn Ala Arg Trp Asp Arg Arg Thr Ala Leu His
 210 215 220
 Tyr Leu Pro Ile Leu Ala Glu Ala Gly Val Glu Leu Phe Glu Gln Pro
 225 230 235 240
 Thr Pro Ala Asp Asp Leu Glu Thr Leu Arg Glu Ile Thr Arg Arg Thr
 245 250 255
 Asn Val Ser Val Met Ala Asp Glu Ser Val Trp Thr Pro Ala Glu Ala
 260 265 270
 Leu Ala Val Val Lys Ala Gln Ala Ala Asp Val Ile Ala Leu Lys Thr
 275 280 285
 Thr Lys His Gly Gly Leu Leu Glu Ser Lys Lys Ile Ala Ala Ile Ala
 290 295 300
 Glu Ala Gly Gly Leu Ala Cys His Gly Ala Thr Ser Leu Glu Gly Pro
 305 310 315 320
 Ile Gly Thr Ala Ala Ser Leu Gln Phe Ala Ala Ser Thr Lys Ala Ile
 325 330 335
 Ser Tyr Gly Thr Glu Leu Phe Gly Pro Gln Leu Leu Lys Asp Thr Tyr
 340 345 350
 Ile Val Gln Glu Phe Glu Tyr Lys Asp Gly Gln Val Ala Ile Pro Gln
 355 360 365
 Gly Pro Gly Leu Gly Val Asp Val Asp Met Asp Lys Val Asn Phe Tyr
 370 375 380
 Thr Arg Lys
 385

<210> 375

<211> 1137

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)...(1114)

<223> RXA02316

<400> 375

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tcgacgacca	cggcgtccac	ctaatttagg	atggttcccc	atg	agc	acc	cca	act	115
				Met	Ser	Thr	Pro	Thr	
				1				5	
gtt gat gag att cta gag cgc gcc cac gtg gtg tcg ctg ccg atg cgt	163								
Val Asp Glu Ile Leu Glu Arg Ala His Val Val Ser Leu Pro Met Arg									
	10	15	20						
gtg aag ttt cgt ggc gtc acc acc agg gag gct ttg ctg att gaa ggc	211								
Val Lys Phe Arg Gly Val Thr Thr Arg Glu Ala Leu Leu Ile Glu Gly									
	25	30	35						
cct gct ggt tgg gga gag ttc gcg ccc ttc ctt gag tat gac ccg caa	259								
Pro Ala Gly Trp Gly Glu Phe Ala Pro Phe Leu Glu Tyr Asp Pro Gln									
	40	45	50						
gaa tcg gcc agt tgg cta aag tcc ggc att gaa gca gcg tgg gag ggt	307								
Glu Ser Ala Ser Trp Leu Lys Ser Gly Ile Glu Ala Ala Trp Glu Gly									
	55	60	65						
ttt ccg gcg ccg ttg cgt gat cgc gtg gaa gtc aat gcc acc atc cca	355								
Phe Pro Ala Pro Leu Arg Asp Arg Val Glu Val Asn Ala Thr Ile Pro									
	70	75	80					85	
gct gtt ccg gcc gat caa gtg gca gaa gtt ttg gac cgt ttc cca ggc	403								
Ala Val Pro Ala Asp Gln Val Ala Glu Val Leu Asp Arg Phe Pro Gly									
	90	95	100						
tgt cgc acc atc aaa gta aag gtc gcg gaa cca ggc cag acc ttg gct	451								
Cys Arg Thr Ile Lys Val Lys Val Ala Glu Pro Gly Gln Thr Leu Ala									
	105	110	115						
gat gac atc gcg cga gtt gcc gct gcc cgt gag gca cgc ccc ggc gcg	499								
Asp Asp Ile Ala Arg Val Ala Ala Ala Arg Glu Ala Arg Pro Gly Ala									
	120	125	130						
atc atc cgt gtt gat gcc aat tgt ggg tgg agt gtg gag cag gcg gtg	547								
Ile Ile Arg Val Asp Ala Asn Cys Gly Trp Ser Val Glu Gln Ala Val									
	135	140	145						
gag gcg gct cag gcg ttg gcg ccg ttg gat tat tta gag cag ccg tgt	595								
Glu Ala Ala Gln Ala Leu Ala Pro Leu Asp Tyr Leu Glu Gln Pro Cys									
	150	155	160					165	
gcc acc gtg gag gaa ctg gcg gaa gtg cgc atg acg gtg cag cgg cgc	643								
Ala Thr Val Glu Glu Leu Ala Glu Val Arg Met Thr Val Gln Arg Arg									
	170	175	180						
gga ctt ttt gtg cgc gtt gca gcg gat gaa tcg atc aga aaa tct gat	691								
Gly Leu Phe Val Arg Val Ala Ala Asp Glu Ser Ile Arg Lys Ser Asp									
	185	190	195						
gat cct tat ccg gtg gcg gat ctg cgt gct gcg gat gtg gct gtg gtg	739								
Asp Pro Tyr Arg Val Ala Asp Leu Arg Ala Ala Asp Val Ala Val Val									
	200	205	210						
aag gtt gct cct ttg ggt ggt gtg aaa agg gta ctt gag gtg gtg caa	787								
Lys Val Ala Pro Leu Gly Gly Val Lys Arg Val Leu Glu Val Val Gln									
	215	220	225						
cat ttg ccg gcg cgc acg atg gac atc act gta gca agt gcg ttg gac	835								

His Leu Arg Ala Arg Thr Met Asp Ile Thr Val Ala Ser Ala Leu Asp
 230 235 240 245
 acg gtt gtg ggg atg aat gct ggg ttg gct gcg gtg gcg gcg ttg ccg 883
 Thr Val Val Gly Met Asn Ala Gly Leu Ala Ala Val Ala Ala Leu Pro
 250 255 260
 aag ttg gat gat gac gat ctc att gat gtg cca cca gcg gcg gcg ggt 931
 Lys Leu Asp Asp Asp Asp Leu Ile Asp Val Pro Pro Ala Ala Ala Gly
 265 270 275
 ctt gcg act tcg cag ttg ttc ctg gag gat gtc gcg acc ccg cac gca 979
 Leu Ala Thr Ser Gln Leu Phe Leu Glu Asp Val Ala Thr Pro His Ala
 280 285 290
 atc act gat ggg ttc atg gaa acg cgt gta att gcc ccg gaa atg gat 1027
 Ile Thr Asp Gly Phe Met Glu Thr Arg Val Ile Ala Pro Glu Met Asp
 295 300 305
 cgt ttg gaa acg ctt gct gcc agc aaa gat agg cgt gat tgg tgg ttt 1075
 Arg Leu Glu Thr Leu Ala Ala Ser Lys Asp Arg Arg Asp Trp Trp Phe
 310 315 320 325
 gag cgc gtg cgt gaa tcg tat ccg tac ctg gag acg atc tagactgttg 1124
 Glu Arg Val Arg Glu Ser Tyr Pro Tyr Leu Glu Thr Ile
 330 335
 tgcattgtcca gca 1137

<210> 376

<211> 338

<212> PRT

<213> Corynebacterium glutamicum

<400> 376

Met Ser Thr Pro Thr Val Asp Glu Ile Leu Glu Arg Ala His Val Val
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 Ser Leu Pro Met Arg Val Lys Phe Arg Gly Val Thr Thr Arg Glu Ala
 20 25 30
 Leu Leu Ile Glu Gly Pro Ala Gly Trp Gly Glu Phe Ala Pro Phe Leu
 35 40 45
 Glu Tyr Asp Pro Gln Glu Ser Ala Ser Trp Leu Lys Ser Gly Ile Glu
 50 55 60
 Ala Ala Trp Glu Gly Phe Pro Ala Pro Leu Arg Asp Arg Val Glu Val
 65 70 75 80
 Asn Ala Thr Ile Pro Ala Val Pro Ala Asp Gln Val Ala Glu Val Leu
 85 90 95
 Asp Arg Phe Pro Gly Cys Arg Thr Ile Lys Val Lys Val Ala Glu Pro
 100 105 110
 Gly Gln Thr Leu Ala Asp Asp Ile Ala Arg Val Ala Ala Ala Arg Glu
 115 120 125
 Ala Arg Pro Gly Ala Ile Ile Arg Val Asp Ala Asn Cys Gly Trp Ser

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      130              135              140
Val Glu Gln Ala Val Glu Ala Ala Gln Ala Leu Ala Pro Leu Asp Tyr
145              150              155              160
Leu Glu Gln Pro Cys Ala Thr Val Glu Glu Leu Ala Glu Val Arg Met
165              170
Thr Val Gln Arg Arg Gly Leu Phe Val Arg Val Ala Ala Asp Glu Ser
180              185              190
Ile Arg Lys Ser Asp Asp Pro Tyr Arg Val Ala Asp Leu Arg Ala Ala
195              200              205
Asp Val Ala Val Val Lys Val Ala Pro Leu Gly Gly Val Lys Arg Val
210              215              220
Leu Glu Val Val Gln His Leu Arg Ala Arg Thr Met Asp Ile Thr Val
225              230              235
Ala Ser Ala Leu Asp Thr Val Val Gly Met Asn Ala Gly Leu Ala Ala
245              250              255
Val Ala Ala Leu Pro Lys Leu Asp Asp Asp Asp Leu Ile Asp Val Pro
260              265              270
Pro Ala Ala Ala Gly Leu Ala Thr Ser Gln Leu Phe Leu Glu Asp Val
275              280              285
Ala Thr Pro His Ala Ile Thr Asp Gly Phe Met Glu Thr Arg Val Ile
290              295              300
Ala Pro Glu Met Asp Arg Leu Glu Thr Leu Ala Ala Ser Lys Asp Arg
305              310              315
Arg Asp Trp Trp Phe Glu Arg Val Arg Glu Ser Tyr Pro Tyr Leu Glu
325              330              335

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Thr Ile

<210> 377
 <211> 414
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(391)
 <223> RXA01464

<400> 377
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caaagtcaac ttctacaccc gtaaataagg agaattatcg atg ctg ttt cta gca 115
 Met Leu Phe Leu Ala
 1 5

cgc atg gac gtc gtc ttc cct gat tcc atg gac gcc gat gtg atg gca 163
 Arg Met Asp Val Val Phe Pro Asp Ser Met Asp Ala Asp Val Met Ala

	10	15	20	
gat ttc cag gct aag gaa aag gcc tac tcc gga gac ctg caa tcc cgt				211
Asp Phe Gln Ala Lys Glu Lys Ala Tyr Ser Gly Asp Leu Gln Ser Arg				
	25	30	35	
gga atc atg aaa gca atc tgg cga gtc gtc ggc gag tat gca aac tac				259
Gly Ile Met Lys Ala Ile Trp Arg Val Val Gly Glu Tyr Ala Asn Tyr				
	40	45	50	
tcc att ttc gat gtc gat gac cac gac gag ctg cat gca att ctt agt				307
Ser Ile Phe Asp Val Asp Asp His Asp Glu Leu His Ala Ile Leu Ser				
	55	60	65	
ggc ttt ccg atg ttc aaa tac atg aat gtc aag atc act cca ctg gca				355
Gly Phe Pro Met Phe Lys Tyr Met Asn Val Lys Ile Thr Pro Leu Ala				
	70	75	80	85
aaa cac ccc aat gct ctg gag tat tac ctc aag gga tagttgaggt				401
Lys His Pro Asn Ala Leu Glu Tyr Tyr Leu Lys Gly				
	90	95		
tctaaccgct cta				414

<210> 378

<211> 97

<212> PRT

<213> Corynebacterium glutamicum

<400> 378

Met	Leu	Phe	Leu	Ala	Arg	Met	Asp	Val	Val	Phe	Pro	Asp	Ser	Met	Asp
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Ala	Asp	Val	Met	Ala	Asp	Phe	Gln	Ala	Lys	Glu	Lys	Ala	Tyr	Ser	Gly
			20					25					30		

Asp	Leu	Gln	Ser	Arg	Gly	Ile	Met	Lys	Ala	Ile	Trp	Arg	Val	Val	Gly
		35					40					45			

Glu	Tyr	Ala	Asn	Tyr	Ser	Ile	Phe	Asp	Val	Asp	Asp	His	Asp	Glu	Leu
	50					55					60				

His	Ala	Ile	Leu	Ser	Gly	Phe	Pro	Met	Phe	Lys	Tyr	Met	Asn	Val	Lys
65					70					75					80

Ile	Thr	Pro	Leu	Ala	Lys	His	Pro	Asn	Ala	Leu	Glu	Tyr	Tyr	Leu	Lys
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Gly

<210> 379

<211> 1119

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1096)

<400> 379

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Val Ser Glu His Ala
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gct gaa cat cac cgc gat acc caa aat ttc tta acc tcc gaa ccg cac 163
Ala Glu His His Arg Asp Thr Gln Asn Phe Leu Thr Ser Glu Pro His
10 15 20

acc acg gca atc gaa gac aac aag aag cgc caa ccg ccg aaa aac ctt 211
Thr Thr Ala Ile Glu Asp Asn Lys Lys Arg Gln Pro Pro Lys Asn Leu
25 30 35

gct gac ggc atg atc aag gcg ctg cgc ccc aag cag tgg gtc aag aac 259
Ala Asp Gly Met Ile Lys Ala Leu Arg Pro Lys Gln Trp Val Lys Asn
40 45 50

ggt ctt gtg cta gca gca cca ctt gct gct ggt gca gat gcg atc ttc 307
Val Leu Val Leu Ala Ala Pro Leu Ala Ala Gly Ala Asp Ala Ile Phe
55 60 65

aac cag cgc acg atc atc gac gtt gct atc gca ttc gta gtg ttc tgc 355
Asn Gln Arg Thr Ile Ile Asp Val Ala Ile Ala Phe Val Val Phe Cys
70 75 80 85

ttc ggt gca tca gcc att tac ttg gtt aat gat gcc cgt gac gtg gaa 403
Phe Gly Ala Ser Ala Ile Tyr Leu Val Asn Asp Ala Arg Asp Val Glu
90 95 100

gct gac cgc gag cac cca acc aag cgt ttc cgc ccc atc gct gca gga 451
Ala Asp Arg Glu His Pro Thr Lys Arg Phe Arg Pro Ile Ala Ala Gly
105 110 115

gtc ctg cca gta gga atg gca tac ggc atg gcc gtg gcg ctc att gca 499
Val Leu Pro Val Gly Met Ala Tyr Gly Met Ala Val Ala Leu Ile Ala
120 125 130

cta tcc atc gga ctg tct ttc ctc gcc acc gac ggc gtg gca ctt gcc 547
Leu Ser Ile Gly Leu Ser Phe Leu Ala Thr Asp Gly Val Ala Leu Ala
135 140 145

tgc	gtg	att	ggc	gtg	tac	att	gcg	ctg	cag	ctg	gga	tac	tgc	ttc	ggt	595
Cys	Val	Ile	Gly	Val	Tyr	Ile	Ala	Leu	Gln	Leu	Gly	Tyr	Cys	Phe	Gly	
150					155					160					165	

tgg	aag	cac	atg	cca	gtg	atc	gat	att	gcg	ctt	gtc	tcc	tcc	gga	ttc	643
Trp	Lys	His	Met	Pro	Val	Ile	Asp	Ile	Ala	Leu	Val	Ser	Ser	Gly	Phe	
				170					175					180		

atg ctc cgc gca atg gca ggt ggt gtc gca gca ggc atc gag cta tcc 691
Met Leu Arg Ala Met Ala Gly Gly Val Ala Ala Gly Ile Glu Leu Ser
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cag tgg ttc ctg cta gtc gct gcg ttt ggt tcc ctg ttc atg gca tct 739
Gln Trp Phe Leu Leu Val Ala Ala Phe Gly Ser Leu Phe Met Ala Ser
200 205 210

gga aag cgc tac gca gaa atc ctt ctg cac gag cgc acc ggc gct aag 787
 Gly Lys Arg Tyr Ala Glu Ile Leu Leu His Glu Arg Thr Gly Ala Lys
 215 220 225

 atc cgc aag tcc ctg gaa agc tac acc ccc acc tac ctg cgc ttc gtt 835
 Ile Arg Lys Ser Leu Glu Ser Tyr Thr Pro Thr Tyr Leu Arg Phe Val
 230 235 240 245

 tgg acc atg gca gca aca gca gtg gtc atg tcc tac gca ctg tgg ggc 883
 Trp Thr Met Ala Ala Thr Ala Val Val Met Ser Tyr Ala Leu Trp Gly
 250 255 260

 ttc gac ctt tcc caa cac tcc acc gac gca ggt ccg tgg tac caa atc 931
 Phe Asp Leu Ser Gln His Ser Thr Asp Ala Gly Pro Trp Tyr Gln Ile
 265 270 275

 tcc atg gtt cca ttc acc atc gcc atc ctg cgc tac gca gcc ggc gta 979
 Ser Met Val Pro Phe Thr Ile Ala Ile Leu Arg Tyr Ala Ala Gly Val
 280 285 290

 gac acc ggc gac ggc ggt gcc cct gac gaa gtg gca ctc agc gac aaa 1027
 Asp Thr Gly Asp Gly Gly Ala Pro Asp Glu Val Ala Leu Ser Asp Lys
 295 300 305

 gtt ctg cag gta cta gcc cta gca tgg gtt ttc tgc atc gtg atg gct 1075
 Val Leu Gln Val Leu Ala Leu Ala Trp Val Phe Cys Ile Val Met Ala
 310 315 320 325

 gtg tac atc atg ccg atg ttt tgaatattta ccaatgaaca tgc 1119
 Val Tyr Ile Met Pro Met Phe
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<210> 380

<211> 332

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 380

Val Ser Glu His Ala Ala Glu His His Arg Asp Thr Gln Asn Phe Leu
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Thr Ser Glu Pro His Thr Thr Ala Ile Glu Asp Asn Lys Lys Arg Gln
 20 25 30

Pro Pro Lys Asn Leu Ala Asp Gly Met Ile Lys Ala Leu Arg Pro Lys
 35 40 45

Gln Trp Val Lys Asn Val Leu Val Leu Ala Ala Pro Leu Ala Ala Gly
 50 55 60

Ala Asp Ala Ile Phe Asn Gln Arg Thr Ile Ile Asp Val Ala Ile Ala
 65 70 75 80

Phe Val Val Phe Cys Phe Gly Ala Ser Ala Ile Tyr Leu Val Asn Asp
 85 90 95

Ala Arg Asp Val Glu Ala Asp Arg Glu His Pro Thr Lys Arg Phe Arg
 100 105 110

Pro Ile Ala Ala Gly Val Leu Pro Val Gly Met Ala Tyr Gly Met Ala

115 120 125
 Val Ala Leu Ile Ala Leu Ser Ile Gly Leu Ser Phe Leu Ala Thr Asp
 130 135 140
 Gly Val Ala Leu Ala Cys Val Ile Gly Val Tyr Ile Ala Leu Gln Leu
 145 150 155 160
 Gly Tyr Cys Phe Gly Trp Lys His Met Pro Val Ile Asp Ile Ala Leu
 165 170 175
 Val Ser Ser Gly Phe Met Leu Arg Ala Met Ala Gly Gly Val Ala Ala
 180 185 190
 Gly Ile Glu Leu Ser Gln Trp Phe Leu Leu Val Ala Ala Phe Gly Ser
 195 200 205
 Leu Phe Met Ala Ser Gly Lys Arg Tyr Ala Glu Ile Leu Leu His Glu
 210 215 220
 Arg Thr Gly Ala Lys Ile Arg Lys Ser Leu Glu Ser Tyr Thr Pro Thr
 225 230 235 240
 Tyr Leu Arg Phe Val Trp Thr Met Ala Ala Thr Ala Val Val Met Ser
 245 250 255
 Tyr Ala Leu Trp Gly Phe Asp Leu Ser Gln His Ser Thr Asp Ala Gly
 260 265 270
 Pro Trp Tyr Gln Ile Ser Met Val Pro Phe Thr Ile Ala Ile Leu Arg
 275 280 285
 Tyr Ala Ala Gly Val Asp Thr Gly Asp Gly Gly Ala Pro Asp Glu Val
 290 295 300
 Ala Leu Ser Asp Lys Val Leu Gln Val Leu Ala Leu Ala Trp Val Phe
 305 310 315 320
 Cys Ile Val Met Ala Val Tyr Ile Met Pro Met Phe
 325 330

<210> 381
 <211> 470
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(447)
 <223> RXN02839

<400> 381
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 Cys Val Val Asn Asp Tyr Ala Asp Arg Lys Phe Asp Gly His Val Lys
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cgc acg gcg aac cga cca ctt ccc agc ggc gcg gta aca gag aaa gag 96
 Arg Thr Ala Asn Arg Pro Leu Pro Ser Gly Ala Val Thr Glu Lys Glu
 20 25 30

gcg cgc gcg ctg ttt gtc gtg ctg gta ctg att tcg ttt tta ctg gtg 144
 Ala Arg Ala Leu Phe Val Val Leu Val Leu Ile Ser Phe Leu Leu Val
 35 40 45

ctg acg ctg aat acg atg acc att ctg ttg tcg att gcc gcg cta gcg 192
 Leu Thr Leu Asn Thr Met Thr Ile Leu Leu Ser Ile Ala Ala Leu Ala
 50 55 60

ctg gcg tgg gtg tac ccg ttt atg aag cgg tat acc cat cta ccg caa 240
 Leu Ala Trp Val Tyr Pro Phe Met Lys Arg Tyr Thr His Leu Pro Gln
 65 70 75 80

gtg gtg ctg ggc gcg gcg ttt ggc tgg tcg att cca atg gct ttt gcc 288
 Val Val Leu Gly Ala Ala Phe Gly Trp Ser Ile Pro Met Ala Phe Ala
 85 90 95

gct gtg agt gag tcg gtg cca ttg agt tgc tgg tta atg ttc ctc gcc 336
 Ala Val Ser Glu Ser Val Pro Leu Ser Cys Trp Leu Met Phe Leu Ala
 100 105 110

aat att ctc tgg gcg gtg gct tac gac acg cag tat gcg atg gtt gac 384
 Asn Ile Leu Trp Ala Val Ala Tyr Asp Thr Gln Tyr Ala Met Val Asp
 115 120 125

cgc gat gat gat gtg aag att ggc att aaa tcc acg gca atc ctg ttg 432
 Arg Asp Asp Asp Val Lys Ile Gly Ile Lys Ser Thr Ala Ile Leu Leu
 130 135 140

gcc aat acg ata aat tgatattggg attttgcaga ttg 470
 Ala Asn Thr Ile Asn
 145

<210> 382

<211> 149

<212> PRT

<213> Corynebacterium glutamicum

<400> 382

Cys Val Val Asn Asp Tyr Ala Asp Arg Lys Phe Asp Gly His Val Lys
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Arg Thr Ala Asn Arg Pro Leu Pro Ser Gly Ala Val Thr Glu Lys Glu
 20 25 30

Ala Arg Ala Leu Phe Val Val Leu Val Leu Ile Ser Phe Leu Leu Val
 35 40 45

Leu Thr Leu Asn Thr Met Thr Ile Leu Leu Ser Ile Ala Ala Leu Ala
 50 55 60

Leu Ala Trp Val Tyr Pro Phe Met Lys Arg Tyr Thr His Leu Pro Gln
 65 70 75 80

Val Val Leu Gly Ala Ala Phe Gly Trp Ser Ile Pro Met Ala Phe Ala
 85 90 95

Ala Val Ser Glu Ser Val Pro Leu Ser Cys Trp Leu Met Phe Leu Ala
 100 105 110

Asn Ile Leu Trp Ala Val Ala Tyr Asp Thr Gln Tyr Ala Met Val Asp

115 120 125
 Arg Asp Asp Asp Val Lys Ile Gly Ile Lys Ser Thr Ala Ile Leu Leu
 130 135 140

Ala Asn Thr Ile Asn
 145

<210> 383
 <211> 417
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(417)
 <223> FRXA02839

<400> 383
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 Cys Val Val Asn Asp Tyr Ala Asp Arg Lys Phe Asp Gly His Val Lys
 1 5 10 15
 cgc acg gcg aac cga cca ctt ccc agc ggc gcg gta aca gag aaa gag 96
 Arg Thr Ala Asn Arg Pro Leu Pro Ser Gly Ala Val Thr Glu Lys Glu
 20 25 30
 gcg cgc gcg ctg ttt gtc gtg ctg gta ctg att tcg ttt tta ctg gtg 144
 Ala Arg Ala Leu Phe Val Val Leu Val Leu Ile Ser Phe Leu Leu Val
 35 40 45
 ctg acg ctg aat acg atg acc att ctg ttg tcg att gcc gcg cta gcg 192
 Leu Thr Leu Asn Thr Met Thr Ile Leu Leu Ser Ile Ala Ala Leu Ala
 50 55 60
 ctg gcg tgg gtg tac ccg ttt atg aag cgg tat acc cat cta ccg caa 240
 Leu Ala Trp Val Tyr Pro Phe Met Lys Arg Tyr Thr His Leu Pro Gln
 65 70 75 80
 gtg gtg ctg ggc gcg gcg ttt ggc tgg tcg att cca atg gct ttt gcc 288
 Val Val Leu Gly Ala Ala Phe Gly Trp Ser Ile Pro Met Ala Phe Ala
 85 90 95
 gct gtg agt gag tcg gtg cca ttg agt tgc tgg tta atg ttc ctc gcc 336
 Ala Val Ser Glu Ser Val Pro Leu Ser Cys Trp Leu Met Phe Leu Ala
 100 105 110
 aat att ctc tgg gcg gtg gct tac gac acg cag tat gcg atg gtt gac 384
 Asn Ile Leu Trp Ala Val Ala Tyr Asp Thr Gln Tyr Ala Met Val Asp
 115 120 125
 cgc gat gat gat gtg aag att ggc att aaa tcc 417
 Arg Asp Asp Asp Val Lys Ile Gly Ile Lys Ser
 130 135

<210> 384
 <211> 139
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 384

Cys Val Val Asn Asp Tyr Ala Asp Arg Lys Phe Asp Gly His Val Lys
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 Ala Arg Ala Leu Phe Val Val Leu Val Leu Ile Ser Phe Leu Leu Val
 35 40 45
 Leu Thr Leu Asn Thr Met Thr Ile Leu Leu Ser Ile Ala Ala Leu Ala
 50 55 60
 Leu Ala Trp Val Tyr Pro Phe Met Lys Arg Tyr Thr His Leu Pro Gln
 65 70 75 80
 Val Val Leu Gly Ala Ala Phe Gly Trp Ser Ile Pro Met Ala Phe Ala
 85 90 95
 Ala Val Ser Glu Ser Val Pro Leu Ser Cys Trp Leu Met Phe Leu Ala
 100 105 110
 Asn Ile Leu Trp Ala Val Ala Tyr Asp Thr Gln Tyr Ala Met Val Asp
 115 120 125
 Arg Asp Asp Asp Val Lys Ile Gly Ile Lys Ser
 130 135

<210> 385

<211> 1356

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1333)

<223> RXA01502

<400> 385

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 ggcgctgacc gtccactttt ttagggacta ggagtacagc atg agc aca cca caa 115
 Met Ser Thr Pro Gln
 1 5
 agc atc gtc att atc ggc ggc ggt tta gcc gga gcg aaa acc gca gag 163
 Ser Ile Val Ile Ile Gly Gly Gly Leu Ala Gly Ala Lys Thr Ala Glu
 10 15 20
 gca cta cgt gta aac ggg tat gaa ggc tcc atc acg ctc atc gca gca 211
 Ala Leu Arg Val Asn Gly Tyr Glu Gly Ser Ile Thr Leu Ile Ala Ala
 25 30 35
~~gag-gat-tat-ctg-cca-tat-gag-cgc-cca-ccg-ctg-tca-aag-gag-tac-atg-259-~~
 Glu Asp Tyr Leu Pro Tyr Glu Arg Pro Pro Leu Ser Lys Glu Tyr Met
 40 45 50
 gct gga aaa gtg ggc ttt gac aag gcg att gtt cac ccg gcg gag tgg 307
 Ala Gly Lys Val Gly Phe Asp Lys Ala Ile Val His Pro Ala Glu Trp

55	60	65	
tac aaa gaa aac aat gtc acg ctg cgt caa ggt gtg cgt gca acg gca			355
Tyr Lys Glu Asn Asn Val Thr Leu Arg Gln Gly Val Arg Ala Thr Ala			
70	75	80	85
att gat gcg ggt tca cgc caa gtc acc gtt gat gat ggc gga aac act			403
Ile Asp Ala Gly Ser Arg Gln Val Thr Val Asp Asp Gly Gly Asn Thr			
	90	95	100
gag acc att aac tac gac aaa cta gtt ctt gct act gga tca gca gtg			451
Glu Thr Ile Asn Tyr Asp Lys Leu Val Leu Ala Thr Gly Ser Ala Val			
	105	110	115
cgc aaa ctt cca att ccg gga gcc gac gcc tct aat gtg cac tac ctg			499
Arg Lys Leu Pro Ile Pro Gly Ala Asp Ala Ser Asn Val His Tyr Leu			
	120	125	130
cgc acc gtg gaa gac tct gac gcg atc aag gca acc ttc ggt gaa ggt			547
Arg Thr Val Glu Asp Ser Asp Ala Ile Lys Ala Thr Phe Gly Glu Gly			
	135	140	145
aaa aag ctg gtc ctc atc ggt ggt ggc tgg atc gga ctc gaa gtc gca			595
Lys Lys Leu Val Leu Ile Gly Gly Gly Trp Ile Gly Leu Glu Val Ala			
	150	155	160
tca gcg gca cga gga gct ggc act gac gtc act gtt ttg gaa ggt gga			643
Ser Ala Ala Arg Gly Ala Gly Thr Asp Val Thr Val Leu Glu Gly Gly			
	170	175	180
aag ctc cca ctt ttg aaa gtc ctt ggt gaa acg gtc gcg caa gtc ttt			691
Lys Leu Pro Leu Leu Lys Val Leu Gly Glu Thr Val Ala Gln Val Phe			
	185	190	195
gcc gat ctg cat gtg gca aac ggc gtt gac ctg cgc acc gaa gtg aaa			739
Ala Asp Leu His Val Ala Asn Gly Val Asp Leu Arg Thr Glu Val Lys			
	200	205	210
att acg gac atc gtc acc gaa gat gga cgt gca gtt ggc gtg cga ctt			787
Ile Thr Asp Ile Val Thr Glu Asp Gly Arg Ala Val Gly Val Arg Leu			
	215	220	225
gat gac ggc gaa gtg gtt ccc gca gac gca gta gtc att ggc atc ggt			835
Asp Asp Gly Glu Val Val Pro Ala Asp Ala Val Val Ile Gly Ile Gly			
	230	235	240
gtc acc cca gtg att gac cta gcg gaa act gct gga ctg gaa atc gac			883
Val Thr Pro Val Ile Asp Leu Ala Glu Thr Ala Gly Leu Glu Ile Asp			
	250	255	260
aat ggt gtt ttg gtg gac gca gca ctg cgt acc agc gac ccg gat atc			931
Asn Gly Val Leu Val Asp Ala Ala Leu Arg Thr Ser Asp Pro Asp Ile			
	265	270	275
tac gca gtt gga gac att gcg aac cac gat cac cca gtt cta gga cac			979
Tyr Ala Val Gly Asp Ile Ala Asn His Asp His Pro Val Leu Gly His			
	280	285	290
cgc atc cgc gtg gag cac tgg gcc acc gcg ttg aat caa cct gcg gct			1027
Arg Ile Arg Val Glu His Trp Ala Thr Ala Leu Asn Gln Pro Ala Ala			
	295	300	305

gcg gtg aaa tcc cta ctt ggc aaa gac gcc gag ttt acc aac ctt ccg 1075
 Ala Val Lys Ser Leu Leu Gly Lys Asp Ala Glu Phe Thr Asn Leu Pro
 310 315 320 325

tac ttc ttt aca gat caa ttc gat ctg ggt tgt gaa tac gtc ggc cac 1123
 Tyr Phe Phe Thr Asp Gln Phe Asp Leu Gly Cys Glu Tyr Val Gly His
 330 335 340

gcc acc ggt tcg cag gag aag gta ttc atc cgt gga aac ctt gaa aca 1171
 Ala Thr Gly Ser Gln Glu Lys Val Phe Ile Arg Gly Asn Leu Glu Thr
 345 350 355

cga gaa ttt gtc gcc ttc tgg gtt gat act gaa aac cga att ctc gcc 1219
 Arg Glu Phe Val Ala Phe Trp Val Asp Thr Glu Asn Arg Ile Leu Ala
 360 365 370

gca atg aac gtg aat gtg tgg gat gtt cct gat caa atc aag cct ctc 1267
 Ala Met Asn Val Asn Val Trp Asp Val Pro Asp Gln Ile Lys Pro Leu
 375 380 385

atc gca tca gga aag agc gtt gac acc gag aag cta gtg gat cca gaa 1315
 Ile Ala Ser Gly Lys Ser Val Asp Thr Glu Lys Leu Val Asp Pro Glu
 390 395 400 405

gtt ccg tat tca gag ctc taagcagtgt gtttgatggc cgc 1356
 Val Pro Tyr Ser Glu Leu
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<210> 386

<211> 411

<212> PRT

<213> Corynebacterium glutamicum

<400> 386

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Ala Lys Thr Ala Glu Ala Leu Arg Val Asn Gly Tyr Glu Gly Ser Ile
 20 25 30

Thr Leu Ile Ala Ala Glu Asp Tyr Leu Pro Tyr Glu Arg Pro Pro Leu
 35 40 45

Ser Lys Glu Tyr Met Ala Gly Lys Val Gly Phe Asp Lys Ala Ile Val
 50 55 60

His Pro Ala Glu Trp Tyr Lys Glu Asn Asn Val Thr Leu Arg Gln Gly
 65 70 75 80

Val Arg Ala Thr Ala Ile Asp Ala Gly Ser Arg Gln Val Thr Val Asp
 85 90 95

Asp Gly Gly Asn Thr Glu Thr Ile Asn Tyr Asp Lys Leu Val Leu Ala
 100 105 110

Thr Gly Ser Ala Val Arg Lys Leu Pro Ile Pro Gly Ala Asp Ala Ser
 115 120 125

Asn Val His Tyr Leu Arg Thr Val Glu Asp Ser Asp Ala Ile Lys Ala

130	135	140
Thr Phe Gly Glu Gly Lys Lys Leu Val Leu Ile Gly Gly Gly Trp Ile 145 150 155 160		
Gly Leu Glu Val Ala Ser Ala Ala Arg Gly Ala Gly Thr Asp Val Thr 165 170 175		
Val Leu Glu Gly Gly Lys Leu Pro Leu Leu Lys Val Leu Gly Glu Thr 180 185 190		
Val Ala Gln Val Phe Ala Asp Leu His Val Ala Asn Gly Val Asp Leu 195 200 205		
Arg Thr Glu Val Lys Ile Thr Asp Ile Val Thr Glu Asp Gly Arg Ala 210 215 220		
Val Gly Val Arg Leu Asp Asp Gly Glu Val Val Pro Ala Asp Ala Val 225 230 235 240		
Val Ile Gly Ile Gly Val Thr Pro Val Ile Asp Leu Ala Glu Thr Ala 245 250 255		
Gly Leu Glu Ile Asp Asn Gly Val Leu Val Asp Ala Ala Leu Arg Thr 260 265 270		
Ser Asp Pro Asp Ile Tyr Ala Val Gly Asp Ile Ala Asn His Asp His 275 280 285		
Pro Val Leu Gly His Arg Ile Arg Val Glu His Trp Ala Thr Ala Leu 290 295 300		
Asn Gln Pro Ala Ala Ala Val Lys Ser Leu Leu Gly Lys Asp Ala Glu 305 310 315 320		
Phe Thr Asn Leu Pro Tyr Phe Phe Thr Asp Gln Phe Asp Leu Gly Cys 325 330 335		
Glu Tyr Val Gly His Ala Thr Gly Ser Gln Glu Lys Val Phe Ile Arg 340 345 350		
Gly Asn Leu Glu Thr Arg Glu Phe Val Ala Phe Trp Val Asp Thr Glu 355 360 365		
Asn Arg Ile Leu Ala Ala Met Asn Val Asn Val Trp Asp Val Pro Asp 370 375 380		
Gln Ile Lys Pro Leu Ile Ala Ser Gly Lys Ser Val Asp Thr Glu Lys 385 390 395 400		
Leu Val Asp Pro Glu Val Pro Tyr Ser Glu Leu 405 410		

<210> 387

<211> 572

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (15)..(572)

<223> RXA02828

<400> 387

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ggc acc ctc tcg ctg ggc ggn ttt gcg ccc caa ctg ctg ctg gcc caa 98
Gly Thr Leu Ser Leu Gly Gly Phe Ala Pro Gln Leu Leu Leu Ala Gln
          15          20          25

ggg atg aat cag cca atg cgc gcg ccc att cat gtg ggt aaa tcg ggc 146
Gly Met Asn Gln Pro Met Arg Ala Pro Ile His Val Gly Lys Ser Gly
          30          35          40

ctg cgc gcc cgc gac gcc gag gcg ctt gcc acc tgg tac caa agc cac 194
Leu Arg Ala Arg Asp Ala Glu Ala Leu Ala Thr Trp Tyr Gln Ser His
          45          50          55          60

gtc ggc ctg caa gaa att ggc cgc gac ggc gcg acg atc cac atg ggt 242
Val Gly Leu Gln Glu Ile Gly Arg Asp Gly Ala Thr Ile His Met Gly
          65          70          75

gcg ggc ggc acc gtg ctg ctg gaa atc acg cag tac gac ggt atc gtg 290
Ala Gly Gly Thr Val Leu Leu Glu Ile Thr Gln Tyr Asp Gly Ile Val
          80          85          90

ctg gcg ccc atg cgc gtc gcg ggc ctt tat cac aac gcg ttc ctg ctg 338
Leu Ala Pro Met Arg Val Ala Gly Leu Tyr His Asn Ala Phe Leu Leu
          95          100          105

ccc gcg cgc gcg gat ctg gcg cgg tgg gtg ctg gac gcc tcg gca cgg 386
Pro Ala Arg Ala Asp Leu Ala Arg Trp Val Leu Asp Ala Ser Ala Arg
          110          115          120

caa ctg cgg atc gac ggc tat gcc gac cac ctt gtc agc gag gcg atg 434
Gln Leu Arg Ile Asp Gly Tyr Ala Asp His Leu Val Ser Glu Ala Met
          125          130          135          140

tac ctg acc gac ccc gaa ggc aac ggc gtc gaa atc tac gcc gac cgc 482
Tyr Leu Thr Asp Pro Glu Gly Asn Gly Val Glu Ile Tyr Ala Asp Arg
          145          150          155

ccc gcc agc gac tgg gtc tgg cgc aat ggt cag gtc gag atg gac agc 530
Pro Ala Ser Asp Trp Val Trp Arg Asn Gly Gln Val Glu Met Asp Ser
          160          165          170

ctg caa atc gac ttc tac agc atg atc gcc acg ctt gac ggc 572
Leu Gln Ile Asp Phe Tyr Ser Met Ile Ala Thr Leu Asp Gly
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<210> 388

<211> 186

<212> PRT

<213> Corynebacterium glutamicum

<400> 388

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 Pro Met Arg Ala Pro Ile His Val Gly Lys Ser Gly Leu Arg Ala Arg
 35 40 45
 Asp Ala Glu Ala Leu Ala Thr Trp Tyr Gln Ser His Val Gly Leu Gln
 50 55 60
 Glu Ile Gly Arg Asp Gly Ala Thr Ile His Met Gly Ala Gly Gly Thr
 65 70 75 80
 Val Leu Leu Glu Ile Thr Gln Tyr Asp Gly Ile Val Leu Ala Pro Met
 85 90 95
 Arg Val Ala Gly Leu Tyr His Asn Ala Phe Leu Leu Pro Ala Arg Ala
 100 105 110
 Asp Leu Ala Arg Trp Val Leu Asp Ala Ser Ala Arg Gln Leu Arg Ile
 115 120 125
 Asp Gly Tyr Ala Asp His Leu Val Ser Glu Ala Met Tyr Leu Thr Asp
 130 135 140
 Pro Glu Gly Asn Gly Val Glu Ile Tyr Ala Asp Arg Pro Ala Ser Asp
 145 150 155 160
 Trp Val Trp Arg Asn Gly Gln Val Glu Met Asp Ser Leu Gln Ile Asp
 165 170 175
 Phe Tyr Ser Met Ile Ala Thr Leu Asp Gly
 180 185

<210> 389

<211> 762

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(739)

<223> RXA02064

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ggtacttcac atctcgcttg ctcgctctag actataacgc gtg agt aac gcc ttc 115
 Val Ser Asn Ala Phe
 1 5

gag tat ctt cgc act tat gtc gag tcc act act gaa acc gac gct gct 163
 Glu Tyr Leu Arg Thr Tyr Val Glu Ser Thr Thr Glu Thr Asp Ala Ala
 10 15 20

gta gcg cgc gct cgt gaa gac gcc gcc gag ttc ggt ctc ccc gcc ccg 211
 Val Ala Arg Ala Arg Glu Asp Ala Ala Glu Phe Gly Leu Pro Ala Pro
 25 30 35

gat gaa atg act ggc cag ctg cta acc act ttg gct gcc acc acc aat 259

Asp Glu Met Thr Gly Gln Leu Leu Thr Thr Leu Ala Ala Thr Thr Asn
 40 45 50
 ggc aac ggc tcc act ggt gcc atc gcg att acc ccg gct gcc ggg ttg 307
 Gly Asn Gly Ser Thr Gly Ala Ile Ala Ile Thr Pro Ala Ala Gly Leu
 55 60 65
 gtg ggt ctg tat atc ctg aac gga ctg gcc gat aac acc aca ctg acc 355
 Val Gly Leu Tyr Ile Leu Asn Gly Leu Ala Asp Asn Thr Thr Leu Thr
 70 75 80 85
 tgc att gat cct gaa tca gag cat cag cgc cag gcc aaa gca ctc ttc 403
 Cys Ile Asp Pro Glu Ser Glu His Gln Arg Gln Ala Lys Ala Leu Phe
 90 95 100
 cgc gag gcc ggc tat tcc ccc agc cgc gta cgc ttc ttg ctc tcg cgc 451
 Arg Glu Ala Gly Tyr Ser Pro Ser Arg Val Arg Phe Leu Leu Ser Arg
 105 110 115
 ccg ctc gac gtg atg agt cgc ctt gcc aac gac agc tat cag ctt gtc 499
 Pro Leu Asp Val Met Ser Arg Leu Ala Asn Asp Ser Tyr Gln Leu Val
 120 125 130
 ttc ggc caa gtc tcc ccc atg gat tta aag gcg ctt gtc gac gcc gcc 547
 Phe Gly Gln Val Ser Pro Met Asp Leu Lys Ala Leu Val Asp Ala Ala
 135 140 145
 tgg ccg ctt ctt cga cga ggc ggt gcg ctg gtg ctc gcc gat gcg ctc 595
 Trp Pro Leu Leu Arg Arg Gly Gly Ala Leu Val Leu Ala Asp Ala Leu
 150 155 160 165
 ctt gac ggc acc att gcg gat caa acc cgc aag gat cgt gac acc caa 643
 Leu Asp Gly Thr Ile Ala Asp Gln Thr Arg Lys Asp Arg Asp Thr Gln
 170 175 180
 gca gca cgt gac gcc gat gaa tat att cgt tcc att gaa ggc gca cac 691
 Ala Ala Arg Asp Ala Asp Glu Tyr Ile Arg Ser Ile Glu Gly Ala His
 185 190 195
 gtt gct cgc ctg ccc ctt ggt gca ggc tta acc gtg gtg act aaa gcc 739
 Val Ala Arg Leu Pro Leu Gly Ala Gly Leu Thr Val Val Thr Lys Ala
 200 205 210
 tagaggggga cgtcgagaag cga 762

<210> 390

<211> 213

<212> PRT

<213> Corynebacterium glutamicum

<400> 390

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Glu Thr Asp Ala Val Ala Arg Ala Arg Glu Asp Ala Ala Glu Phe
 20 25 30

Gly Leu Pro Ala Pro Asp Glu Met Thr Gly Gln Leu Leu Thr Thr Leu
 35 40 45

Ala Ala Thr Thr Asn Gly Asn Gly Ser Thr Gly Ala Ile Ala Ile Thr
 50 55 60

Pro Ala Ala Gly Leu Val Gly Leu Tyr Ile Leu Asn Gly Leu Ala Asp
 65 70 75 80

Asn Thr Thr Leu Thr Cys Ile Asp Pro Glu Ser Glu His Gln Arg Gln
 85 90 95

Ala Lys Ala Leu Phe Arg Glu Ala Gly Tyr Ser Pro Ser Arg Val Arg
 100 105 110

Phe Leu Leu Ser Arg Pro Leu Asp Val Met Ser Arg Leu Ala Asn Asp
 115 120 125

Ser Tyr Gln Leu Val Phe Gly Gln Val Ser Pro Met Asp Leu Lys Ala
 130 135 140

Leu Val Asp Ala Ala Trp Pro Leu Leu Arg Arg Gly Gly Ala Leu Val
 145 150 155 160

Leu Ala Asp Ala Leu Leu Asp Gly Thr Ile Ala Asp Gln Thr Arg Lys
 165 170 175

Asp Arg Asp Thr Gln Ala Ala Arg Asp Ala Asp Glu Tyr Ile Arg Ser
 180 185 190

Ile Glu Gly Ala His Val Ala Arg Leu Pro Leu Gly Ala Gly Leu Thr
 195 200 205

Val Val Thr Lys Ala
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<210> 391
 <211> 978
 <212> DNA
 <213> Corynebacterium glutamicum

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 <223> RXN00639

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 Met Thr Ser Ala Glu
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cag atc gtt gat cca aca gcc cac gat tcg ggc aac aag gca act gac 163
 Gln Ile Val Asp Pro Thr Ala His Asp Ser Gly Asn Lys Ala Thr Asp
 10 15 20

aag ttc aag gca aac cgc gtt tcc tcc gat acc tcc aag gaa cgc gca 211
 Lys Phe Lys Ala Asn Arg Val Ser Ser Asp Thr Ser Lys Glu Arg Ala
 25 30 35

aac gcg atc tac gta gat ctg ctc gcg gcg atc gcc cag gtt gct cac 259
 Asn Ala Ile Tyr Val Asp Leu Leu Ala Ala Ile Ala Gln Val Ala His

40					45					50							
aag	cac	gaa	gtc	acc	tac	gaa	gag	tac	gca	gtg	ctc	aag	cag	tgg	atg	307	
Lys	His	Glu	Val	Thr	Tyr	Glu	Glu	Tyr	Ala	Val	Leu	Lys	Gln	Trp	Met		
55					60					65							
atc	gac	gtt	gga	gaa	tac	ggc	gag	tgg	cca	ctg	tgg	ttg	gac	gtt	ttc	355	
Ile	Asp	Val	Gly	Glu	Tyr	Gly	Glu	Trp	Pro	Leu	Trp	Leu	Asp	Val	Phe		
70					75					80					85		
gtt	gag	cat	gag	atc	gaa	gag	atc	aac	tac	aac	cgc	cac	gac	tac	acc	403	
Val	Glu	His	Glu	Ile	Glu	Glu	Ile	Asn	Tyr	Asn	Arg	His	Asp	Tyr	Thr		
90					95					100							
gga	acc	aag	ggt	tcc	atc	gaa	ggc	cct	tat	tac	gta	gag	aac	tct	ccg	451	
Gly	Thr	Lys	Gly	Ser	Ile	Glu	Gly	Pro	Tyr	Tyr	Val	Glu	Asn	Ser	Pro		
105					110					115							
aag	ctc	cct	tgg	gat	gct	gaa	atg	cca	atg	cgt	gac	aag	gac	cgc	gca	499	
Lys	Leu	Pro	Trp	Asp	Ala	Glu	Met	Pro	Met	Arg	Asp	Lys	Asp	Arg	Ala		
120					125					130							
tgc	acc	cca	ctg	atc	ttc	gag	ggg	cag	gtt	act	gac	ctc	gac	ggc	aac	547	
Cys	Thr	Pro	Leu	Ile	Phe	Glu	Gly	Gln	Val	Thr	Asp	Leu	Asp	Gly	Asn		
135					140					145							
ggt	ctt	gat	gga	gca	gaa	gtt	gag	ctc	tgg	cac	gca	gat	gag	gac	gga	595	
Gly	Leu	Asp	Gly	Ala	Glu	Val	Glu	Leu	Trp	His	Ala	Asp	Glu	Asp	Gly		
150					155					160					165		
tac	tac	tcc	cag	ttc	gcg	cct	gga	atc	cca	gag	tgg	aac	ctg	cgt	ggc	643	
Tyr	Tyr	Ser	Gln	Phe	Ala	Pro	Gly	Ile	Pro	Glu	Trp	Asn	Leu	Arg	Gly		
170					175					180							
acc	atc	gtt	acc	gat	gag	gaa	ggc	cgc	tac	aag	atc	aag	acc	ctg	cag	691	
Thr	Ile	Val	Thr	Asp	Glu	Glu	Gly	Arg	Tyr	Lys	Ile	Lys	Thr	Leu	Gln		
185					190					195							
cct	gcg	cct	tac	cag	atc	cct	cat	gat	ggc	cca	acc	ggt	tgg	ttc	att	739	
Pro	Ala	Pro	Tyr	Gln	Ile	Pro	His	Asp	Gly	Pro	Thr	Gly	Trp	Phe	Ile		
200					205					210							
gag	tct	tac	ggt	ggg	cac	cca	tgg	cgc	cca	gcc	cac	ctc	cac	ttg	cgc	787	
Glu	Ser	Tyr	Gly	Gly	His	Pro	Trp	Arg	Pro	Ala	His	Leu	His	Leu	Arg		
215					220					225							
gtt	tcc	cac	ccg	ggc	tac	cgc	acc	atc	acc	acc	cag	ctt	tac	ttc	gag	835	
Val	Ser	His	Pro	Gly	Tyr	Arg	Thr	Ile	Thr	Thr	Gln	Leu	Tyr	Phe	Glu		
230					235					240					245		
ggt	ggc	gag	tgg	gtc	gaa	aac	gac	gtt	gca	acc	gct	gtg	aag	cca	gaa	883	
Gly	Gly	Glu	Trp	Val	Glu	Asn	Asp	Val	Ala	Thr	Ala	Val	Lys	Pro	Glu		
250					255					260							
ctg	gtc	ctg	cac	cct	gag	act	ggc	gag	gat	ggt	aac	cac	gtt	cac	tac	931	
Leu	Val	Leu	His	Pro	Glu	Thr	Gly	Glu	Asp	Gly	Asn	His	Val	His	Tyr		
265					270					275							
cca	ttc	gtc	ctg	gat	aag	gaa	gac	tagtttttct	acctagctag	cat						978	
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<210> 392

<211> 285

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 392

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Asn Lys Ala Thr Asp Lys Phe Lys Ala Asn Arg Val Ser Ser Asp Thr
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Ser Lys Glu Arg Ala Asn Ala Ile Tyr Val Asp Leu Leu Ala Ala Ile
 35 40 45

Ala Gln Val Ala His Lys His Glu Val Thr Tyr Glu Glu Tyr Ala Val
 50 55 60

Leu Lys Gln Trp Met Ile Asp Val Gly Glu Tyr Gly Glu Trp Pro Leu
 65 70 75 80

Trp Leu Asp Val Phe Val Glu His Glu Ile Glu Glu Ile Asn Tyr Asn
 85 90 95

Arg His Asp Tyr Thr Gly Thr Lys Gly Ser Ile Glu Gly Pro Tyr Tyr
 100 105 110

Val Glu Asn Ser Pro Lys Leu Pro Trp Asp Ala Glu Met Pro Met Arg
 115 120 125

Asp Lys Asp Arg Ala Cys Thr Pro Leu Ile Phe Glu Gly Gln Val Thr
 130 135 140

Asp Leu Asp Gly Asn Gly Leu Asp Gly Ala Glu Val Glu Leu Trp His
 145 150 155 160

Ala Asp Glu Asp Gly Tyr Tyr Ser Gln Phe Ala Pro Gly Ile Pro Glu
 165 170 175

Trp Asn Leu Arg Gly Thr Ile Val Thr Asp Glu Glu Gly Arg Tyr Lys
 180 185 190

Ile Lys Thr Leu Gln Pro Ala Pro Tyr Gln Ile Pro His Asp Gly Pro
 195 200 205

Thr Gly Trp Phe Ile Glu Ser Tyr Gly Gly His Pro Trp Arg Pro Ala
 210 215 220

His Leu His Leu Arg Val Ser His Pro Gly Tyr Arg Thr Ile Thr Thr
 225 230 235 240

Gln Leu Tyr Phe Glu Gly Gly Glu Trp Val Glu Asn Asp Val Ala Thr
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Ala Val Lys Pro Glu Leu Val Leu His Pro Glu Thr Gly Glu Asp Gly
 260 265 270

Asn His Val His Tyr Pro Phe Val Leu Asp Lys Glu Asp
 275 280 285

<400> 393																
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gcaccccccta cttcaccccc aaagtctcta ggagtatgac atg act tca gct gaa 115																
Met Thr Ser Ala Glu 5																
cag atc gtt gat cca aca gcc cac gat tcg ggc aac aag gca act gac 163																
Gln Ile Val Asp Pro Thr Ala His Asp Ser Gly Asn Lys Ala Thr Asp 20																
aag ttc aag gca aac cgc gtt tcc tcc gat acc tcc aag gaa cgc gca 211																
Lys Phe Lys Ala Asn Arg Val Ser Ser Asp Thr Ser Lys Glu Arg Ala 35																
aac gcg atc tac gta gat ctg ctc gcg gcg atc gcc cag gtt gct cac 259																
Asn Ala Ile Tyr Val Asp Leu Leu Ala Ala Ile Ala Gln Val Ala His 50																
aag cac gaa gtc acc tac gaa gag tac gca gtg ctc aag cag tgg atg 307																
Lys His Glu Val Thr Tyr Glu Glu Tyr Ala Val Leu Lys Gln Trp Met 65																
atc gac gtt gga gaa tac ggc gag tgg cca ctg tgg ttg gac gtt ttc 355																
Ile Asp Val Gly Glu Tyr Gly Glu Trp Pro Leu Trp Leu Asp Val Phe 85																
gtt gag cat gag atc gaa gag atc aac tac aac cgc cac gac tac acc 403																
Val Glu His Glu Ile Glu Glu Ile Asn Tyr Asn Arg His Asp Tyr Thr 100																
gga acc aag ggt tcc atc gaa ggc cct tat tac gta gag aac tct ccg 451																
Gly Thr Lys Gly Ser Ile Glu Gly Pro Tyr Tyr Val Glu Asn Ser Pro 115																
aag ctc cct tgg gat gct gaa atg cca atg cgt gac aag gac cgc gca 499																
Lys Leu Pro Trp Asp Ala Glu Met Pro Met Arg Asp Lys Asp Arg Ala 130																
tgc acc cca ctg atc ttc gag ggg cag gtt act gac ctc gac ggc aac 547																
Cys Thr Pro Leu Ile Phe Glu Gly Gln Val Thr Asp Leu Asp Gly Asn 145																
ggt ctt gat gga gca gaa gtt gag ctc tgg cac gca gat gag gac gga 595																
Gly Leu Asp Gly Ala Glu Val Glu Leu Trp His Ala Asp Glu Asp Gly 165																
tac tac tcc cag ttc gcg cct gga atc cca gag tgg aac ctg cgt ggc 643																
Tyr Tyr Ser Gln Phe Ala Pro Gly Ile Pro Glu Trp Asn Leu Arg Gly																

170										175					180					
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Thr	Ile	Val	Thr	Asp	Glu	Glu	Gly	Arg	Tyr	Lys	Ile	Lys	Thr	Leu	Gln					
			185					190					195							
cct	gcg	cct	tac	cag	atc	cct	cat	gat	ggc	cca	acc	ggg	tgg	ttc	att	739				
Pro	Ala	Pro	Tyr	Gln	Ile	Pro	His	Asp	Gly	Pro	Thr	Gly	Trp	Phe	Ile					
		200					205					210								
gag	tct	tac	ggg	ggg	cac	cca										760				
Glu	Ser	Tyr	Gly	Gly	His	Pro														
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<212> PRT

<213> Corynebacterium glutamicum

<400> 394

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Ser	Lys	Glu	Arg	Ala	Asn	Ala	Ile	Tyr	Val	Asp	Leu	Leu	Ala	Ala	Ile	
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Leu	Lys	Gln	Trp	Met	Ile	Asp	Val	Gly	Glu	Tyr	Gly	Glu	Trp	Pro	Leu	
65					70					75					80	
Trp	Leu	Asp	Val	Phe	Val	Glu	His	Glu	Ile	Glu	Glu	Ile	Asn	Tyr	Asn	
				85					90					95		
Arg	His	Asp	Tyr	Thr	Gly	Thr	Lys	Gly	Ser	Ile	Glu	Gly	Pro	Tyr	Tyr	
		100						105					110			
Val	Glu	Asn	Ser	Pro	Lys	Leu	Pro	Trp	Asp	Ala	Glu	Met	Pro	Met	Arg	
		115					120					125				
Asp	Lys	Asp	Arg	Ala	Cys	Thr	Pro	Leu	Ile	Phe	Glu	Gly	Gln	Val	Thr	
	130					135					140					
Asp	Leu	Asp	Gly	Asn	Gly	Leu	Asp	Gly	Ala	Glu	Val	Glu	Leu	Trp	His	
145				150					155					160		
Ala	Asp	Glu	Asp	Gly	Tyr	Tyr	Ser	Gln	Phe	Ala	Pro	Gly	Ile	Pro	Glu	
				165					170					175		
Trp	Asn	Leu	Arg	Gly	Thr	Ile	Val	Thr	Asp	Glu	Glu	Gly	Arg	Tyr	Lys	
			180					185					190			
Ile	Lys	Thr	Leu	Gln	Pro	Ala	Pro	Tyr	Gln	Ile	Pro	His	Asp	Gly	Pro	
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Thr	Gly	Trp	Phe	Ile	Glu	Ser	Tyr	Gly	Gly	His	Pro					

210

215

220

<210> 395

<211> 1584

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(1561)

<223> RXN01653

<400> 395

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 Met Ala Thr Ala Glu
 1 5

aac aca aca cag gag aat cgg aaa atc ctg ttc aac gca ttt gat atg 163
 Asn Thr Thr Gln Glu Asn Arg Lys Ile Leu Phe Asn Ala Phe Asp Met
 10 15 20

aac tgc gtt gcg cat cag tcc cca gga ctg tgg aca cac ccg aag gat 211
 Asn Cys Val Ala His Gln Ser Pro Gly Leu Trp Thr His Pro Lys Asp
 25 30 35

aag gcg cga gac tac aac act ctt gat tac tgg gtg cac ctt gcc aag 259
 Lys Ala Arg Asp Tyr Asn Thr Leu Asp Tyr Trp Val His Leu Ala Lys
 40 45 50

act ttg gag aag ggc ctt ttc gac ggc ctt ttc atc gca gat gtg ctt 307
 Thr Leu Glu Lys Gly Leu Phe Asp Gly Leu Phe Ile Ala Asp Val Leu
 55 60 65

gga act tac gat gtt tat ggt tct agt aat gaa gcg gcg ttg agc agt 355
 Gly Thr Tyr Asp Val Tyr Gly Ser Ser Asn Glu Ala Ala Leu Ser Ser
 70 75 80 85

ggt gcg cag gtg cct gtc aat gat ccg atc ctt ctt gtt tct gcg atg 403
 Gly Ala Gln Val Pro Val Asn Asp Pro Ile Leu Leu Val Ser Ala Met
 90 95 100

gcc tat gcc aca aag aac ctc ggg ttt ggc att act gca ggt act gcc 451
 Ala Tyr Ala Thr Lys Asn Leu Gly Phe Gly Ile Thr Ala Gly Thr Ala
 105 110 115

tat gag cac ccg tat cct ttt gcg cgg cgt ctg gcc aca ctt gat cac 499
 Tyr Glu His Pro Tyr Pro Phe Ala Arg Arg Leu Ala Thr Leu Asp His
 120 125 130

ctg act aat ggg cgt gtg ggg tgg aat gtg gtt act ggc tat ctt ccc 547
 Leu Thr Asn Gly Arg Val Gly Trp Asn Val Val Thr Gly Tyr Leu Pro
 135 140 145

tct gct gct caa aac atg ggt gac acc gat cag ctg cca cat gat gag 595
 Ser Ala Ala Gln Asn Met Gly Asp Thr Asp Gln Leu Pro His Asp Glu
 150 155 160 165

cgc tat gac aaa gca gat gaa tac ctg gaa gtg atc tac aag ctt ctc 643

Arg	Tyr	Asp	Lys	Ala	Asp	Glu	Tyr	Leu	Glu	Val	Ile	Tyr	Lys	Leu	Leu		
				170					175					180			
gag	ggc	tcc	tgg	gaa	gac	gat	gct	gtt	caa	aac	aat	acg	gag	acg	agt	691	
Glu	Gly	Ser	Trp	Glu	Asp	Asp	Ala	Val	Gln	Asn	Asn	Thr	Glu	Thr	Ser		
			185					190					195				
gtc	ttt	acg	gac	tcc	tcc	aaa	gtg	cac	gcc	att	aat	cat	cat	ggc	aag	739	
Val	Phe	Thr	Asp	Ser	Ser	Lys	Val	His	Ala	Ile	Asn	His	His	Gly	Lys		
		200					205				210						
tac	ttt	gat	gtg	ccg	ggc	att	gcc	atc	act	gag	ccg	agt	gtg	cag	cgt	787	
Tyr	Phe	Asp	Val	Pro	Gly	Ile	Ala	Ile	Thr	Glu	Pro	Ser	Val	Gln	Arg		
	215					220				225							
acg	ccg	gtg	atc	tac	cag	gcg	ggg	gca	tcg	ccg	cgc	gga	ttg	aaa	ttc	835	
Thr	Pro	Val	Ile	Tyr	Gln	Ala	Gly	Ala	Ser	Pro	Arg	Gly	Leu	Lys	Phe		
230					235				240					245			
gct	ggg	gag	aat	gca	gaa	gca	gtg	ttt	atc	aat	tcc	agc	acc	gtg	gag	883	
Ala	Gly	Glu	Asn	Ala	Glu	Ala	Val	Phe	Ile	Asn	Ser	Ser	Thr	Val	Glu		
				250				255						260			
gca	atc	acc	aag	act	gtc	gca	aaa	att	cgc	gct	gct	gcg	gtc	gct	gcg	931	
Ala	Ile	Thr	Lys	Thr	Val	Ala	Lys	Ile	Arg	Ala	Ala	Ala	Val	Ala	Ala		
			265				270						275				
gga	cgt	gat	cca	cat	gcg	gtg	aag	atc	ttt	gcg	atg	caa	acc	atc	atc	979	
Gly	Arg	Asp	Pro	His	Ala	Val	Lys	Ile	Phe	Ala	Met	Gln	Thr	Ile	Ile		
		280					285				290						
act	ggg	gaa	aca	gaa	gca	gat	gcg	cag	gca	aag	ctg	gag	gaa	tac	agt	1027	
Thr	Gly	Glu	Thr	Glu	Ala	Asp	Ala	Gln	Ala	Lys	Leu	Glu	Glu	Tyr	Ser		
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cgc	tat	atc	gat	cct	gtc	ggg	ggg	ctg	acc	ttg	atg	tct	gga	tgg	acc	1075	
Arg	Tyr	Ile	Asp	Pro	Val	Gly	Gly	Leu	Thr	Leu	Met	Ser	Gly	Trp	Thr		
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ggc	gcg	gat	ctg	tcg	cag	tat	gac	ctg	gat	gaa	ccg	atc	acc	aat	att	1123	
Gly	Ala	Asp	Leu	Ser	Gln	Tyr	Asp	Leu	Asp	Glu	Pro	Ile	Thr	Asn	Ile		
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gag	tca	aac	gct	att	cag	tcc	act	gca	gcc	acc	att	agc	aac	ggc	acc	1171	
Glu	Ser	Asn	Ala	Ile	Gln	Ser	Thr	Ala	Ala	Thr	Ile	Ser	Asn	Gly	Thr		
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ggg	gaa	ggg	gcg	tgg	acg	gta	cgc	aaa	ctg	ggg	gag	gca	acc	ggc	atc	1219	
Gly	Glu	Gly	Ala	Trp	Thr	Val	Arg	Lys	Leu	Gly	Glu	Ala	Thr	Gly	Ile		
		360				365				370							
ggc	ggc	ttc	gga	cca	gtg	ctt	gtg	gga	tct	ggc	gct	aac	gtt	gcc	gcg	1267	
Gly	Gly	Phe	Gly	Pro	Val	Leu	Val	Gly	Ser	Gly	Ala	Asn	Val	Ala	Ala		
	375					380				385							
gaa	ctt	gca	cgc	atc	cag	gat	ctc	agc	gat	gtt	gat	ggg	ttc	aac	ctt	1315	
Glu	Leu	Ala	Arg	Ile	Gln	Asp	Leu	Ser	Asp	Val	Asp	Gly	Phe	Asn	Leu		
390					395					400				405			
gct	tat	gcc	atc	acc	cca	gga	act	ttt	gaa	gat	gtc	gtg	gac	ttt	gtg	1363	
Ala	Tyr	Ala	Ile	Thr	Pro	Gly	Thr	Phe	Glu	Asp	Val	Val	Asp	Phe	Val		

410										415					420					
gtg	cct	gag	ctg	caa	aaa	ctt	agc	cgc	tac	aag	acg	gaa	tac	gcg	ccg	1411				
Val	Pro	Glu	Leu	Gln	Lys	Leu	Ser	Arg	Tyr	Lys	Thr	Glu	Tyr	Ala	Pro					
			425					430					435							
ggc	tcc	ttg	cgc	aac	aaa	ttg	ctc	ggc	aaa	ggc	gat	cgc	ctg	gac	gat	1459				
Gly	Ser	Leu	Arg	Asn	Lys	Leu	Leu	Gly	Lys	Gly	Asp	Arg	Leu	Asp	Asp					
		440					445					450								
acc	cac	cgc	ggc	gca	agc	tac	cgc	cta	ggc	gct	cgc	aac	tcc	acc	gcc	1507				
Thr	His	Arg	Gly	Ala	Ser	Tyr	Arg	Leu	Gly	Ala	Arg	Asn	Ser	Thr	Ala					
		455				460					465									
act	att	gat	ctc	agt	tcc	ata	tcc	gcc	caa	cta	gtt	tcc	cag	gga	gcc	1555				
Thr	Ile	Asp	Leu	Ser	Ser	Ile	Ser	Ala	Gln	Leu	Val	Ser	Gln	Gly	Ala					
470					475					480					485					
cac	tca	tgatctcacc	gcaaacaatc	atc												1584				
His	Ser																			

<210> 396

<211> 487

<212> PRT

<213> Corynebacterium glutamicum

<400> 396

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			20					25					30			
Thr	His	Pro	Lys	Asp	Lys	Ala	Arg	Asp	Tyr	Asn	Thr	Leu	Asp	Tyr	Trp	
		35					40					45				
Val	His	Leu	Ala	Lys	Thr	Leu	Glu	Lys	Gly	Leu	Phe	Asp	Gly	Leu	Phe	
	50					55					60					
Ile	Ala	Asp	Val	Leu	Gly	Thr	Tyr	Asp	Val	Tyr	Gly	Ser	Ser	Asn	Glu	
65				70					75						80	
Ala	Ala	Leu	Ser	Ser	Gly	Ala	Gln	Val	Pro	Val	Asn	Asp	Pro	Ile	Leu	
				85					90					95		
Leu	Val	Ser	Ala	Met	Ala	Tyr	Ala	Thr	Lys	Asn	Leu	Gly	Phe	Gly	Ile	
			100					105					110			
Thr	Ala	Gly	Thr	Ala	Tyr	Glu	His	Pro	Tyr	Pro	Phe	Ala	Arg	Arg	Leu	
		115					120					125				
Ala	Thr	Leu	Asp	His	Leu	Thr	Asn	Gly	Arg	Val	Gly	Trp	Asn	Val	Val	
		130				135					140					
Thr	Gly	Tyr	Leu	Pro	Ser	Ala	Ala	Gln	Asn	Met	Gly	Asp	Thr	Asp	Gln	
145					150					155					160	
Leu	Pro	His	Asp	Glu	Arg	Tyr	Asp	Lys	Ala	Asp	Glu	Tyr	Leu	Glu	Val	
				165					170					175		

Ile Tyr Lys Leu Leu Glu Gly Ser Trp Glu Asp Asp Ala Val Gln Asn
 180 185 190
 Asn Thr Glu Thr Ser Val Phe Thr Asp Ser Ser Lys Val His Ala Ile
 195 200 205
 Asn His His Gly Lys Tyr Phe Asp Val Pro Gly Ile Ala Ile Thr Glu
 210 215 220
 Pro Ser Val Gln Arg Thr Pro Val Ile Tyr Gln Ala Gly Ala Ser Pro
 225 230 235 240
 Arg Gly Leu Lys Phe Ala Gly Glu Asn Ala Glu Ala Val Phe Ile Asn
 245 250 255
 Ser Ser Thr Val Glu Ala Ile Thr Lys Thr Val Ala Lys Ile Arg Ala
 260 265 270
 Ala Ala Val Ala Ala Gly Arg Asp Pro His Ala Val Lys Ile Phe Ala
 275 280 285
 Met Gln Thr Ile Ile Thr Gly Glu Thr Glu Ala Asp Ala Gln Ala Lys
 290 295 300
 Leu Glu Glu Tyr Ser Arg Tyr Ile Asp Pro Val Gly Gly Leu Thr Leu
 305 310 315 320
 Met Ser Gly Trp Thr Gly Ala Asp Leu Ser Gln Tyr Asp Leu Asp Glu
 325 330 335
 Pro Ile Thr Asn Ile Glu Ser Asn Ala Ile Gln Ser Thr Ala Ala Thr
 340 345 350
 Ile Ser Asn Gly Thr Gly Glu Gly Ala Trp Thr Val Arg Lys Leu Gly
 355 360 365
 Glu Ala Thr Gly Ile Gly Gly Phe Gly Pro Val Leu Val Gly Ser Gly
 370 375 380
 Ala Asn Val Ala Ala Glu Leu Ala Arg Ile Gln Asp Leu Ser Asp Val
 385 390 395 400
 Asp Gly Phe Asn Leu Ala Tyr Ala Ile Thr Pro Gly Thr Phe Glu Asp
 405 410 415
 Val Val Asp Phe Val Val Pro Glu Leu Gln Lys Leu Ser Arg Tyr Lys
 420 425 430
 Thr Glu Tyr Ala Pro Gly Ser Leu Arg Asn Lys Leu Leu Gly Lys Gly
 435 440 445
 Asp Arg Leu Asp Asp Thr His Arg Gly Ala Ser Tyr Arg Leu Gly Ala
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~~Arg Asn Ser Thr Ala Thr Ile Asp Leu Ser Ser Ile Ser Ala Gln Leu~~
 465 470 475 480
 Val Ser Gln Gly Ala His Ser
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<210> 398
<211> 120
<212> PRT
<213> Corynebacterium glutamicum
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  1                      5                      10                     15
Asn Ala Phe Asp Met Asn Cys Val Ala His Gln Ser Pro Gly Leu Trp

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20	25	30
Thr His Pro Lys Asp Lys Ala Arg Asp Tyr Asn Thr Leu Asp Tyr Trp		
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Val His Leu Ala Lys Thr Leu Glu Lys Gly Leu Phe Asp Gly Leu Phe		
50	55	60
Ile Ala Asp Val Leu Gly Thr Tyr Asp Val Tyr Gly Ser Ser Asn Glu		
65	70	75
Ala Ala Leu Ser Ser Gly Ala Gln Val Pro Val Asn Asp Pro Ile Leu		
85	90	95
Leu Val Ser Ala Met Ala Tyr Ala Thr Lys Asn Leu Gly Phe Gly Ile		
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Thr Ala Gly Thr Ala Tyr Glu His		
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 <213> Corynebacterium glutamicum

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 <222> (1)..(939)
 <223> FRXA01653

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Gly Ser Asp Leu Gln Ala Ser Arg Gly Leu Glu Asp Asp Ala Val	
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caa aac aat acg gag acg agt gtc ttt acg gac tcc tcc aaa gtg cac	96
Gln Asn Asn Thr Glu Thr Ser Val Phe Thr Asp Ser Ser Lys Val His	
20 25 30	
gcc att aat cat cat ggc aag tac ttt gat gtg ccg ggc att gcc atc	144
Ala Ile Asn His His Gly Lys Tyr Phe Asp Val Pro Gly Ile Ala Ile	
35 40 45	
act gag ccg agt gtg cag cgt acg ccg gtg atc tac cag gcg ggt gca	192
Thr Glu Pro Ser Val Gln Arg Thr Pro Val Ile Tyr Gln Ala Gly Ala	
50 55 60	
tcg ccg cgc gga ttg aaa ttc gct ggt gag aat gca gaa gca gtg ttt	240
Ser Pro Arg Gly Leu Lys Phe Ala Gly Glu Asn Ala Glu Ala Val Phe	
65 70 75 80	
atc aat tcc agc acc gtg gag gca atc acc aag act gtc gca aaa att	288
Ile Asn Ser Ser Thr Val Glu Ala Ile Thr Lys Thr Val Ala Lys Ile	
85 90 95	
cgc gct gct gcg gtc gct gcg gga cgt gat cca cat gcg gtg aag atc	336
Arg Ala Ala Ala Val Ala Ala Gly Arg Asp Pro His Ala Val Lys Ile	
100 105 110	
ttt gcg atg caa acc atc atc act ggt gaa aca gaa gca gat gcg cag	384

Phe Ala Met Gln Thr Ile Ile Thr Gly Glu Thr Glu Ala Asp Ala Gln
 115 120 125
 gca aag ctg gag gaa tac agt cgc tat atc gat cct gtc ggt ggt ctg 432
 Ala Lys Leu Glu Glu Tyr Ser Arg Tyr Ile Asp Pro Val Gly Gly Leu
 130 135 140
 acc ttg atg tct gga tgg acc ggc gcg gat ctg tcg cag tat gac ctg 480
 Thr Leu Met Ser Gly Trp Thr Gly Ala Asp Leu Ser Gln Tyr Asp Leu
 145 150 155 160
 gat gaa ccg atc acc aat att gag tca aac gct att cag tcc act gca 528
 Asp Glu Pro Ile Thr Asn Ile Glu Ser Asn Ala Ile Gln Ser Thr Ala
 165 170 175
 gcc acc att agc aac ggc acc ggt gaa ggt gcg tgg acg gta cgc aaa 576
 Ala Thr Ile Ser Asn Gly Thr Gly Glu Gly Ala Trp Thr Val Arg Lys
 180 185 190
 ctg ggt gag gca acc ggc atc ggc ggc ttc gga cca gtg ctt gtg gga 624
 Leu Gly Glu Ala Thr Gly Ile Gly Gly Phe Gly Pro Val Leu Val Gly
 195 200 205
 tct ggc gct aac gtt gcc gcg gaa ctt gca cgc atc cag gat ctc agc 672
 Ser Gly Ala Asn Val Ala Glu Leu Ala Arg Ile Gln Asp Leu Ser
 210 215 220
 gat gtt gat ggt ttc aac ctt gct tat gcc atc acc cca gga act ttt 720
 Asp Val Asp Gly Phe Asn Leu Ala Tyr Ala Ile Thr Pro Gly Thr Phe
 225 230 235 240
 gaa gat gtc gtg gac ttt gtg gtg cct gag ctg caa aaa ctt agc cgc 768
 Glu Asp Val Val Asp Phe Val Val Pro Glu Leu Gln Lys Leu Ser Arg
 245 250 255
 tac aag acg gaa tac gcg ccg ggt tcc ttg cgc aac aaa ttg ctc ggt 816
 Tyr Lys Thr Glu Tyr Ala Pro Gly Ser Leu Arg Asn Lys Leu Leu Gly
 260 265 270
 aaa ggt gat cgc ctg gac gat acc cac cgc ggc gca agc tac cgc cta 864
 Lys Gly Asp Arg Leu Asp Asp Thr His Arg Gly Ala Ser Tyr Arg Leu
 275 280 285
 ggc gct cgg aac tcc acc gcc act att gat ctc agt tcc ata tcc gcc 912
 Gly Ala Arg Asn Ser Thr Ala Thr Ile Asp Leu Ser Ser Ile Ser Ala
 290 295 300
 caa cta gtt tcc cag gga gcc cac tca tgatctcacc gcaaacaatc atc 962
 Gln Leu Val Ser Gln Gly Ala His Ser
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<211> 313

<212> PRT

<213> ~~Corynebacterium-glutamicum~~

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Gln Asn Asn Thr Glu Thr Ser Val Phe Thr Asp Ser Ser Lys Val His
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 Ala Ile Asn His His Gly Lys Tyr Phe Asp Val Pro Gly Ile Ala Ile
 35 40 45
 Thr Glu Pro Ser Val Gln Arg Thr Pro Val Ile Tyr Gln Ala Gly Ala
 50 55 60
 Ser Pro Arg Gly Leu Lys Phe Ala Gly Glu Asn Ala Glu Ala Val Phe
 65 70 75 80
 Ile Asn Ser Ser Thr Val Glu Ala Ile Thr Lys Thr Val Ala Lys Ile
 85 90 95
 Arg Ala Ala Ala Val Ala Ala Gly Arg Asp Pro His Ala Val Lys Ile
 100 105 110
 Phe Ala Met Gln Thr Ile Ile Thr Gly Glu Thr Glu Ala Asp Ala Gln
 115 120 125
 Ala Lys Leu Glu Glu Tyr Ser Arg Tyr Ile Asp Pro Val Gly Gly Leu
 130 135 140
 Thr Leu Met Ser Gly Trp Thr Gly Ala Asp Leu Ser Gln Tyr Asp Leu
 145 150 155 160
 Asp Glu Pro Ile Thr Asn Ile Glu Ser Asn Ala Ile Gln Ser Thr Ala
 165 170 175
 Ala Thr Ile Ser Asn Gly Thr Gly Glu Gly Ala Trp Thr Val Arg Lys
 180 185 190
 Leu Gly Glu Ala Thr Gly Ile Gly Gly Phe Gly Pro Val Leu Val Gly
 195 200 205
 Ser Gly Ala Asn Val Ala Ala Glu Leu Ala Arg Ile Gln Asp Leu Ser
 210 215 220
 Asp Val Asp Gly Phe Asn Leu Ala Tyr Ala Ile Thr Pro Gly Thr Phe
 225 230 235 240
 Glu Asp Val Val Asp Phe Val Val Pro Glu Leu Gln Lys Leu Ser Arg
 245 250 255
 Tyr Lys Thr Glu Tyr Ala Pro Gly Ser Leu Arg Asn Lys Leu Leu Gly
 260 265 270
 Lys Gly Asp Arg Leu Asp Asp Thr His Arg Gly Ala Ser Tyr Arg Leu
 275 280 285
 Gly Ala Arg Asn Ser Thr Ala Thr Ile Asp Leu Ser Ser Ile Ser Ala
 290 295 300
 Gln Leu Val Ser Gln Gly Ala His Ser
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<220>

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<222> (101) .. (757)

<223> RXN02530

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Met Ser Thr Asn Tyr
1 5

gaa gca atc atc att gga gca ggt cag gct gga ctc gcg gcg gcg cat 163
Glu Ala Ile Ile Ile Gly Ala Gly Gln Ala Gly Leu Ala Ala Ala His
10 15 20

gaa ctt tcc cgc cgc ggt ttc act ccc gga aaa gat ttt ctc gtc ctc 211
Glu Leu Ser Arg Arg Gly Phe Thr Pro Gly Lys Asp Phe Leu Val Leu
25 30 35

gat tcc aac gac ggg ccc ggt ggc gcc tgg cgg cat agg tgg gat tca 259
Asp Ser Asn Asp Gly Pro Gly Gly Ala Trp Arg His Arg Trp Asp Ser
40 45 50

ctc aca tta ggt aaa gcc cac gga atc gcc gat ctc cca ggg ctt ccc 307
Leu Thr Leu Gly Lys Ala His Gly Ile Ala Asp Leu Pro Gly Leu Pro
55 60 65

atg aat cgc ccc gat ccg aaa act ccg gct tcc aca ttg gtt gct ggt 355
Met Asn Arg Pro Asp Pro Lys Thr Pro Ala Ser Thr Leu Val Ala Gly
70 75 80 85

tat	tac	ggc	gct	tac	gag	aac	gag	ttc	tcc	ttc	gca	gtt	gtg	cgc	cca	403
Tyr	Tyr	Gly	Ala	Tyr	Glu	Asn	Glu	Phe	Ser	Phe	Ala	Val	Val	Arg	Pro	
				90		/			95					100		

gtc aaa gtc tca cga gtt gag ccc act tcc gag gat cct tcg agc cca 451
Val Lys Val Ser Arg Val Glu Pro Thr Ser Glu Asp Pro Ser Ser Pro
105 110 115

ttg	cgc	gtg	agc	agc	gac	gat	ggt	cga	gag	tgg	att	acc	cgc	atg	gtt	499
Leu	Arg	Val	Ser	Ser	Asp	Asp	Gly	Arg	Glu	Trp	Ile	Thr	Arg	Met	Val	
		120					125					130				

ctt aat gca aca ggt acg tgg aca aac cct tat gtt ccg tac att cct 547
 Leu Asn Ala Thr Gly Thr Trp Thr Asn Pro Tyr Val Pro Tyr Ile Pro
 135 140 145

ggc atc gat aaa ttc cag ggc aag cag ctc cac acc gtt aat tac cgc 595
Gly Ile Asp Lys Phe Gln Gly Lys Gln Leu His Thr Val Asn Tyr Arg
150 155 160 165

aag gcc gag gat ttc aaa ggt aag aaa gtc ctg gtc gtc ggc ggt ggt 643
Lys Ala Glu Asp Phe Lys Gly Lys Lys Val Leu Val Val Gly Gly Gly
170 175 180

ttg agt gct gtg caa ttt ctg ctg gag ttg gaa ggc ttg gcg gaa acc 691
Leu Ser Ala Val Gln Phe Leu Leu Glu Leu Glu Gly Leu Ala Glu Thr
185 190 195

cgg ctg ggg cat tgc ggt tgagcgcgcc gtccgcgaac gca 780
 Arg Leu Gly His Cys Gly
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<210> 402
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<213> Corynebacterium glutamicum
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Leu	Ala	Ala	Ala 20	His	Glu	Leu	Ser	Arg 25	Arg	Gly	Phe	Thr	Pro 30	Gly	Lys	
Asp	Phe 35	Leu	Val	Leu	Asp	Ser	Asn 40	Asp	Gly	Pro	Gly	Gly 45	Ala	Trp	Arg	
His 50	Arg	Trp	Asp	Ser	Leu	Thr 55	Leu	Gly	Lys	Ala	His 60	Gly	Ile	Ala	Asp	
Leu 65	Pro	Gly	Leu	Pro	Met 70	Asn	Arg	Pro	Asp	Pro 75	Lys	Thr	Pro	Ala	Ser 80	
Thr	Leu	Val	Ala	Gly 85	Tyr	Tyr	Gly	Ala	Tyr 90	Glu	Asn	Glu	Phe	Ser 95	Phe	
Ala	Val	Val	Arg 100	Pro	Val	Lys	Val	Ser 105	Arg	Val	Glu	Pro	Thr 110	Ser	Glu	
Asp	Pro	Ser 115	Ser	Pro	Leu	Arg	Val 120	Ser	Ser	Asp	Asp	Gly 125	Arg	Glu	Trp	
Ile 130	Thr	Arg	Met	Val	Leu	Asn 135	Ala	Thr	Gly	Thr	Trp 140	Thr	Asn	Pro	Tyr	
Val 145	Pro	Tyr	Ile	Pro	Gly 150	Ile	Asp	Lys	Phe	Gln 155	Gly	Lys	Gln	Leu	His 160	
Thr	Val	Asn	Tyr	Arg 165	Lys	Ala	Glu	Asp	Phe 170	Lys	Gly	Lys	Lys	Val 175	Leu	
Val	Val	Gly	Gly 180	Gly	Leu	Ser	Ala	Val 185	Gln	Phe	Leu	Leu	Glu 190	Leu	Glu	
Gly	Leu 195	Ala	Glu	Thr	Thr	Trp	Ala 200	Thr	Arg	Arg	Pro	Arg 205	Thr	Tyr	Ala	
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<223> FRXA02530

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 Thr Leu Val Ala Gly Tyr Tyr Gly Ala Tyr Glu Asn Glu Phe Ser Phe
 15 20 25

gca gtt gtg cgc cca gtc aaa gtc tca cga gtt gag ccc act tcc gag 148
 Ala Val Val Arg Pro Val Lys Val Ser Arg Val Glu Pro Thr Ser Glu
 30 35 40

gat cct tcg agc cca ttg cgc gtg agc agc gac gat ggt cga gag tgg 196
 Asp Pro Ser Ser Pro Leu Arg Val Ser Ser Asp Asp Gly Arg Glu Trp
 45 50 55

att acc cgc atg gtt ctt aat gca aca ggt acg tgg aca aac cct tat 244
 Ile Thr Arg Met Val Leu Asn Ala Thr Gly Thr Trp Thr Asn Pro Tyr
 60 65 70 75

gtt ccg tac att cct ggc atc gat aaa ttc cag ggc aag cag ctc cac 292
 Val Pro Tyr Ile Pro Gly Ile Asp Lys Phe Gln Gly Lys Gln Leu His
 80 85 90

acc gtt aat tac cgc aag gcc gag gat ttc aaa ggt aag aaa gtc ctg 340
 Thr Val Asn Tyr Arg Lys Ala Glu Asp Phe Lys Gly Lys Lys Val Leu
 95 100 105

gtc gtc ggc ggt ggt ttg agt gct gtg caa ttt ctg ctg gag ttg gaa 388
 Val Val Gly Gly Gly Leu Ser Ala Val Gln Phe Leu Leu Glu Leu Glu
 110 115 120

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<213> Corynebacterium glutamicum

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 Lys Ala Glu Asp Phe Lys Gly Lys Lys Val Leu Val Val Gly Gly Gly
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 Met Glu Met Val Met
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 Lys Asn Lys Arg Val Ala Ile Ile Gly Ala Gly Pro Ser Gly Ile Ala
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 Gln Leu Arg Ala Phe Glu Ser Ala Glu Lys Gln Gly His Glu Ile Pro
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 Glu Leu Val Cys Phe Glu Lys Gln Asp Thr Trp Gly Gly Gln Trp Asn
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 Tyr Ser Trp Arg Thr Gly Thr Asp Ser Tyr Gly Glu Pro Val His Ser
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Thr Phe Ser Tyr Arg Ser Asn Pro Met Gly Tyr Glu Trp Pro Glu Glu	
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 Gly Gly Gln Trp Asn Tyr Ser Trp Arg Thr Gly Thr Asp Ser Tyr Gly
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His	Val	Val	Arg	Trp	Val	Ser	Phe	Asp	Glu	Ala	Thr	Lys	Leu	Phe	Thr		
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His His Thr Pro Trp Met Ile Glu Leu Asp Asp Ser Leu Glu Arg Tyr
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Tyr Phe Arg Ser Ile Pro Tyr Ala Lys Ala Arg Pro Phe Ala Asp Ala
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Glu Lys Leu Glu Pro Leu Arg Ile Asp Ala Thr Gly Lys His Glu Gly
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Leu Tyr Leu Thr Leu Ala Thr Pro Glu Ala Arg Phe Gly Ala Asp Ala
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Pro Val Ile Val Tyr Ile His Gly Gly Gly Tyr Asp Gly Gly Thr Arg
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Phe Asp Ala Arg Thr Glu Pro Thr Phe Phe Arg Glu Gln Gly Phe Val
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Ala	Leu	Glu	Trp	Val	Gln	Lys	Asn	Ile	Glu	His	Phe	Gly	Gly	Asp	Pro		
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Tyr	Gly	His	Arg	Ala	Gly	Leu	Trp	Phe	Asp	Gln	Arg	Gly	Phe	Gly	Ala		
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 Pro Phe Ala Asp Ala Glu Lys Leu Glu Pro Leu Arg Ile Asp Ala Thr
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 Gly Phe Ala Arg Phe His Asp Asp Glu Ala Asn Arg Tyr Arg Gly Ile
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 Asp Asp Cys Val Leu Ala Leu Glu Trp Val Gln Lys Asn Ile Glu His
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 Ala Gly Ile Ala Leu Trp Leu Thr Arg Leu Asp His Tyr Lys Gly Ala
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 Arg Ala Ser Leu Ala Gly Ile Lys Pro Ala Arg Leu Asp Lys Gly Tyr
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 Arg Arg Phe Ala Arg Arg Tyr Phe Thr Asp Leu Ala Leu Gly Pro Thr
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Phe Val Lys Gly Val Lys Gly Pro Gly Leu Lys Thr Trp Arg Gly Ile
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Pro Tyr Gly Arg Asn Thr Gly Gly Lys Tyr Arg Phe Arg Ala Pro Arg
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 Glu Asn Tyr Asp Met Leu Glu Trp Gly Thr Gly Arg Pro Asp Leu Ala
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 Asn Glu Leu Asp Phe Ile Glu Pro Glu Glu Thr Glu Glu Glu Gln Gln
 520 525 530

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Phe Arg Ala Pro Arg Pro Ala Lys Lys Trp Asp Gly Val Arg Asp Cys
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Ser Met Phe Gly Glu Val Ala Ser Gln Pro Thr Tyr Ser Trp Thr Asp
 65 70 75 80

Lys Ile Arg Gly Ser Glu Asp Cys Leu Asn Leu Asp Val Val Arg Pro
 85 90 95

Asp Ser Glu Glu Lys Leu Pro Val Val Val Tyr Leu His Gly Gly Ser
 100 105 110

~~Phe Ile Met Gly Ser Ser Ser Glu Lys Ala Leu Arg Gly Tyr Asn Leu~~
 115 120 125

Val Thr Asn Met Asn Val Val Tyr Val Ser Val Asn Phe Arg Leu Gly
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Ala	Leu	Gly	Tyr	Leu	Asp	Leu	Arg	Ser	Val	Gly	Glu	Asp	Cys	Val	Ala	
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Asn	Pro	Ala	Leu	His	Asp	Gln	Leu	Leu	Ala	Leu	Gln	Trp	Val	Ser	Arg	
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Glu	Ser	Ala	Gly	Ala	Ala	Ala	Val	Val	Ala	Leu	Met	Cys	Val	Pro	Ala	
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Ser	Val	His	Ser	Ser	Thr	Gln	Ala	Lys	Phe	Trp	Ala	Arg	Glu	Leu	Ile	
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Glu	Ser	Ala	Asp	Asp	Leu	Val	Arg	Ala	Gly	Gln	Ser	Met	Met	Trp	Arg	
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Ser	Gly	Glu	Leu	Leu	Gln	Leu	Asn	Ser	Cys	Tyr	Gly	Pro	Thr	Val	Asp	
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Gln	His	Arg	Ile	Pro	Phe	Met	Ile	Gly	Thr	Asn	Asn	Gly	Glu	Thr	Ser	
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Phe	Ser	Lys	Ala	Phe	Tyr	Leu	Arg	Ser	Ser	Ala	Arg	Arg	Arg	Ser	Ala	
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Gln	Ser	Met	Arg	Lys	Leu	Gly	Leu	Gly	Ala	Ile	His	Ser	Phe	Glu	Leu	
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Asn	Ala	Val	Phe	Gly	Asp	His	Glu	Ser	Ser	Arg	Ser	Met	Asn	Leu	Ala	
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Lys	Ile	Ala	Gly	Gly	Met	Asp	His	Leu	Asp	Lys	Val	Thr	Glu	Leu	Val	
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Gln	Glu	His	Trp	Lys	Gln	Phe	Ile	Tyr	Phe	Gly	Arg	Pro	Gly	Glu	Glu	
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Trp	Lys	Ala	Tyr	Arg	Gly	Arg	Ser	Asp	Thr	Glu	Pro	Gly	Arg	Ala	Thr	

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Gln Ala Thr Pro Gln Asp Ser Glu Ser Ala Leu Asn Lys Trp Ala Gln

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Trp Met Glu Glu Ser Glu Asp Ser Pro Leu Asn Arg Phe Thr Pro Glu			
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gcc ggc gac cgc aac gca gtc ttc gat atc aag gct acc tac cag cag			547
Ala Gly Asp Arg Asn Ala Val Phe Asp Ile Lys Ala Thr Tyr Gln Gln			
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cat tac cac tcc ttc gac ctg ttc gat gcg cca gag gtc ttc ttc cca			595
His Tyr His Ser Phe Asp Leu Phe Asp Ala Pro Glu Val Phe Phe Pro			
150	155	160	165
cga gtt gga cca tac aag ctg caa aac ctc gaa aac gtt tgg acc gca			643
Arg Val Gly Pro Tyr Lys Leu Gln Asn Leu Glu Asn Val Trp Thr Ala			
170	175	180	
ctg gat tcc caa gac atc ttt gag tcc cgt ggc atc agt cgc gat ggc			691
Leu Asp Ser Gln Asp Ile Phe Glu Ser Arg Gly Ile Ser Arg Asp Gly			
185	190	195	
gca att gtt gtc gtt cgc cca gac cag tac gtc gca gca gtc ctc cca			739
Ala Ile Val Val Val Arg Pro Asp Gln Tyr Val Ala Ala Val Leu Pro			
200	205	210	
ctc gaa gac acc gca gca ctg gct gag ttc ttc aat ggc aat ctg ctt			787
Leu Glu Asp Thr Ala Ala Leu Ala Glu Phe Phe Asn Gly Asn Leu Leu			
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Ala Glu Glu Phe Thr Ala Gly Phe Leu Thr Glu Tyr Gln Asp Asn Leu			
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Ile Thr Ala Gly Met Glu His Gln Ala Leu Ala Ser Gly Phe Pro Val			
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Gly Arg Arg Phe Lys Ser Asp Ile Ala Leu Arg Arg Cys Asp Ala Val			
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Thr Thr His Ile Gly His Glu His Ser Ala Asp Gly His Trp Arg Ile			
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Tyr Val Phe Ala Gly Gln Ala Thr Pro Gln Asp Ser Glu Ser Ala Leu			
100	105	110	

Asn Lys Trp Ala Gln Trp Met Glu Glu Ser Glu Asp Ser Pro Leu Asn
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 Arg Phe Thr Pro Glu Ala Gly Asp Arg Asn Ala Val Phe Asp Ile Lys
 130 135 140
 Ala Thr Tyr Gln Gln His Tyr His Ser Phe Asp Leu Phe Asp Ala Pro
 145 150 155 160
 Glu Val Phe Phe Pro Arg Val Gly Pro Tyr Lys Leu Gln Asn Leu Glu
 165 170 175
 Asn Val Trp Thr Ala Leu Asp Ser Gln Asp Ile Phe Glu Ser Arg Gly
 180 185 190
 Ile Ser Arg Asp Gly Ala Ile Val Val Val Arg Pro Asp Gln Tyr Val
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 Val Arg His Asp Glu
 1 5
 cac tac cca gct gcg gca aac ctc att gct ttc gat aag gga tgg tcc 163
 His Tyr Pro Ala Ala Ala Asn Leu Ile Ala Phe Asp Lys Gly Trp Ser
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 Thr Leu Ile Ala Pro Gln Leu Glu Asp Pro Glu Ala Glu Glu Phe Thr
 25 30 35
 gcc gga ttc ctc acc gaa tac cag gac aat ctg atc act gcg ggc atg 259
 Ala Gly Phe Leu Thr Glu Tyr Gln Asp Asn Leu Ile Thr Ala Gly Met
 40 45 50
 gag cac cag gcg ctc gcg agc ggc ttc ccg gtg ggg cgt cgc ttc aag 307
 Glu His Gln Ala Leu Ala Ser Gly Phe Pro Val Gly Arg Arg Phe Lys
 55 60 65
 tcc gat att gct tta cga cgc tgc gat gcg gtg acc acc cac atc ggc 355
 Ser Asp Ile Ala Leu Arg Arg Cys Asp Ala Val Thr Thr His Ile Gly

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His Glu His Ser Ala Asp Gly His Trp Arg Ile Tyr Val Phe Ala Gly				
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Gln Ala Thr Pro Gln				
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Ile Thr Ala Gly Met Glu His Gln Ala Leu Ala Ser Gly Phe Pro Val	
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Gly Arg Arg Phe Lys Ser Asp Ile Ala Leu Arg Arg Cys Asp Ala Val	
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	Met Gln Phe His Tyr
	1 5

gaa gga tac gca acc ggt gac cca atg gag atg cgc gcg gaa ggt agc	163
Glu Gly Tyr Ala Thr Gly Asp Pro Met Glu Met Arg Ala Glu Gly Ser	
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gga atc aac cgc ccg gac gat ctc ccc gag gtc atg gat gtt ctc atc	211

Gly	Ile	Asn	Arg	Pro	Asp	Asp	Leu	Pro	Glu	Val	Met	Asp	Val	Leu	Ile		
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Val	Gly	Ala	Gly	Pro	Ala	Gly	Thr	Ile	Ala	Ala	Ala	Gln	Leu	Ser	Arg		
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Phe	Pro	Asn	Val	Thr	Thr	Arg	Leu	Val	Glu	Arg	Ser	Asp	Arg	Arg	Leu		
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gaa	cta	gcc	aat	gca	gat	ggc	gtg	cac	tcc	cga	acc	att	gaa	act	ttc	355	
Glu	Leu	Ala	Asn	Ala	Asp	Gly	Val	His	Ser	Arg	Thr	Ile	Glu	Thr	Phe		
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Gln	Ala	Phe	Gly	Phe	Ala	His	Glu	Ile	Leu	Ala	Glu	Ala	His	Glu	Ile		
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Thr	Asp	Met	Ala	Phe	Trp	Lys	Pro	Asp	Pro	Gln	Asn	Pro	Arg	Glu	Ile		
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Pro	Met	Ala	Leu	Leu	Thr	Gln	Thr	Arg	Ile	Ile	Asp	His	Phe	Asn	Arg		
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Phe	Met	Lys	Asn	Ser	Pro	Thr	Arg	Met	Lys	Pro	Asp	Tyr	Gly	Tyr	Glu		
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Phe	Val	Asp	Phe	Glu	Val	Glu	Glu	Asp	Ala	Glu	Tyr	Pro	Val	Ile	Val		
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acc	ctc	cgc	cgc	acc	agt	ggc	gag	caa	act	ggc	gaa	ttg	gtc	acc	gtc	691	
Thr	Leu	Arg	Arg	Thr	Ser	Gly	Glu	Gln	Thr	Gly	Glu	Leu	Val	Thr	Val		
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Arg	Thr	Lys	Tyr	Leu	Val	Gly	Ala	Asp	Gly	Ala	Arg	Ser	Gln	Val	Arg		
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Lys	Ser	Leu	Gly	Tyr	Arg	Leu	Gln	Gly	Lys	Gln	Ala	Asn	His	Ala	Trp		
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Gly	Val	Met	Asp	Ile	His	Ala	Asn	Thr	Glu	Phe	Pro	Asp	Val	Arg	Lys		
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Lys	Cys	Thr	Ile	Lys	Ser	Asp	Ser	Gly	Arg	Thr	Ile	Leu	Leu	Ile	Pro		
				250					255					260			
cgt	gag	ggt	ggc	ttc	ctc	ttc	cgt	ctc	tac	gtt	gac	ctg	ggc	gaa	gta	931	
Arg	Glu	Gly	Gly	Phe	Leu	Phe	Arg	Leu	Tyr	Val	Asp	Leu	Gly	Glu	Val		

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cct	gat	gat	ggc	agc	aag	gct	ggt	cgt	gat	acc	cca	ctc	cag	gat	gtc	979		
Pro	Asp	Asp	Gly	Ser	Lys	Ala	Val	Arg	Asp	Thr	Pro	Leu	Gln	Asp	Val			
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Ile	Asp	Thr	Ala	Asn	Gln	Ile	Met	Ala	Pro	Phe	Thr	Leu	Asp	Val	Lys			
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aac	ggt	gtg	tgg	aac	tcc	atc	tac	gag	gta	ggc	cac	cgc	gtc	gca	gac	1075		
Asn	Val	Val	Trp	Asn	Ser	Ile	Tyr	Glu	Val	Gly	His	Arg	Val	Ala	Asp			
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cat	ttc	gat	gac	cgt	ggt	tca	gaa	aaa	acc	tcg	agc	gaa	cac	cca	cgc	1123		
His	Phe	Asp	Asp	Arg	Val	Ser	Glu	Lys	Thr	Ser	Ser	Glu	His	Pro	Arg			
				330					335					340				
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Ile	Phe	Ile	Ala	Gly	Asp	Ala	Cys	His	Thr	His	Ser	Ala	Lys	Ala	Gly			
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cag	ggc	atg	aac	gtg	tcc	atg	cag	gac	gga	ttc	aac	ctt	ggc	tgg	aag	1219		
Gln	Gly	Met	Asn	Val	Ser	Met	Gln	Asp	Gly	Phe	Asn	Leu	Gly	Trp	Lys			
		360					365					370						
ctt	gga	cat	gtg	gcc	agc	gga	aat	agc	cca	cgc	gaa	cta	ctt	cag	acc	1267		
Leu	Gly	His	Val	Ala	Ser	Gly	Asn	Ser	Pro	Arg	Glu	Leu	Leu	Gln	Thr			
		375				380					385							
tac	gct	gaa	gag	cgc	gaa	gac	att	gcc	tac	aag	ctc	atc	gag	tac	gac	1315		
Tyr	Ala	Glu	Glu	Arg	Glu	Asp	Ile	Ala	Tyr	Lys	Leu	Ile	Glu	Tyr	Asp			
		390			395					400					405			
aag	aac	tgg	tca	aca	ctc	atg	gca	aag	cca	agc	agc	gaa	atg	ggc	agt	1363		
Lys	Asn	Trp	Ser	Thr	Leu	Met	Ala	Lys	Pro	Ser	Ser	Glu	Met	Gly	Ser			
				410					415					420				
gcc	caa	gac	ctt	gag	gat	ttc	tac	cgc	gcg	aac	tct	gag	ttc	aat	gcc	1411		
Ala	Gln	Asp	Leu	Glu	Asp	Phe	Tyr	Arg	Ala	Asn	Ser	Glu	Phe	Asn	Ala			
			425					430					435					
ggc	tac	atg	acc	cac	tat	cct	cct	tct	tcc	atc	aca	atg	gat	ggc	agc	1459		
Gly	Tyr	Met	Thr	His	Tyr	Pro	Pro	Ser	Ser	Ile	Thr	Met	Asp	Gly	Ser			
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Asn	Gln	Asp	Leu	Ala	Lys	Gly	Tyr	Pro	Ile	Gly	Arg	Arg	Phe	Lys	Ser			
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Ala	Met	Val	Gly	Arg	Val	Cys	Asp	Phe	Thr	Glu	Thr	His	Leu	Gly	His			
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caa	gca	aca	gcc	gac	gga	cgc	atg	cgc	gca	tac	gtc	ttc	gca	gga	tcc	1603		
Gln	Ala	Thr	Ala	Asp	Gly	Arg	Met	Arg	Ala	Tyr	Val	Phe	Ala	Gly	Ser			
			490						495					500				
gat	gca	ctt	aac	ggc	gag	ggt	tct	gag	cta	gac	cgc	tgg	gca	gaa	tgg	1651		
Asp	Ala	Leu	Asn	Gly	Glu	Gly	Ser	Glu	Leu	Asp	Arg	Trp	Ala	Glu	Trp			
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gca gag gcg aac ctt gac ccc acg ctt gtc gac gcc aag gtg att tac 1699
 Ala Glu Ala Asn Leu Asp Pro Thr Leu Val Asp Ala Lys Val Ile Tyr
 520 525 530

caa agc cct tat acc gag ctc gac acc cgc cag gtt cca tcc gtg ttc 1747
 Gln Ser Pro Tyr Thr Glu Leu Asp Thr Arg Gln Val Pro Ser Val Phe
 535 540 545

aaa cct gca gtc ggg atc ttc gaa ctg acc aat gtg gaa aac tcc ttc 1795
 Lys Pro Ala Val Gly Ile Phe Glu Leu Thr Asn Val Glu Asn Ser Phe
 550 555 560 565

ggt atc acc acg gac tcc gac atc ttt gat agt cgc gag atc tcc cgc 1843
 Gly Ile Thr Thr Asp Ser Asp Ile Phe Asp Ser Arg Glu Ile Ser Arg
 570 575 580

gat ggt gtc gtg gtg gta gtc cga cca gac caa tac gtt tcc gga atc 1891
 Asp Gly Val Val Val Val Val Arg Pro Asp Gln Tyr Val Ser Gly Ile
 585 590 595

ttc cca ctc act gat acc caa ggg ctt ggc gaa ttc ctc acc gga tac 1939
 Phe Pro Leu Thr Asp Thr Gln Gly Leu Gly Glu Phe Leu Thr Gly Tyr
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Met Asp Val Leu Ile Val Gly Ala Gly Pro Ala Gly Thr Ile Ala Ala
 35 40 45

Ala Gln Leu Ser Arg Phe Pro Asn Val Thr Thr Arg Leu Val Glu Arg
 50 55 60

Ser Asp Arg Arg Leu Glu Leu Ala Asn Ala Asp Gly Val His Ser Arg
 65 70 75 80

Thr Ile Glu Thr Phe Gln Ala Phe Gly Phe Ala His Glu Ile Leu Ala
 85 90 95

Glu Ala His Glu Ile Thr Asp Met Ala Phe Trp Lys Pro Asp Pro Gln
 100 105 110

Asn Pro Arg Glu Ile Ile Arg Asp Asn Ser Thr Arg Glu Leu Pro Gln
 115 120 125

His	Ile	Ser	Glu	Phe	Pro	Met	Ala	Leu	Leu	Thr	Gln	Thr	Arg	Ile	Ile	130	135	140
Asp	His	Phe	Asn	Arg	Phe	Met	Lys	Asn	Ser	Pro	Thr	Arg	Met	Lys	Pro	145	150	155 160
Asp	Tyr	Gly	Tyr	Glu	Phe	Val	Asp	Phe	Glu	Val	Glu	Glu	Asp	Ala	Glu	165	170	175
Tyr	Pro	Val	Ile	Val	Thr	Leu	Arg	Arg	Thr	Ser	Gly	Glu	Gln	Thr	Gly	180	185	190
Glu	Leu	Val	Thr	Val	Arg	Thr	Lys	Tyr	Leu	Val	Gly	Ala	Asp	Gly	Ala	195	200	205
Arg	Ser	Gln	Val	Arg	Lys	Ser	Leu	Gly	Tyr	Arg	Leu	Gln	Gly	Lys	Gln	210	215	220
Ala	Asn	His	Ala	Trp	Gly	Val	Met	Asp	Ile	His	Ala	Asn	Thr	Glu	Phe	225	230	235 240
Pro	Asp	Val	Arg	Lys	Lys	Cys	Thr	Ile	Lys	Ser	Asp	Ser	Gly	Arg	Thr	245	250	255
Ile	Leu	Leu	Ile	Pro	Arg	Glu	Gly	Gly	Phe	Leu	Phe	Arg	Leu	Tyr	Val	260	265	270
Asp	Leu	Gly	Glu	Val	Pro	Asp	Asp	Gly	Ser	Lys	Ala	Val	Arg	Asp	Thr	275	280	285
Pro	Leu	Gln	Asp	Val	Ile	Asp	Thr	Ala	Asn	Gln	Ile	Met	Ala	Pro	Phe	290	295	300
Thr	Leu	Asp	Val	Lys	Asn	Val	Val	Trp	Asn	Ser	Ile	Tyr	Glu	Val	Gly	305	310	315 320
His	Arg	Val	Ala	Asp	His	Phe	Asp	Asp	Arg	Val	Ser	Glu	Lys	Thr	Ser	325	330	335
Ser	Glu	His	Pro	Arg	Ile	Phe	Ile	Ala	Gly	Asp	Ala	Cys	His	Thr	His	340	345	350
Ser	Ala	Lys	Ala	Gly	Gln	Gly	Met	Asn	Val	Ser	Met	Gln	Asp	Gly	Phe	355	360	365
Asn	Leu	Gly	Trp	Lys	Leu	Gly	His	Val	Ala	Ser	Gly	Asn	Ser	Pro	Arg	370	375	380
Glu	Leu	Leu	Gln	Thr	Tyr	Ala	Glu	Glu	Arg	Glu	Asp	Ile	Ala	Tyr	Lys	385	390	395 400
Leu	Ile	Glu	Tyr	Asp	Lys	Asn	Trp	Ser	Thr	Leu	Met	Ala	Lys	Pro	Ser	405	410	415
Ser	Glu	Met	Gly	Ser	Ala	Gln	Asp	Leu	Glu	Asp	Phe	Tyr	Arg	Ala	Asn	420	425	430
Ser	Glu	Phe	Asn	Ala	Gly	Tyr	Met	Thr	His	Tyr	Pro	Pro	Ser	Ser	Ile	435	440	445

Thr Met Asp Gly Ser Asn Gln Asp Leu Ala Lys Gly Tyr Pro Ile Gly
 450 455 460
 Arg Arg Phe Lys Ser Ala Met Val Gly Arg Val Cys Asp Phe Thr Glu
 465 470 475 480
 Thr His Leu Gly His Gln Ala Thr Ala Asp Gly Arg Met Arg Ala Tyr
 485 490 495
 Val Phe Ala Gly Ser Asp Ala Leu Asn Gly Glu Gly Ser Glu Leu Asp
 500 505 510
 Arg Trp Ala Glu Trp Ala Glu Ala Asn Leu Asp Pro Thr Leu Val Asp
 515 520 525
 Ala Lys Val Ile Tyr Gln Ser Pro Tyr Thr Glu Leu Asp Thr Arg Gln
 530 535 540
 Val Pro Ser Val Phe Lys Pro Ala Val Gly Ile Phe Glu Leu Thr Asn
 545 550 555 560
 Val Glu Asn Ser Phe Gly Ile Thr Thr Asp Ser Asp Ile Phe Asp Ser
 565 570 575
 Arg Glu Ile Ser Arg Asp Gly Val Val Val Val Arg Pro Asp Gln
 580 585 590
 Tyr Val Ser Gly Ile Phe Pro Leu Thr Asp Thr Gln Gly Leu Gly Glu
 595 600 605
 Phe Leu Thr Gly Tyr Phe Pro Lys Met Lys Gly Ala His Gln Leu Ile
 610 615 620
 Asn Ala Asn
 625

<210> 417
 <211> 735
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(712)
 <223> RXN01461

<400> 417
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gtggccgcaa cgccacccca tttgagtaaa gggttttgca atg att gat aca ggg 115
 Met Ile Asp Thr Gly
 1 5

aag aac ggc gag ttc cgc tac gag cag tcg aat atc atc gat cag aac 163
 Lys Asn Gly Glu Phe Arg Tyr Glu Gln Ser Asn Ile Ile Asp Gln Asn
 10 15 20

gaa gcc gag ttc ggc atc act cct tca cag acc gtg ggc cct tac gtc 211
 Glu Ala Glu Phe Gly Ile Thr Pro Ser Gln Thr Val Gly Pro Tyr Val
 25 30 35

cac atc ggt ttg acc ctt gaa ggt gcg gag cat ctc gtg gag cca ggt 259
 His Ile Gly Leu Thr Leu Glu Gly Ala Glu His Leu Val Glu Pro Gly
 40 45 50
 tcg gaa ggc gcg gtg tcc ttt act gtt tcc gca act gat ggc aac ggc 307
 Ser Glu Gly Ala Val Ser Phe Thr Val Ser Ala Thr Asp Gly Asn Gly
 55 60 65
 gac ccc atc gcg gat gcc atg ttt gaa ctg tgg cag gcc gat cca gag 355
 Asp Pro Ile Ala Asp Ala Met Phe Glu Leu Trp Gln Ala Asp Pro Glu
 70 75 80 85
 ggc atc cac aac tct gat ttg gat cca aac cgc aca gca cca gca acc 403
 Gly Ile His Asn Ser Asp Leu Asp Pro Asn Arg Thr Ala Pro Ala Thr
 90 95 100
 gca gat ggc ttc cgc ggg ctt ggt cgc gcg atg gca aac gcg cag ggt 451
 Ala Asp Gly Phe Arg Gly Leu Gly Arg Ala Met Ala Asn Ala Gln Gly
 105 110 115
 gag gca acg ttc acc act ttg gtt ccg gga gca ttc gca gat gag gca 499
 Glu Ala Thr Phe Thr Thr Leu Val Pro Gly Ala Phe Ala Asp Glu Ala
 120 125 130
 cca cac ttc aag gtt ggt gtg ttc gcc cgt ggc atg ctg gag cgt ctg 547
 Pro His Phe Lys Val Gly Val Phe Ala Arg Gly Met Leu Glu Arg Leu
 135 140 145
 tac act cgc gca tac ctg cca gac gcc gat ttg agc acc gac cca gtt 595
 Tyr Thr Arg Ala Tyr Leu Pro Asp Ala Asp Leu Ser Thr Asp Pro Val
 150 155 160 165
 ttg gct gtg gtc cca gct gat cga cgt gac ctc ctg gtg gct caa aag 643
 Leu Ala Val Val Pro Ala Asp Arg Arg Asp Leu Leu Val Ala Gln Lys
 170 175 180
 acc gat gat gga ttc cgc ttc gac atc act gtc cag gct gaa gac aat 691
 Thr Asp Asp Gly Phe Arg Phe Asp Ile Thr Val Gln Ala Glu Asp Asn
 185 190 195
 gaa acc cca ttt ttt gga ctc taaattgacc cgatctttat act 735
 Glu Thr Pro Phe Phe Gly Leu
 200

<210> 418

<211> 204

<212> PRT

<213> Corynebacterium glutamicum

<400> 418

Met Ile Asp Thr Gly Lys Asn Gly Glu Phe Arg Tyr Glu Gln Ser Asn
 1 5 10 15

~~Ile Ile Asp Gln Asn Glu Ala Glu Phe Gly Ile Thr Pro Ser Gln Thr~~
 20 25 30

Val Gly Pro Tyr Val His Ile Gly Leu Thr Leu Glu Gly Ala Glu His
 35 40 45

Leu Val Glu Pro Gly Ser Glu Gly Ala Val Ser Phe Thr Val Ser Ala
 50 55 60
 Thr Asp Gly Asn Gly Asp Pro Ile Ala Asp Ala Met Phe Glu Leu Trp
 65 70 75 80
 Gln Ala Asp Pro Glu Gly Ile His Asn Ser Asp Leu Asp Pro Asn Arg
 85 90 95
 Thr Ala Pro Ala Thr Ala Asp Gly Phe Arg Gly Leu Gly Arg Ala Met
 100 105 110
 Ala Asn Ala Gln Gly Glu Ala Thr Phe Thr Thr Leu Val Pro Gly Ala
 115 120 125
 Phe Ala Asp Glu Ala Pro His Phe Lys Val Gly Val Phe Ala Arg Gly
 130 135 140
 Met Leu Glu Arg Leu Tyr Thr Arg Ala Tyr Leu Pro Asp Ala Asp Leu
 145 150 155 160
 Ser Thr Asp Pro Val Leu Ala Val Val Pro Ala Asp Arg Arg Asp Leu
 165 170 175
 Leu Val Ala Gln Lys Thr Asp Asp Gly Phe Arg Phe Asp Ile Thr Val
 180 185 190
 Gln Ala Glu Asp Asn Glu Thr Pro Phe Phe Gly Leu
 195 200

<210> 419

<211> 559

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(559)

<223> FRXA01461

<400> 419

tcgactatga cgagaccgt gaaaacttcg cgcttggtta caagttcgac atcgtccttc 60

gtggccgcaa cgccacccca tttgagtaaa gggttttgca atg att gat aca ggg 115
 Met Ile Asp Thr Gly
 1 5

aag aac ggc gag ttc cgc tac gag cag tcg aat atc atc gat cag aac 163
 Lys Asn Gly Glu Phe Arg Tyr Glu Gln Ser Asn Ile Ile Asp Gln Asn
 10 15 20

gaa gcc gag ttc ggc atc act cct tca cag acc gtg ggc cct tac gtc 211
 Glu Ala Glu Phe Gly Ile Thr Pro Ser Gln Thr Val Gly Pro Tyr Val
 25 30 35

cac atc ggt ttg acc ctt gaa ggt gcg gag cat ctc gtg gag cca ggt 259
 His Ile Gly Leu Thr Leu Glu Gly Ala Glu His Leu Val Glu Pro Gly
 40 45 50

tcg gaa ggc gcg gtg tcc ttt act gtt tcc gca act gat ggc aac ggc 307

Ser Glu Gly Ala Val Ser Phe Thr Val Ser Ala Thr Asp Gly Asn Gly
 55 60 65
 gac ccc atc gcg gat gcc atg ttt gaa ctg tgg cag gcc gat cca gag 355
 Asp Pro Ile Ala Asp Ala Met Phe Glu Leu Trp Gln Ala Asp Pro Glu
 70 75 80 85
 ggc atc cac aac tct gat ttg gat cca aac cgc aca gca cca gca acc 403
 Gly Ile His Asn Ser Asp Leu Asp Pro Asn Arg Thr Ala Pro Ala Thr
 90 95 100
 gca gat ggc ttc cgc ggg ctt ggt cgc gcg atg gca aac gcg cag ggt 451
 Ala Asp Gly Phe Arg Gly Leu Gly Arg Ala Met Ala Asn Ala Gln Gly
 105 110 115
 gag gca acg ttc acc act ttg gtt ccg gga gca ttc gca gat gag gca 499
 Glu Ala Thr Phe Thr Thr Leu Val Pro Gly Ala Phe Ala Asp Glu Ala
 120 125 130
 cca cac ttc aag gtt ggt gtg ttc gcc cgt ggc atg ctg gag cgt ctg 547
 Pro His Phe Lys Val Gly Val Phe Ala Arg Gly Met Leu Glu Arg Leu
 135 140 145
 tac act cgc gca 559
 Tyr Thr Arg Ala
 150

<210> 420

<211> 153

<212> PRT

<213> Corynebacterium glutamicum

<400> 420

Met Ile Asp Thr Gly Lys Asn Gly Glu Phe Arg Tyr Glu Gln Ser Asn
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 Ile Ile Asp Gln Asn Glu Ala Glu Phe Gly Ile Thr Pro Ser Gln Thr
 20 25 30
 Val Gly Pro Tyr Val His Ile Gly Leu Thr Leu Glu Gly Ala Glu His
 35 40 45
 Leu Val Glu Pro Gly Ser Glu Gly Ala Val Ser Phe Thr Val Ser Ala
 50 55 60
 Thr Asp Gly Asn Gly Asp Pro Ile Ala Asp Ala Met Phe Glu Leu Trp
 65 70 75 80
 Gln Ala Asp Pro Glu Gly Ile His Asn Ser Asp Leu Asp Pro Asn Arg
 85 90 95
 Thr Ala Pro Ala Thr Ala Asp Gly Phe Arg Gly Leu Gly Arg Ala Met
 100 105 110
 --- Ala-Asn-Ala-Gln-Gly-Glu-Ala-Thr-Phe-Thr-Thr-Leu-Val-Pro-Gly-Ala ---
 115 120 125
 Phe Ala Asp Glu Ala Pro His Phe Lys Val Gly Val Phe Ala Arg Gly
 130 135 140

Met Leu Glu Arg Leu Tyr Thr Arg Ala
145 150

<210> 421
<211> 813
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(790)
<223> RXA01462

<400> 421
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tacttttgaga tctatatcac tagacgcaga aagggtctcgc atg gac atc cca cac 115
Met Asp Ile Pro His
1 5
ttc gcc ccg acg gga ggc gaa tac tcc cca ctg cac ttc ccg gag tac 163
Phe Ala Pro Thr Gly Gly Glu Tyr Ser Pro Leu His Phe Pro Glu Tyr
10 15 20
cgg acc acc atc aag cgc aac cca agc aac gat ctc atc atg gtt cct 211
Arg Thr Thr Ile Lys Arg Asn Pro Ser Asn Asp Leu Ile Met Val Pro
25 30 35
agt cgc ctc ggc gag tcc acg gga cct gtc ttc ggc gac cgc gac ttg 259
Ser Arg Leu Gly Glu Ser Thr Gly Pro Val Phe Gly Asp Arg Asp Leu
40 45 50
gga gac atc gac aac gac atg acc aag gtg aac ggt ggc gag gct atc 307
Gly Asp Ile Asp Asn Asp Met Thr Lys Val Asn Gly Gly Glu Ala Ile
55 60 65
ggc cag cgc atc ttc gtt cac ggc cgt gtc ctc ggt ttc gat ggc aag 355
Gly Gln Arg Ile Phe Val His Gly Arg Val Leu Gly Phe Asp Gly Lys
70 75 80 85
cca gtt ccg cac acc ttg gtc gag gcg tgg cag gca aac gcc gca ggc 403
Pro Val Pro His Thr Leu Val Glu Ala Trp Gln Ala Asn Ala Ala Gly
90 95 100
cgt tac cgc cac aag aat gac tcc tgg cca gcg cca ctg gat cca cac 451
Arg Tyr Arg His Lys Asn Asp Ser Trp Pro Ala Pro Leu Asp Pro His
105 110 115
ttc aac ggt gtt gca cgt act ctc acc gac aag gac ggc cag tac cac 499
Phe Asn Gly Val Ala Arg Thr Leu Thr Asp Lys Asp Gly Gln Tyr His
120 125 130
ttc tgg acc gtt atg cca ggt aat tac cct tgg ggt aac cac cac aac 547
Phe Trp Thr Val Met Pro Gly Asn Tyr Pro Trp Gly Asn His His Asn
135 140 145
gca tgg cgc ccg gcg cac att cac ttc tcg ctc tat ggt cgt cag ttt 595
Ala Trp Arg Pro Ala His Ile His Phe Ser Leu Tyr Gly Arg Gln Phe
150 155 160 165

acg gag cgt ctg gtc acc cag atg tac ttc ccg aac gat cca ttg ttc 643
 Thr Glu Arg Leu Val Thr Gln Met Tyr Phe Pro Asn Asp Pro Leu Phe
 170 175 180

ttc cag gat ccg atc tac aac gcg gtg cca aag ggt gca cgt gag cgc 691
 Phe Gln Asp Pro Ile Tyr Asn Ala Val Pro Lys Gly Ala Arg Glu Arg
 185 190 195

atg atc gca acg ttc gac tat gac gag acc cgt gaa aac ttc gcg ctt 739
 Met Ile Ala Thr Phe Asp Tyr Asp Glu Thr Arg Glu Asn Phe Ala Leu
 200 205 210

ggt tac aag ttc gac atc gtc ctt cgt ggc cgc aac gcc acc cca ttt 787
 Gly Tyr Lys Phe Asp Ile Val Leu Arg Gly Arg Asn Ala Thr Pro Phe
 215 220 225

gag taaaggggttt tgcaatgatt gat 813
 Glu
 230

<210> 422

<211> 230

<212> PRT

<213> Corynebacterium glutamicum

<400> 422

Met Asp Ile Pro His Phe Ala Pro Thr Gly Gly Glu Tyr Ser Pro Leu
 1 5 10 15

His Phe Pro Glu Tyr Arg Thr Thr Ile Lys Arg Asn Pro Ser Asn Asp
 20 25 30

Leu Ile Met Val Pro Ser Arg Leu Gly Glu Ser Thr Gly Pro Val Phe
 35 40 45

Gly Asp Arg Asp Leu Gly Asp Ile Asp Asn Asp Met Thr Lys Val Asn
 50 55 60

Gly Gly Glu Ala Ile Gly Gln Arg Ile Phe Val His Gly Arg Val Leu
 65 70 75 80

Gly Phe Asp Gly Lys Pro Val Pro His Thr Leu Val Glu Ala Trp Gln
 85 90 95

Ala Asn Ala Ala Gly Arg Tyr Arg His Lys Asn Asp Ser Trp Pro Ala
 100 105 110

Pro Leu Asp Pro His Phe Asn Gly Val Ala Arg Thr Leu Thr Asp Lys
 115 120 125

Asp Gly Gln Tyr His Phe Trp Thr Val Met Pro Gly Asn Tyr Pro Trp
 130 135 140

Gly Asn His His Asn Ala Trp Arg Pro Ala His Ile His Phe Ser Leu
 145 150 155 160

Tyr Gly Arg Gln Phe Thr Glu Arg Leu Val Thr Gln Met Tyr Phe Pro
 165 170 175

Asn Asp Pro Leu Phe Phe Gln Asp Pro Ile Tyr Asn Ala Val Pro Lys

180 185 190

Gly Ala Arg Glu Arg Met Ile Ala Thr Phe Asp Tyr Asp Glu Thr Arg
195 200 205

Glu Asn Phe Ala Leu Gly Tyr Lys Phe Asp Ile Val Leu Arg Gly Arg
210 215 220

Asn Ala Thr Pro Phe Glu
225 230

<210> 423
<211> 1614
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1591)
<223> RXN00641

<400> 423
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gtggcaatac caacttcttt tcactctctt ggagggttcac atg tcc aca cca gtt 115
Met Ser Thr Pro Val
1 5

tca aat ttg gca agc gtt cag aaa act ctg gac cat gcg ctt gag gac 163
Ser Asn Leu Ala Ser Val Gln Lys Thr Leu Asp His Ala Leu Glu Asp
10 15 20

cgc cct gaa gag gga atc gtc cgc gtc aac cgc aac atc ttc act gac 211
Arg Pro Glu Glu Gly Ile Val Arg Val Asn Arg Asn Ile Phe Thr Asp
25 30 35

cct gag atc ttc gag ctg gag atg cgc cac atc ttc gaa ggc atc tgg 259
Pro Glu Ile Phe Glu Leu Glu Met Arg His Ile Phe Glu Gly Ile Trp
40 45 50

atg gac atg gct cac gag tcc cag atc cct aac ggt gga gac tac ttc 307
Met Asp Met Ala His Glu Ser Gln Ile Pro Asn Gly Gly Asp Tyr Phe
55 60 65

acc acc tac att ggc tgc cag cgg atc atg atc acc cgt tcc aag gaa 355
Thr Thr Tyr Ile Gly Cys Gln Arg Ile Met Ile Thr Arg Ser Lys Glu
70 75 80 85

ggc aca ctc aac ggc ctg atc aac gcg tgt tct cac cgt ggc gcc atg 403
Gly Thr Leu Asn Gly Leu Ile Asn Ala Cys Ser His Arg Gly Ala Met
90 95 100

ctc tgc cgt ggc aag agt gac aac cgc acc tcc ttg acc tgc cca ttc 451
Leu Cys Arg Gly Lys Ser Asp Asn Arg Thr Ser Leu Thr Cys Pro Phe
105 110 115

cac ggc tgg cca ttc tgc aac ggc ggc gca ctg ctc aag gtc aag ggc 499
His Gly Trp Pro Phe Cys Asn Gly Gly Ala Leu Leu Lys Val Lys Gly
120 125 130

gaa	aaa	gaa	ggc	gcc	tac	cca	gag	aat	ttc	cgc	acc	gac	ggc	tcc	cac	547
Glu	Lys	Glu	Gly	Ala	Tyr	Pro	Glu	Asn	Phe	Arg	Thr	Asp	Gly	Ser	His	
135						140					145					
gat	gtg	cgt	cgc	gtt	cct	aag	tta	gag	tcc	tac	cgt	ggc	ttc	ctc	ttc	595
Asp	Val	Arg	Arg	Val	Pro	Lys	Leu	Glu	Ser	Tyr	Arg	Gly	Phe	Leu	Phe	
150					155					160					165	
ggc	tcc	ctc	aac	gat	gat	gtc	gtt	tct	ttg	gaa	gag	cac	ctc	ggc	gac	643
Gly	Ser	Leu	Asn	Asp	Asp	Val	Val	Ser	Leu	Glu	Glu	His	Leu	Gly	Asp	
				170					175					180		
acc	cgt	acc	gtc	att	gac	atg	ctg	gtt	gac	caa	tcc	cca	gaa	ggc	ctc	691
Thr	Arg	Thr	Val	Ile	Asp	Met	Leu	Val	Asp	Gln	Ser	Pro	Glu	Gly	Leu	
			185					190					195			
gaa	gta	ctg	cgc	gga	tcc	tcc	acc	tac	acc	tac	gac	ggc	aac	tgg	aag	739
Glu	Val	Leu	Arg	Gly	Ser	Ser	Thr	Tyr	Thr	Tyr	Asp	Gly	Asn	Trp	Lys	
	200						205					210				
ctc	cag	acc	gaa	aac	ggt	gca	gac	ggc	tac	cac	gtt	tcc	tcc	acc	cac	787
Leu	Gln	Thr	Glu	Asn	Gly	Ala	Asp	Gly	Tyr	His	Val	Ser	Ser	Thr	His	
	215					220					225					
tgg	aac	tac	gct	gca	acc	acc	tcc	cgc	cgt	ggc	act	ggt	gaa	tcc	gcg	835
Trp	Asn	Tyr	Ala	Ala	Thr	Thr	Ser	Arg	Arg	Gly	Thr	Gly	Glu	Ser	Ala	
230					235					240					245	
aac	gaa	acc	aag	gca	atg	gac	gct	ggt	acc	tgg	ggc	aag	cag	ggt	ggc	883
Asn	Glu	Thr	Lys	Ala	Met	Asp	Ala	Gly	Thr	Trp	Gly	Lys	Gln	Gly	Gly	
				250				255						260		
gga	tac	ttc	tcc	tac	cct	tac	ggc	cac	atg	ctg	ctg	tgg	atg	tgg	tgg	931
Gly	Tyr	Phe	Ser	Tyr	Pro	Tyr	Gly	His	Met	Leu	Leu	Trp	Met	Trp	Trp	
			265					270					275			
ggc	aac	cca	gaa	gac	cgc	cca	ctg	ttc	gag	cgc	cgc	gac	gag	ttc	aag	979
Gly	Asn	Pro	Glu	Asp	Arg	Pro	Leu	Phe	Glu	Arg	Arg	Asp	Glu	Phe	Lys	
		280					285					290				
aag	gaa	ttc	ggc	gaa	gaa	aag	ggc	gag	ttc	atg	gtt	ggt	gct	tcc	cgc	1027
Lys	Glu	Phe	Gly	Glu	Glu	Lys	Gly	Glu	Phe	Met	Val	Gly	Ala	Ser	Arg	
	295					300					305					
aat	ctg	tgc	ctc	tac	ccc	aat	gtt	tac	ctg	atg	gat	cag	ttc	tcc	tca	1075
Asn	Leu	Cys	Leu	Tyr	Pro	Asn	Val	Tyr	Leu	Met	Asp	Gln	Phe	Ser	Ser	
310					315					320					325	
cag	atc	cgc	cac	atc	cgc	cca	atc	tca	gtt	gat	cag	acc	gaa	gtc	acc	1123
Gln	Ile	Arg	His	Ile	Arg	Pro	Ile	Ser	Val	Asp	Gln	Thr	Glu	Val	Thr	
				330					335					340		
atc	tac	tgc	atc	gca	cct	aag	ggc	gag	tcc	gcg	gaa	gca	cgt	gca	aac	1171
Ile	Tyr	Cys	Ile	Ala	Pro	Lys	Gly	Glu	Ser	Ala	Glu	Ala	Arg	Ala	Asn	
			345				350						355			
cgc	atc	cgc	cag	tac	gaa	gac	ttc	ttc	aac	gca	acg	ggc	atg	gca	acc	1219
Arg	Ile	Arg	Gln	Tyr	Glu	Asp	Phe	Phe	Asn	Ala	Thr	Gly	Met	Ala	Thr	
		360					365					370				
cca	gat	gac	ctg	gag	gaa	ttc	cgc	tcc	tgc	cag	aag	acc	tac	cag	gca	1267

Pro Asp Asp Leu Glu Glu Phe Arg Ser Cys Gln Lys Thr Tyr Gln Ala
 375 380 385

tct gcc ttc cca tgg aat gac atg acc cgc ggt ttg ggc cac cag gta 1315
 Ser Ala Phe Pro Trp Asn Asp Met Thr Arg Gly Leu Gly His Gln Val
 390 395 400 405

cag gga cca aac gag gtt gcc aag ggc cta ggc atg aac gaa gtt ctt 1363
 Gln Gly Pro Asn Glu Val Ala Lys Gly Leu Gly Met Asn Glu Val Leu
 410 415 420

tcc tcc gga gca cgc acc gaa gat gaa ggc ctc tac cca atc cag cac 1411
 Ser Ser Gly Ala Arg Thr Glu Asp Glu Gly Leu Tyr Pro Ile Gln His
 425 430 435

ggc ttc tgg cat gaa ctc atg cag gag gct gtg aat aag cag agc atc 1459
 Gly Phe Trp His Glu Leu Met Gln Glu Ala Val Asn Lys Gln Ser Ile
 440 445 450

aag gaa aag gaa ttg gct gac gat acc gct tct tcc ctt gcc acc gta 1507
 Lys Glu Lys Glu Leu Ala Asp Asp Thr Ala Ser Ser Leu Ala Thr Val
 455 460 465

gct gca gcc aaa atc cgt gag gaa gca aag gca gcc gcg aag tcc gac 1555
 Ala Ala Ala Lys Ile Arg Glu Glu Ala Lys Ala Ala Ala Lys Ser Asp
 470 475 480 485

gct gga gag cct cgc cgc cgt cgt cgc acc cgc ggt tagtcgtcga 1601
 Ala Gly Glu Pro Arg Arg Arg Arg Arg Thr Arg Gly
 490 495

aaagcaaaaa atc 1614

<210> 424

<211> 497

<212> PRT

<213> Corynebacterium glutamicum

<400> 424

Met Ser Thr Pro Val Ser Asn Leu Ala Ser Val Gln Lys Thr Leu Asp
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His Ala Leu Glu Asp Arg Pro Glu Glu Gly Ile Val Arg Val Asn Arg
 20 25 30

Asn Ile Phe Thr Asp Pro Glu Ile Phe Glu Leu Glu Met Arg His Ile
 35 40 45

Phe Glu Gly Ile Trp Met Asp Met Ala His Glu Ser Gln Ile Pro Asn
 50 55 60

Gly Gly Asp Tyr Phe Thr Thr Tyr Ile Gly Cys Gln Arg Ile Met Ile
 65 70 75 80

Thr Arg Ser Lys Glu Gly Thr Leu Asn Gly Leu Ile Asn Ala Cys Ser
 85 90 95

His Arg Gly Ala Met Leu Cys Arg Gly Lys Ser Asp Asn Arg Thr Ser
 100 105 110

Leu Thr Cys Pro Phe His Gly Trp Pro Phe Cys Asn Gly Gly Ala Leu
 115 120 125
 Leu Lys Val Lys Gly Glu Lys Glu Gly Ala Tyr Pro Glu Asn Phe Arg
 130 135 140
 Thr Asp Gly Ser His Asp Val Arg Arg Val Pro Lys Leu Glu Ser Tyr
 145 150 155 160
 Arg Gly Phe Leu Phe Gly Ser Leu Asn Asp Asp Val Val Ser Leu Glu
 165 170 175
 Glu His Leu Gly Asp Thr Arg Thr Val Ile Asp Met Leu Val Asp Gln
 180 185 190
 Ser Pro Glu Gly Leu Glu Val Leu Arg Gly Ser Ser Thr Tyr Thr Tyr
 195 200 205
 Asp Gly Asn Trp Lys Leu Gln Thr Glu Asn Gly Ala Asp Gly Tyr His
 210 215 220
 Val Ser Ser Thr His Trp Asn Tyr Ala Ala Thr Thr Ser Arg Arg Gly
 225 230 235 240
 Thr Gly Glu Ser Ala Asn Glu Thr Lys Ala Met Asp Ala Gly Thr Trp
 245 250 255
 Gly Lys Gln Gly Gly Gly Tyr Phe Ser Tyr Pro Tyr Gly His Met Leu
 260 265 270
 Leu Trp Met Trp Trp Gly Asn Pro Glu Asp Arg Pro Leu Phe Glu Arg
 275 280 285
 Arg Asp Glu Phe Lys Lys Glu Phe Gly Glu Glu Lys Gly Glu Phe Met
 290 295 300
 Val Gly Ala Ser Arg Asn Leu Cys Leu Tyr Pro Asn Val Tyr Leu Met
 305 310 315 320
 Asp Gln Phe Ser Ser Gln Ile Arg His Ile Arg Pro Ile Ser Val Asp
 325 330 335
 Gln Thr Glu Val Thr Ile Tyr Cys Ile Ala Pro Lys Gly Glu Ser Ala
 340 345 350
 Glu Ala Arg Ala Asn Arg Ile Arg Gln Tyr Glu Asp Phe Phe Asn Ala
 355 360 365
 Thr Gly Met Ala Thr Pro Asp Asp Leu Glu Glu Phe Arg Ser Cys Gln
 370 375 380
 Lys Thr Tyr Gln Ala Ser Ala Phe Pro Trp Asn Asp Met Thr Arg Gly
 385 390 395 400
 Leu Gly His Gln Val Gln Gly Pro Asn Glu Val Ala Lys Gly Leu Gly
 405 410 415
 Met Asn Glu Val Leu Ser Ser Gly Ala Arg Thr Glu Asp Glu Gly Leu
 420 425 430
 Tyr Pro Ile Gln His Gly Phe Trp His Glu Leu Met Gln Glu Ala Val

435	440	445
Asn Lys Gln Ser Ile Lys Glu Lys Glu Leu Ala Asp Asp Thr Ala Ser		
450	455	460
Ser Leu Ala Thr Val Ala Ala Ala Lys Ile Arg Glu Glu Ala Lys Ala		
465	470	475 480
Ala Ala Lys Ser Asp Ala Gly Glu Pro Arg Arg Arg Arg Arg Thr Arg		
	485	490 495

Gly

<210> 425
 <211> 372
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(349)
 <223> FRXA00640

<220>
 <223> All occurrences of n = any nucleotide

<400> 425
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 gtggcaatac caacttcttt tcactctctt ggaggttcac atg tcc aca cca gtt 115
 Met Ser Thr Pro Val
 1 5
 tca aat ttg gca agc gtt cag aaa act ctg gac cat gcg ctt gag gac 163
 Ser Asn Leu Ala Ser Val Gln Lys Thr Leu Asp His Ala Leu Glu Asp
 10 15 20
 cgc cct gaa gag gga atc gtc cgc gtc aac cgc aac atc ttc act gac 211
 Arg Pro Glu Glu Gly Ile Val Arg Val Asn Arg Asn Ile Phe Thr Asp
 25 30 35
 cct gag atc ttc gag ctg gag atg cgc cac atc ttc gaa ggc atc tgg 259
 Pro Glu Ile Phe Glu Leu Glu Met Arg His Ile Phe Glu Gly Ile Trp
 40 45 50
 atg gac atg gct cac gag tcc cag atc cct aac ggt gga gac tac ttc 307
 Met Asp Met Ala His Glu Ser Gln Ile Pro Asn Gly Gly Asp Tyr Phe
 55 60 65
 acc acc tac att ggc tgc cag cgg atc atg atc acc cgt tcc 349
 Thr Thr Tyr Ile Gly Cys Gln Arg Ile Met Ile Thr Arg Ser
 70 75 80

naggnnggca cactnaangg cct 372

<210> 426
 <211> 83
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<213> Corynebacterium glutamicum

<400> 426

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Met Ser Thr Pro Val Ser Asn Leu Ala Ser Val Gln Lys Thr Leu Asp
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His Ala Leu Glu Asp Arg Pro Glu Glu Gly Ile Val Arg Val Asn Arg
      20             25             30

Asn Ile Phe Thr Asp Pro Glu Ile Phe Glu Leu Glu Met Arg His Ile
      35             40             45

Phe Glu Gly Ile Trp Met Asp Met Ala His Glu Ser Gln Ile Pro Asn
      50             55             60

Gly Gly Asp Tyr Phe Thr Thr Tyr Ile Gly Cys Gln Arg Ile Met Ile
      65             70             75             80

Thr Arg Ser

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<210> 427

<211> 1164

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1141)

<223> FRXA00641

<220>

<223> All occurrences of n = any nucleotide

<400> 427

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cncctaccca gagtatttcc gcaccgangg ntcccangat  gtg cgt cgc gtt cct  115
                                         Val Arg Arg Val Pro
                                         1             5

aag tta gag tcc tac cgt ggc ttc ctc ttc ggc tcc ctc aac gat gat  163
Lys Leu Glu Ser Tyr Arg Gly Phe Leu Phe Gly Ser Leu Asn Asp Asp
      10             15             20

gtc gtt tct ttg gaa gag cac ctc ggc gac acc cgt acc gtc att gac  211
Val Val Ser Leu Glu Glu His Leu Gly Asp Thr Arg Thr Val Ile Asp
      25             30             35

atg ctg gtt gac caa tcc cca gaa ggc ctc gaa gta ctg cgc gga tcc  259
Met Leu Val Asp Gln Ser Pro Glu Gly Leu Glu Val Leu Arg Gly Ser
      40             45             50

tcc acc tac acc tac gac ggc aac tgg aag ctc cag acc gaa aac ggt  307
Ser Thr Tyr Thr Tyr Asp Gly Asn Trp Lys Leu Gln Thr Glu Asn Gly
      55             60             65

gca gac ggc tac cac gtt tcc tcc acc cac tgg aac tac gct gca acc  355
Ala Asp Gly Tyr His Val Ser Ser Thr His Trp Asn Tyr Ala Ala Thr
      70             75             80             85

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acc tcc cgc cgt ggc act ggt gaa tcc gcg aac gaa acc aag gca atg	403
Thr Ser Arg Arg Gly Thr Gly Glu Ser Ala Asn Glu Thr Lys Ala Met	
90 95 100	
gac gct ggt acc tgg ggc aag cag ggt ggc gga tac ttc tcc tac cct	451
Asp Ala Gly Thr Trp Gly Lys Gln Gly Gly Tyr Phe Ser Tyr Pro	
105 110 115	
tac ggc cac atg ctg ctg tgg atg tgg tgg ggc aac cca gaa gac cgc	499
Tyr Gly His Met Leu Leu Trp Met Trp Trp Gly Asn Pro Glu Asp Arg	
120 125 130	
cca ctg ttc gag cgc cgc gac gag ttc aag aag gaa ttc ggc gaa gaa	547
Pro Leu Phe Glu Arg Arg Asp Glu Phe Lys Lys Glu Phe Gly Glu Glu	
135 140 145	
aag ggc gag ttc atg gtt ggt gct tcc cgc aat ctg tgc ctc tac ccc	595
Lys Gly Glu Phe Met Val Gly Ala Ser Arg Asn Leu Cys Leu Tyr Pro	
150 155 160 165	
aat gtt tac ctg atg gat cag ttc tcc tca cag atc cgc cac atc cgc	643
Asn Val Tyr Leu Met Asp Gln Phe Ser Ser Gln Ile Arg His Ile Arg	
170 175 180	
cca atc tca gtt gat cag acc gaa gtc acc atc tac tgc atc gca cct	691
Pro Ile Ser Val Asp Gln Thr Glu Val Thr Ile Tyr Cys Ile Ala Pro	
185 190 195	
aag ggc gag tcc gcg gaa gca cgt gca aac cgc atc cgc cag tac gaa	739
Lys Gly Glu Ser Ala Glu Ala Arg Ala Asn Arg Ile Arg Gln Tyr Glu	
200 205 210	
gac ttc ttc aac gca acg ggc atg gca acc cca gat gac ctg gag gaa	787
Asp Phe Phe Asn Ala Thr Gly Met Ala Thr Pro Asp Asp Leu Glu Glu	
215 220 225	
ttc cgc tcc tgc cag aag acc tac cag gca tct gcc ttc cca tgg aat	835
Phe Arg Ser Cys Gln Lys Thr Tyr Gln Ala Ser Ala Phe Pro Trp Asn	
230 235 240 245	
gac atg acc cgc ggt ttg ggc cac cag gta cag gga cca aac gag gtt	883
Asp Met Thr Arg Gly Leu Gly His Gln Val Gln Gly Pro Asn Glu Val	
250 255 260	
gcc aag ggc cta ggc atg aac gaa gtt ctt tcc tcc gga gca cgc acc	931
Ala Lys Gly Leu Gly Met Asn Glu Val Leu Ser Ser Gly Ala Arg Thr	
265 270 275	
gaa gat gaa ggc ctc tac cca atc cag cac ggc ttc tgg cat gaa ctc	979
Glu Asp Glu Gly Leu Tyr Pro Ile Gln His Gly Phe Trp His Glu Leu	
280 285 290	
atg cag gag gct gtg aat aag cag agc atc aag gaa aag gaa ttg gct	1027
Met Gln Glu Ala Val Asn Lys Gln Ser Ile Lys Glu Lys Glu Leu Ala	
295 300 305	
gac gat acc gct tct tcc ctt gcc acc gta gct gca gcc aaa atc cgt	1075
Asp Asp Thr Ala Ser Ser Leu Ala Thr Val Ala Ala Lys Ile Arg	
310 315 320 325	

gag gaa gca aag gca gcc gcg aag tcc gac gct gga gag cct cgc cgc 1123
 Glu Glu Ala Lys Ala Ala Ala Lys Ser Asp Ala Gly Glu Pro Arg Arg
 330 335 340

cgt cgt cgc acc cgc ggt tagtcgtcga aaagcaaaaa atc 1164
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 345

<210> 428

<211> 347

<212> PRT

<213> Corynebacterium glutamicum

<400> 428

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 20 25 30

Arg Thr Val Ile Asp Met Leu Val Asp Gln Ser Pro Glu Gly Leu Glu
 35 40 45

Val Leu Arg Gly Ser Ser Thr Tyr Thr Tyr Asp Gly Asn Trp Lys Leu
 50 55 60

Gln Thr Glu Asn Gly Ala Asp Gly Tyr His Val Ser Ser Thr His Trp
 65 70 75 80

Asn Tyr Ala Ala Thr Ser Arg Arg Gly Thr Gly Glu Ser Ala Asn
 85 90 95

Glu Thr Lys Ala Met Asp Ala Gly Thr Trp Gly Lys Gln Gly Gly Gly
 100 105 110

Tyr Phe Ser Tyr Pro Tyr Gly His Met Leu Leu Trp Met Trp Trp Gly
 115 120 125

Asn Pro Glu Asp Arg Pro Leu Phe Glu Arg Arg Asp Glu Phe Lys Lys
 130 135 140

Glu Phe Gly Glu Glu Lys Gly Glu Phe Met Val Gly Ala Ser Arg Asn
 145 150 155 160

Leu Cys Leu Tyr Pro Asn Val Tyr Leu Met Asp Gln Phe Ser Ser Gln
 165 170 175

Ile Arg His Ile Arg Pro Ile Ser Val Asp Gln Thr Glu Val Thr Ile
 180 185 190

Tyr Cys Ile Ala Pro Lys Gly Glu Ser Ala Glu Ala Arg Ala Asn Arg
 195 200 205

Ile Arg Gln Tyr Glu Asp Phe Phe Asn Ala Thr Gly Met Ala Thr Pro
 210 215 220

Asp Asp Leu Glu Glu Phe Arg Ser Cys Gln Lys Thr Tyr Gln Ala Ser
 225 230 235 240

Ala Phe Pro Trp Asn Asp Met Thr Arg Gly Leu Gly His Gln Val Gln

	245		250		255
Gly Pro Asn Glu Val Ala Lys Gly Leu Gly Met Asn Glu Val Leu Ser					
	260		265		270
Ser Gly Ala Arg Thr Glu Asp Glu Gly Leu Tyr Pro Ile Gln His Gly					
	275		280		285
Phe Trp His Glu Leu Met Gln Glu Ala Val Asn Lys Gln Ser Ile Lys					
	290		295		300
Glu Lys Glu Leu Ala Asp Asp Thr Ala Ser Ser Leu Ala Thr Val Ala					
305		310		315	320
Ala Ala Lys Ile Arg Glu Glu Ala Lys Ala Ala Ala Lys Ser Asp Ala					
	325		330		335
Gly Glu Pro Arg Arg Arg Arg Arg Thr Arg Gly					
	340		345		

<210> 429
 <211> 615
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(592)
 <223> RXA00642

<400> 429
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 Met Ser Glu Ile Thr
 1 5
 cgc tct gag atc gaa gct ttc ctc tac tac gag gct cgc ctg ctc gat 163
 Arg Ser Glu Ile Glu Ala Phe Leu Tyr Tyr Glu Ala Arg Leu Leu Asp
 10 15 20
 gac cgt aaa ttt gaa gaa tgg ctc gaa tgc tac cgc gag gac gcc gag 211
 Asp Arg Lys Phe Glu Glu Trp Leu Glu Cys Tyr Arg Glu Asp Ala Glu
 25 30 35
 ttt tgg atg cca gcc tgg gac gac aac ggt gaa ctg act gaa gat cca 259
 Phe Trp Met Pro Ala Trp Asp Asp Asn Gly Glu Leu Thr Glu Asp Pro
 40 45 50
 cag tct gaa att tcc ctc atc tac tac cca aac cgt ggt gga ctt gag 307
 Gln Ser Glu Ile Ser Leu Ile Tyr Tyr Pro Asn Arg Gly Gly Leu Glu
 55 60 65
 gac cgc gtc ttc cgc atc cgc acc gaa cgc tcc tct gca act tcc cta 355
 Asp Arg Val Phe Arg Ile Arg Thr Glu Arg Ser Ser Ala Thr Ser Leu
 70 75 80 85
 cct gaa cca cgc acc ggc cac agc acc acc aac gtg gaa atc ctg gag 403
 Pro Glu Pro Arg Thr Gly His Ser Thr Thr Asn Val Glu Ile Leu Glu
 90 95 100

cgc cgc gac ggc gaa gta gat atc cgc ttc aac tgg atc acc ttc tac 451
 Arg Arg Asp Gly Glu Val Asp Ile Arg Phe Asn Trp Ile Thr Phe Tyr
 105 110 115

tac cgt tac aac acc acc gac acc tac ttc ggc acc acg ttt atc acc 499
 Tyr Arg Tyr Asn Thr Thr Asp Thr Tyr Phe Gly Thr Thr Phe Ile Thr
 120 125 130

ctt gat gtc agt ggt gaa acc ccg aag atc gtc aag aag aag gtc gtt 547
 Leu Asp Val Ser Gly Glu Thr Pro Lys Ile Val Lys Lys Lys Val Val
 135 140 145

ttg aag aac gac tac atc cac cac atc gtc gat att tac cac gtc 592
 Leu Lys Asn Asp Tyr Ile His His Ile Val Asp Ile Tyr His Val
 150 155 160

taggaggcac tcacatgact cac 615

<210> 430

<211> 164

<212> PRT

<213> Corynebacterium glutamicum

<400> 430

Met Ser Glu Ile Thr Arg Ser Glu Ile Glu Ala Phe Leu Tyr Tyr Glu
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Ala Arg Leu Leu Asp Asp Arg Lys Phe Glu Glu Trp Leu Glu Cys Tyr
 20 25 30

Arg Glu Asp Ala Glu Phe Trp Met Pro Ala Trp Asp Asp Asn Gly Glu
 35 40 45

Leu Thr Glu Asp Pro Gln Ser Glu Ile Ser Leu Ile Tyr Tyr Pro Asn
 50 55 60

Arg Gly Gly Leu Glu Asp Arg Val Phe Arg Ile Arg Thr Glu Arg Ser
 65 70 75 80

Ser Ala Thr Ser Leu Pro Glu Pro Arg Thr Gly His Ser Thr Thr Asn
 85 90 95

Val Glu Ile Leu Glu Arg Arg Asp Gly Glu Val Asp Ile Arg Phe Asn
 100 105 110

Trp Ile Thr Phe Tyr Tyr Arg Tyr Asn Thr Thr Asp Thr Tyr Phe Gly
 115 120 125

Thr Thr Phe Ile Thr Leu Asp Val Ser Gly Glu Thr Pro Lys Ile Val
 130 135 140

Lys Lys Lys Val Val Leu Lys Asn Asp Tyr Ile His His Ile Val Asp
 145 150 155 160

Ile Tyr His Val

<210> 431

<211> 1659
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1636)
 <223> RXA00643

<400> 431

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accacatcgt cgatattttac cacgtctagg aggcactcac atg act cac caa gtt 115
 Met Thr His Gln Val
 1 5

gca ctt gcc ttt gaa gac ggc atc acc cga ttc atc gac tgc gaa gat 163
 Ala Leu Ala Phe Glu Asp Gly Ile Thr Arg Phe Ile Asp Cys Glu Asp
 10 15 20

gac caa act gtt gca gat gcc gcc tac cag gca cgc atc aac att cct 211
 Asp Gln Thr Val Ala Asp Ala Ala Tyr Gln Ala Arg Ile Asn Ile Pro
 25 30 35

ttc gac tgc cgc gac ggc gcc tgc gga acc tgc aaa gcg ttc tgc gaa 259
 Phe Asp Cys Arg Asp Gly Ala Cys Gly Thr Cys Lys Ala Phe Cys Glu
 40 45 50

tcc ggc gac ttt gac gaa ggc gac tac atc gac gac gcc ctg tcc gaa 307
 Ser Gly Asp Phe Asp Glu Gly Asp Tyr Ile Asp Asp Ala Leu Ser Glu
 55 60 65

gat gaa gca gcc gac ggc tac tgc ctg cct tgc cag atg acc cca aag 355
 Asp Glu Ala Ala Asp Gly Tyr Cys Leu Pro Cys Gln Met Thr Pro Lys
 70 75 80 85

acc gac ctc atc ttg cag atc gcc acc acc tcc gtg ctg gca aag acc 403
 Thr Asp Leu Ile Leu Gln Ile Ala Thr Thr Ser Val Leu Ala Lys Thr
 90 95 100

ggc gca tcc act ttc gat ggc gag ttg aag gag atc aat cac ttc tct 451
 Gly Ala Ser Thr Phe Asp Gly Glu Leu Lys Glu Ile Asn His Phe Ser
 105 110 115

gat tcc acc atc ggc att gag atc gaa ctg gaa aac cgc caa gat ttg 499
 Asp Ser Thr Ile Gly Ile Glu Ile Glu Leu Glu Asn Arg Gln Asp Leu
 120 125 130

gcg ttc ctc cct ggt caa tac atg aac atc cag gtt cca ggc agc gac 547
 Ala Phe Leu Pro Gly Gln Tyr Met Asn Ile Gln Val Pro Gly Ser Asp
 135 140 145

cag act cgt tcc tac tct ttc tcc tgc gct caa gat tcc ggc aac gtg 595
 Gln Thr Arg Ser Tyr Ser Phe Ser Cys Ala Gln Asp Ser Gly Asn Val
 150 155 160 165

cag ttc ctg atc aag gta acc cca ggt gga ctc atg acc acc tat ctc 643
 Gln Phe Leu Ile Lys Val Thr Pro Gly Gly Leu Met Thr Thr Tyr Leu
 170 175 180

acc gat cac gcg aag gtc ggc gac aag ctc acc ttg acc ggc ccg atg 691

Thr	Asp	His	Ala	Lys	Val	Gly	Asp	Lys	Leu	Thr	Leu	Thr	Gly	Pro	Met	
			185					190					195			
ggt	tcc	ttc	ttc	ctg	cgt	gaa	cct	gtc	cgc	ccg	atc	ctg	ctg	ctc	gcc	739
Gly	Ser	Phe	Phe	Leu	Arg	Glu	Pro	Val	Arg	Pro	Ile	Leu	Leu	Leu	Ala	
		200					205					210				
ggc	gga	act	gga	ctt	gca	ccg	atc	ttg	gct	att	ttg	gaa	aag	ctt	tcc	787
Gly	Gly	Thr	Gly	Leu	Ala	Pro	Ile	Leu	Ala	Ile	Leu	Glu	Lys	Leu	Ser	
	215					220					225					
cgc	gat	gag	ctt	ctc	gac	gtc	cca	atc	cgc	ctg	gtt	tac	ggc	gcg	aac	835
Arg	Asp	Glu	Leu	Leu	Asp	Val	Pro	Ile	Arg	Leu	Val	Tyr	Gly	Ala	Asn	
230					235					240					245	
ttc	acc	cac	gat	ctg	gtg	gaa	ttg	gat	cga	ctt	gat	gcc	ttc	aag	gac	883
Phe	Thr	His	Asp	Leu	Val	Glu	Leu	Asp	Arg	Leu	Asp	Ala	Phe	Lys	Asp	
				250					255					260		
aag	ttc	gac	ttc	gat	tac	atc	acc	gtg	ctt	tcc	gac	aag	gac	acc	gag	931
Lys	Phe	Asp	Phe	Asp	Tyr	Ile	Thr	Val	Leu	Ser	Asp	Lys	Asp	Thr	Glu	
			265					270					275			
cat	cca	cgc	aag	ggc	tac	gtc	cca	gca	cac	ctg	acc	ggc	gaa	tat	gag	979
His	Pro	Arg	Lys	Gly	Tyr	Val	Pro	Ala	His	Leu	Thr	Gly	Glu	Tyr	Glu	
		280					285					290				
cca	gat	gag	gac	act	gat	gtg	tac	ctc	tgc	ggc	cct	cct	cca	atg	gtc	1027
Pro	Asp	Glu	Asp	Thr	Asp	Val	Tyr	Leu	Cys	Gly	Pro	Pro	Pro	Met	Val	
	295					300					305					
gag	gcc	gtg	cgc	caa	ttc	ctg	ggc	acc	ctg	gag	cat	cct	ccg	ctg	gac	1075
Glu	Ala	Val	Arg	Gln	Phe	Leu	Gly	Thr	Leu	Glu	His	Pro	Pro	Leu	Asp	
310					315					320					325	
ttt	tat	tac	gag	aag	ttc	act	tcc	gcc	gct	gcc	cct	gct	gct	ggg	aag	1123
Phe	Tyr	Tyr	Glu	Lys	Phe	Thr	Ser	Ala	Ala	Ala	Pro	Ala	Ala	Gly	Lys	
				330					335					340		
cca	gag	atc	acc	gtg	gag	acc	agc	gaa	gtt	gca	gag	gat	ttc	aac	ctg	1171
Pro	Glu	Ile	Thr	Val	Glu	Thr	Ser	Glu	Val	Ala	Glu	Asp	Phe	Asn	Leu	
			345					350					355			
gtc	gag	gtg	tcc	act	cca	ggc	atg	tct	tcc	ggc	gag	gtg	cac	tct	tct	1219
Val	Glu	Val	Ser	Thr	Pro	Gly	Met	Ser	Ser	Gly	Glu	Val	His	Ser	Ser	
		360					365					370				
gca	acc	cag	ctg	cag	gcc	cgc	atg	gct	ctg	gag	ctc	ggc	gcg	ctg	gag	1267
Ala	Thr	Gln	Leu	Gln	Ala	Arg	Met	Ala	Leu	Glu	Leu	Gly	Ala	Leu	Glu	
	375					380					385					
ctt	gcg	atc	aac	aaa	ctc	ggc	gag	cgc	gac	atc	gag	cga	ttc	cgc	aac	1315
Leu	Ala	Ile	Asn	Lys	Leu	Gly	Glu	Arg	Asp	Ile	Glu	Arg	Phe	Arg	Asn	
390					395					400					405	
ttg	gcc	gac	atc	gcg	aac	tcc	ttc	atc	gac	ggc	gat	aag	ttt	atc	gac	1363
Leu	Ala	Asp	Ile	Ala	Asn	Ser	Phe	Ile	Asp	Gly	Asp	Lys	Phe	Ile	Asp	
				410					415					420		
gcg	gtg	aag	ttc	acc	gag	gcc	aac	gcc	gat	ttc	cac	gag	ttc	ctc	ttc	1411
Ala	Val	Lys	Phe	Thr	Glu	Ala	Asn	Ala	Asp	Phe	His	Glu	Phe	Leu	Phe	

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          425              430              435
cgc cgc gca aac aac gag gcg ctg ctt gcg gcg tac cag aac ctc cag 1459
Arg Arg Ala Asn Asn Glu Ala Leu Leu Ala Ala Tyr Gln Asn Leu Gln
      440              445              450

gtt gtt caa gaa atg aac gca acc ctt cca ggc gcc gag tgg att gat 1507
Val Val Gln Glu Met Asn Ala Thr Leu Pro Gly Ala Glu Trp Ile Asp
      455              460              465

ccg gca att gcc acc gag cac ttg gcg ctt gtc gac gcc gtc tcc cag 1555
Pro Ala Ile Ala Thr Glu His Leu Ala Leu Val Asp Ala Val Ser Gln
      470              475              480

aat gat ctc gag acc gcg aga aca atc att cgt gaa cac gcg gag cac 1603
Asn Asp Leu Glu Thr Ala Arg Thr Ile Ile Arg Glu His Ala Glu His
      490              495              500

ggc att gac act atg gtt aag gcc ctc gag aaa tgagcgcgcc agtaggacaa 1656
Gly Ile Asp Thr Met Val Lys Ala Leu Glu Lys
      505              510

ggc 1659

<210> 432
<211> 512
<212> PRT
<213> Corynebacterium glutamicum

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Met Thr His Gln Val Ala Leu Ala Phe Glu Asp Gly Ile Thr Arg Phe
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Ile Asp Cys Glu Asp Asp Gln Thr Val Ala Asp Ala Ala Tyr Gln Ala
      20              25              30

Arg Ile Asn Ile Pro Phe Asp Cys Arg Asp Gly Ala Cys Gly Thr Cys
      35              40              45

Lys Ala Phe Cys Glu Ser Gly Asp Phe Asp Glu Gly Asp Tyr Ile Asp
      50              55              60

Asp Ala Leu Ser Glu Asp Glu Ala Ala Asp Gly Tyr Cys Leu Pro Cys
      65              70              75              80

Gln Met Thr Pro Lys Thr Asp Leu Ile Leu Gln Ile Ala Thr Thr Ser
      85              90              95

Val Leu Ala Lys Thr Gly Ala Ser Thr Phe Asp Gly Glu Leu Lys Glu
      100              105              110

Ile Asn His Phe Ser Asp Ser Thr Ile Gly Ile Glu Ile Glu Leu Glu
      115              120              125

Asn Arg Gln Asp Leu Ala Phe Leu Pro Gly Gln Tyr Met Asn Ile Gln
      130              135              140

Val Pro Gly Ser Asp Gln Thr Arg Ser Tyr Ser Phe Ser Cys Ala Gln
      145              150              155              160

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Asp Ser Gly Asn Val Gln Phe Leu Ile Lys Val Thr Pro Gly Gly Leu
 165 170 175
 Met Thr Thr Tyr Leu Thr Asp His Ala Lys Val Gly Asp Lys Leu Thr
 180 185 190
 Leu Thr Gly Pro Met Gly Ser Phe Phe Leu Arg Glu Pro Val Arg Pro
 195 200 205
 Ile Leu Leu Leu Ala Gly Gly Thr Gly Leu Ala Pro Ile Leu Ala Ile
 210 215 220
 Leu Glu Lys Leu Ser Arg Asp Glu Leu Leu Asp Val Pro Ile Arg Leu
 225 230 235 240
 Val Tyr Gly Ala Asn Phe Thr His Asp Leu Val Glu Leu Asp Arg Leu
 245 250 255
 Asp Ala Phe Lys Asp Lys Phe Asp Phe Asp Tyr Ile Thr Val Leu Ser
 260 265 270
 Asp Lys Asp Thr Glu His Pro Arg Lys Gly Tyr Val Pro Ala His Leu
 275 280 285
 Thr Gly Glu Tyr Glu Pro Asp Glu Asp Thr Asp Val Tyr Leu Cys Gly
 290 295 300
 Pro Pro Pro Met Val Glu Ala Val Arg Gln Phe Leu Gly Thr Leu Glu
 305 310 315 320
 His Pro Pro Leu Asp Phe Tyr Tyr Glu Lys Phe Thr Ser Ala Ala Ala
 325 330 335
 Pro Ala Ala Gly Lys Pro Glu Ile Thr Val Glu Thr Ser Glu Val Ala
 340 345 350
 Glu Asp Phe Asn Leu Val Glu Val Ser Thr Pro Gly Met Ser Ser Gly
 355 360 365
 Glu Val His Ser Ser Ala Thr Gln Leu Gln Ala Arg Met Ala Leu Glu
 370 375 380
 Leu Gly Ala Leu Glu Leu Ala Ile Asn Lys Leu Gly Glu Arg Asp Ile
 385 390 395 400
 Glu Arg Phe Arg Asn Leu Ala Asp Ile Ala Asn Ser Phe Ile Asp Gly
 405 410 415
 Asp Lys Phe Ile Asp Ala Val Lys Phe Thr Glu Ala Asn Ala Asp Phe
 420 425 430
 His Glu Phe Leu Phe Arg Arg Ala Asn Asn Glu Ala Leu Leu Ala Ala
 435 440 445
 Tyr Gln Asn Leu Gln Val Val Gln Glu Met Asn Ala Thr Leu Pro Gly
 450 455 460
 Ala Glu Trp Ile Asp Pro Ala Ile Ala Thr Glu His Leu Ala Leu Val
 465 470 475 480
 Asp Ala Val Ser Gln Asn Asp Leu Glu Thr Ala Arg Thr Ile Ile Arg

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		Met	Thr	Leu	Ser	Glu	Arg	Lys	Leu	Thr	Thr	Thr	Ala			
		1				5				10						
aag	att	ctt	ccc	cac	cca	ctc	aac	gcc	tgg	tac	gtc	gcc	gct	tgg	gat	99
Lys	Ile	Leu	Pro	His	Pro	Leu	Asn	Ala	Trp	Tyr	Val	Ala	Ala	Trp	Asp	
		15					20					25				
tat	gaa	gtc	aca	tct	aaa	aag	ccc	atg	gcc	agg	aca	atc	gcc	aac	aaa	147
Tyr	Glu	Val	Thr	Ser	Lys	Lys	Pro	Met	Ala	Arg	Thr	Ile	Ala	Asn	Lys	
		30				35					40					
cca	ctc	gct	ttg	tac	cgc	acc	aaa	gat	ggc	cga	gcc	gtt	gcc	ctt	gca	195
Pro	Leu	Ala	Leu	Tyr	Arg	Thr	Lys	Asp	Gly	Arg	Ala	Val	Ala	Leu	Ala	
		45			50					55					60	
gac	gcc	tgc	tgg	cac	cgc	ctc	gca	ccg	cta	tcc	aag	gga	aaa	ctc	gtg	243
Asp	Ala	Cys	Trp	His	Arg	Leu	Ala	Pro	Leu	Ser	Lys	Gly	Lys	Leu	Val	
				65					70					75		
ggc	aca	gac	gga	atc	caa	tgc	cct	tat	cac	ggc	ttg	gag	tac	aac	tcc	291
Gly	Thr	Asp	Gly	Ile	Gln	Cys	Pro	Tyr	His	Gly	Leu	Glu	Tyr	Asn	Ser	
			80					85					90			
gcg	ggc	cgc	tgc	atg	aaa	atg	ccc	gcg	cag	gaa	acc	ctc	aac	ccg	tca	339
Ala	Gly	Arg	Cys	Met	Lys	Met	Pro	Ala	Gln	Glu	Thr	Leu	Asn	Pro	Ser	
		95					100					105				
gca	gcc	gtc	aac	tcc	tac	ccc	gtg	gtg	gaa	gcc	cac	cgc	ttt	gtg	tgg	387
Ala	Ala	Val	Asn	Ser	Tyr	Pro	Val	Val	Glu	Ala	His	Arg	Phe	Val	Trp	
		110				115					120					
gtg	tgg	ctg	ggc	gat	ccc	aca	ttg	gca	gat	ccc	acc	caa	gta	ccc	gat	435
Val	Trp	Leu	Gly	Asp	Pro	Thr	Leu	Ala	Asp	Pro	Thr	Gln	Val	Pro	Asp	
		125			130					135					140	
atg	cac	cag	atg	agc	cac	ccc	gaa	tgg	gca	ggc	gat	gga	cgc	acc	atc	483
Met	His	Gln	Met	Ser	His	Pro	Glu	Trp	Ala	Gly	Asp	Gly	Arg	Thr	Ile	
				145					150					155		
tcc	gct	gac	tgc	aac	tac	caa	tta	gtg	ctg	gac	aac	ttg	atg	gac	ctc	531
Ser	Ala	Asp	Cys	Asn	Tyr	Gln	Leu	Val	Leu	Asp	Asn	Leu	Met	Asp	Leu	
			160					165					170			

acc cac gaa gag ttc gtg cac tcc tcc agc atc gga caa gac gaa ctt 579
 Thr His Glu Glu Phe Val His Ser Ser Ser Ile Gly Gln Asp Glu Leu
 175 180 185

agt gaa tca gag ttc gtg gtc acc cac act gaa gat tcc gtg acg gtc 627
 Ser Glu Ser Glu Phe Val Thr His Thr Glu Asp Ser Val Thr Val
 190 195 200

acc cgc tgg atg cat gac ata gat gca cca ccg ttt tgg caa aag aac 675
 Thr Arg Trp Met His Asp Ile Asp Ala Pro Pro Phe Trp Gln Lys Asn
 205 210 215 220

atg aat gat aag ttc cca gga ttt gaa ggc aag gtg gat cgt tgg cag 723
 Met Asn Asp Lys Phe Pro Gly Phe Glu Gly Lys Val Asp Arg Trp Gln
 225 230 235

atc atc cac tac tac tac cct tcc acc atc tgc att gat gtt ggt gta 771
 Ile Ile His Tyr Tyr Tyr Pro Ser Thr Ile Cys Ile Asp Val Gly Val
 240 245 250

gca aag gct gga act ggc gcg cag gaa ggc gac cgc agc cag ggc gtt 819
 Ala Lys Ala Gly Thr Gly Ala Gln Glu Gly Asp Arg Ser Gln Gly Val
 255 260 265

aat ggg tat gtc atg aac acc att acc cca gat tca gat cgt tcc tct 867
 Asn Gly Tyr Val Met Asn Thr Ile Thr Pro Asp Ser Asp Arg Ser Ser
 270 275 280

cat tac ttc tgg gca ttc atg cgc aac tac cgc ctg gaa agc caa acc 915
 His Tyr Phe Trp Ala Phe Met Arg Asn Tyr Arg Leu Glu Ser Gln Thr
 285 290 295 300

atc acc acc cag ctg cgc gac ggt gta tcc ggt gta ttc aaa gaa gac 963
 Ile Thr Thr Gln Leu Arg Asp Gly Val Ser Gly Val Phe Lys Glu Asp
 305 310 315

gaa gac atg ctg acc gct cag caa gat gcc atc gac gcc aac acc gac 1011
 Glu Asp Met Leu Thr Ala Gln Gln Asp Ala Ile Asp Ala Asn Thr Asp
 320 325 330

tac gag ttt tac agc ctc aac att gat gcc ggt ggc atg tgg gtg cgc 1059
 Tyr Glu Phe Tyr Ser Leu Asn Ile Asp Ala Gly Gly Met Trp Val Arg
 335 340 345

cga atc ctc gag gaa gca ctc tcc aag gaa ggc cga ctg gat atc ccc 1107
 Arg Ile Leu Glu Glu Ala Leu Ser Lys Glu Gly Arg Leu Asp Ile Pro
 350 355 360

acc aca ttc ccc cgc gca aca ccg aag ccg gag gca taaaccatga 1153
 Thr Thr Phe Pro Arg Ala Thr Pro Lys Pro Glu Ala
 365 370 375

actcgcaatg gca 1166

<210> 434

<211> 376

<212> PRT

<213> Corynebacterium glutamicum

<400> 434

Met Thr Leu Ser Glu Arg Lys Leu Thr Thr Thr Ala Lys Ile Leu Pro
 1 5 10 15
 His Pro Leu Asn Ala Trp Tyr Val Ala Ala Trp Asp Tyr Glu Val Thr
 20 25 30
 Ser Lys Lys Pro Met Ala Arg Thr Ile Ala Asn Lys Pro Leu Ala Leu
 35 40 45
 Tyr Arg Thr Lys Asp Gly Arg Ala Val Ala Leu Ala Asp Ala Cys Trp
 50 55 60
 His Arg Leu Ala Pro Leu Ser Lys Gly Lys Leu Val Gly Thr Asp Gly
 65 70 75 80
 Ile Gln Cys Pro Tyr His Gly Leu Glu Tyr Asn Ser Ala Gly Arg Cys
 85 90 95
 Met Lys Met Pro Ala Gln Glu Thr Leu Asn Pro Ser Ala Ala Val Asn
 100 105 110
 Ser Tyr Pro Val Val Glu Ala His Arg Phe Val Trp Val Trp Leu Gly
 115 120 125
 Asp Pro Thr Leu Ala Asp Pro Thr Gln Val Pro Asp Met His Gln Met
 130 135 140
 Ser His Pro Glu Trp Ala Gly Asp Gly Arg Thr Ile Ser Ala Asp Cys
 145 150 155 160
 Asn Tyr Gln Leu Val Leu Asp Asn Leu Met Asp Leu Thr His Glu Glu
 165 170 175
 Phe Val His Ser Ser Ser Ile Gly Gln Asp Glu Leu Ser Glu Ser Glu
 180 185 190
 Phe Val Val Thr His Thr Glu Asp Ser Val Thr Val Thr Arg Trp Met
 195 200 205
 His Asp Ile Asp Ala Pro Pro Phe Trp Gln Lys Asn Met Asn Asp Lys
 210 215 220
 Phe Pro Gly Phe Glu Gly Lys Val Asp Arg Trp Gln Ile Ile His Tyr
 225 230 235 240
 Tyr Tyr Pro Ser Thr Ile Cys Ile Asp Val Gly Val Ala Lys Ala Gly
 245 250 255
 Thr Gly Ala Gln Glu Gly Asp Arg Ser Gln Gly Val Asn Gly Tyr Val
 260 265 270
 Met Asn Thr Ile Thr Pro Asp Ser Asp Arg Ser Ser His Tyr Phe Trp
 275 280 285
 Ala Phe Met Arg Asn Tyr Arg Leu Glu Ser Gln Thr Ile Thr Thr Gln
 290 295 300
 Leu Arg Asp Gly Val Ser Gly Val Phe Lys Glu Asp Glu Asp Met Leu
 305 310 315 320
 Thr Ala Gln Gln Asp Ala Ile Asp Ala Asn Thr Asp Tyr Glu Phe Tyr

<400>																	435
gct	gga	act	ggc	gcg	cag	gat	ggc	gac	cgc	agc	cag	ggc	gtt	aat	ggg	48	
Ala	Gly	Thr	Gly	Ala	Gln	Asp	Gly	Asp	Arg	Ser	Gln	Gly	Val	Asn	Gly		
1				5					10					15			
tat	gtc	atg	aac	acc	att	acc	cca	gat	tca	gat	cgt	ttt	tct	cat	tac	96	
Tyr	Val	Met	Asn	Thr	Ile	Thr	Pro	Asp	Ser	Asp	Arg	Phe	Ser	His	Tyr		
			20					25					30				
ttc	tgg	gca	ttc	atg	cgc	aac	tac	cgc	ctg	gaa	agc	caa	acc	atc	acc	144	
Phe	Trp	Ala	Phe	Met	Arg	Asn	Tyr	Arg	Leu	Glu	Ser	Gln	Thr	Ile	Thr		
		35					40					45					
acc	cag	ctg	cgc	gac	ggg	gta	tcc	ggg	gta	ttc	aaa	gaa	gac	gaa	gac	192	
Thr	Gln	Leu	Arg	Asp	Gly	Val	Ser	Gly	Val	Phe	Lys	Glu	Asp	Glu	Asp		
	50					55					60						
atg	ctg	acc	gct	cag	caa	gat	gcc	atc	gac	gcc	aac	acc	gac	tac	gag	240	
Met	Leu	Thr	Ala	Gln	Gln	Asp	Ala	Ile	Asp	Ala	Asn	Thr	Asp	Tyr	Glu		
65					70				75					80			
ttt	tac	agc	ctc	aac	att	gat	gcc	ggg	ggc	atg	tgg	gtg	cgc	cga	atc	288	
Phe	Tyr	Ser	Leu	Asn	Ile	Asp	Ala	Gly	Gly	Met	Trp	Val	Arg	Arg	Ile		
				85				90						95			
ctc	gag	gaa	gca	ctc	tcc	aag	gaa	ggc	cga	ctg	gat	atc	ccc	acc	aca	336	
Leu	Glu	Glu	Ala	Leu	Ser	Lys	Glu	Gly	Arg	Leu	Asp	Ile	Pro	Thr	Thr		
			100					105					110				
ttc	ccc	cgc	gca	aca	ccg	aag	ccg	gag	gca	taa	acc	atga	actcg	caatg	gca	389	
Phe	Pro	Arg	Ala	Thr	Pro	Lys	Pro	Glu	Ala								
		115					120										

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<210> 436
<211> 122
<212> PRT
<213> Corynebacterium glutamicum
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<400> 436

Ala Gly Thr Gly Ala Gln Asp Gly Asp Arg Ser Gln Gly Val Asn Gly
 1 5 10 15
 Tyr Val Met Asn Thr Ile Thr Pro Asp Ser Asp Arg Phe Ser His Tyr
 20 25 30
 Phe Trp Ala Phe Met Arg Asn Tyr Arg Leu Glu Ser Gln Thr Ile Thr
 35 40 45
 Thr Gln Leu Arg Asp Gly Val Ser Gly Val Phe Lys Glu Asp Glu Asp
 50 55 60
 Met Leu Thr Ala Gln Gln Asp Ala Ile Asp Ala Asn Thr Asp Tyr Glu
 65 70 75 80
 Phe Tyr Ser Leu Asn Ile Asp Ala Gly Gly Met Trp Val Arg Arg Ile
 85 90 95
 Leu Glu Glu Ala Leu Ser Lys Glu Gly Arg Leu Asp Ile Pro Thr Thr
 100 105 110
 Phe Pro Arg Ala Thr Pro Lys Pro Glu Ala
 115 120

<210> 437

<211> 669

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(669)

<223> FRXA02012

<400> 437

ttc acc atg aca ctg tcc gaa cgc aag ctc acc acc acc gcc aag att 48
 Phe Thr Met Thr Leu Ser Glu Arg Lys Leu Thr Thr Thr Ala Lys Ile
 1 5 10 15
 ctt ccc cac cca ctc aac gcc tgg tac gtc gcc gct tgg gat tat gaa 96
 Leu Pro His Pro Leu Asn Ala Trp Tyr Val Ala Ala Trp Asp Tyr Glu
 20 25 30
 gtc aca tct aaa aag ccc atg gcc agg aca atc gcc aac aaa cca ctc 144
 Val Thr Ser Lys Lys Pro Met Ala Arg Thr Ile Ala Asn Lys Pro Leu
 35 40 45
 gct ttg tac cgc acc aaa gat ggc cga gcc gtt gcc ctt gca gac gcc 192
 Ala Leu Tyr Arg Thr Lys Asp Gly Arg Ala Val Ala Leu Ala Asp Ala
 50 55 60
 tgc tgg cac cgc ctc gca ccg cta tcc aag gga aaa ctc gtg ggc aca 240
 Cys Trp His Arg Leu Ala Pro Leu Ser Lys Gly Lys Leu Val Gly Thr
 65 70 75 80
 gac gga atc caa tgc cct tat cac ggc ttg gag tac aac tcc gcg ggc 288
 Asp Gly Ile Gln Cys Pro Tyr His Gly Leu Glu Tyr Asn Ser Ala Gly
 85 90 95

cgc tgc atg aaa atg ccc gcg cag gaa acc ctc aac ccg tca gca gcc 336
 Arg Cys Met Lys Met Pro Ala Gln Glu Thr Leu Asn Pro Ser Ala Ala
 100 105 110

gtc aac tcc tac ccc gtg gtg gaa gcc cac cgc ttt gtg tgg gtg tgg 384
 Val Asn Ser Tyr Pro Val Val Glu Ala His Arg Phe Val Trp Val Trp
 115 120 125

ctg ggc gat ccc aca ttg gca gat ccc acc caa gta ccc gat atg cac 432
 Leu Gly Asp Pro Thr Leu Ala Asp Pro Thr Gln Val Pro Asp Met His
 130 135 140

cag atg agc cac ccc gaa tgg gca ggc gat gga cgc acc atc tcc gct 480
 Gln Met Ser His Pro Glu Trp Ala Gly Asp Gly Arg Thr Ile Ser Ala
 145 150 155 160

gac tgc aac tac caa tta gtg ctg gac aac ttg atg gac ctc acc cac 528
 Asp Cys Asn Tyr Gln Leu Val Leu Asp Asn Leu Met Asp Leu Thr His
 165 170 175

caa gag ttc gtg cac tcc tcc agc atc gga caa gac gaa ctt agt gaa 576
 Gln Glu Phe Val His Ser Ser Ser Ile Gly Gln Asp Glu Leu Ser Glu
 180 185 190

tca gag ttc gtg gtc acc cac act gaa gat tcc gtg acg gtc acc cgc 624
 Ser Glu Phe Val Val Thr His Thr Glu Asp Ser Val Thr Val Thr Arg
 195 200 205

tgg atg cat gac ata gat gca cca ccg ttt tgg caa aag aac atg 669
 Trp Met His Asp Ile Asp Ala Pro Pro Phe Trp Gln Lys Asn Met
 210 215 220

<210> 438

<211> 223

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 438

Phe Thr Met Thr Leu Ser Glu Arg Lys Leu Thr Thr Thr Ala Lys Ile
 1 5 10 15

Leu Pro His Pro Leu Asn Ala Trp Tyr Val Ala Ala Trp Asp Tyr Glu
 20 25 30

Val Thr Ser Lys Lys Pro Met Ala Arg Thr Ile Ala Asn Lys Pro Leu
 35 40 45

Ala Leu Tyr Arg Thr Lys Asp Gly Arg Ala Val Ala Leu Ala Asp Ala
 50 55 60

Cys Trp His Arg Leu Ala Pro Leu Ser Lys Gly Lys Leu Val Gly Thr
 65 70 75 80

Asp Gly Ile Gln Cys Pro Tyr His Gly Leu Glu Tyr Asn Ser Ala Gly
 85 90 95

Arg Cys Met Lys Met Pro Ala Gln Glu Thr Leu Asn Pro Ser Ala Ala
 100 105 110

Val Asn Ser Tyr Pro Val Val Glu Ala His Arg Phe Val Trp Val Trp

115	120	125
Leu Gly Asp Pro Thr Leu Ala Asp Pro Thr Gln Val Pro Asp Met His		
130	135	140
Gln Met Ser His Pro Glu Trp Ala Gly Asp Gly Arg Thr Ile Ser Ala		
145	150	155
Asp Cys Asn Tyr Gln Leu Val Leu Asp Asn Leu Met Asp Leu Thr His		
165	170	175
Gln Glu Phe Val His Ser Ser Ser Ile Gly Gln Asp Glu Leu Ser Glu		
180	185	190
Ser Glu Phe Val Val Thr His Thr Glu Asp Ser Val Thr Val Thr Arg		
195	200	205
Trp Met His Asp Ile Asp Ala Pro Pro Phe Trp Gln Lys Asn Met		
210	215	220

<210> 439
 <211> 1098
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1075)
 <223> RXA01994

<400> 439
 gtgggtgctgc cgaatcctcg aggaagcact ctccaaggaa ggccgactgg atatccccac 60

cacattcccc cgcgcaacac cgaagccgga ggcataaac atg aac tcg caa tgg 115
 Met Asn Ser Gln Trp
 1 5

caa gat gca cat gtt gtt tcc agc gaa atc atc gct gca gac att cgg 163
 Gln Asp Ala His Val Val Ser Ser Glu Ile Ile Ala Ala Asp Ile Arg
 10 15 20

cga ata gaa cta tcc ccg aaa ttt gcg att cca gta aaa ccc ggc gaa 211
 Arg Ile Glu Leu Ser Pro Lys Phe Ala Ile Pro Val Lys Pro Gly Glu
 25 30 35

cat ctc aag atc atg gtg ccc cta aaa act gga cag gaa aag aga tcg 259
 His Leu Lys Ile Met Val Pro Leu Lys Thr Gly Gln Glu Lys Arg Ser
 40 45 50

tac tcc atc gtt gac gct cgt cac gac ggt tcg act ctc gcc ctg agc 307
 Tyr Ser Ile Val Asp Ala Arg His Asp Gly Ser Thr Leu Ala Leu Ser
 55 60 65

gta ctc aaa acc aga aac tcc cgt gga gga tct gag ttc atg cat acg 355
 Val Leu Lys Thr Arg Asn Ser Arg Gly Gly Ser Glu Phe Met His Thr
 70 75 80 85

ctt cga gct gga gac aca gtt act gtc tcc agg ccg tct cag gat ttt 403
 Leu Arg Ala Gly Asp Thr Val Thr Val Ser Arg Pro Ser Gln Asp Phe
 90 95 100

cct ctc cgc gtg ggt gcg cct gag tat gta ctt gtt gcc ggc gga att	451
Pro Leu Arg Val Gly Ala Pro Glu Tyr Val Leu Val Ala Gly Gly Ile	
105 110 115	
gga atc aca gcg atc cgt tca atg gca tct tta tta aag aaa ttg gga	499
Gly Ile Thr Ala Ile Arg Ser Met Ala Ser Leu Leu Lys Lys Leu Gly	
120 125 130	
gcg aac tac cgc atc cat ttc gca gca cgc agc ctt gat gcc atg gct	547
Ala Asn Tyr Arg Ile His Phe Ala Ala Arg Ser Leu Asp Ala Met Ala	
135 140 145	
tac aaa gat gag ctc gtg gca gaa cac ggc gac aag ctg cac ctg cat	595
Tyr Lys Asp Glu Leu Val Ala Glu His Gly Asp Lys Leu His Leu His	
150 155 160 165	
cta gat tct gaa ggc acc acc atc gat gtc cca gca ttg atc gaa acc	643
Leu Asp Ser Glu Gly Thr Thr Ile Asp Val Pro Ala Leu Ile Glu Thr	
170 175 180	
tta aac ccc cac act gag ctt tat atg tgc ggc ccc atc cgc ttg atg	691
Leu Asn Pro His Thr Glu Leu Tyr Met Cys Gly Pro Ile Arg Leu Met	
185 190 195	
gat gcc atc cgg cgc gca tgg aac acc cgc gga ctt gac ccc acc aat	739
Asp Ala Ile Arg Arg Ala Trp Asn Thr Arg Gly Leu Asp Pro Thr Asn	
200 205 210	
ctg cgt ttc gaa acg ttt gga aac agt gga tgg ttc tcc cca gag gtt	787
Leu Arg Phe Glu Thr Phe Gly Asn Ser Gly Trp Phe Ser Pro Glu Val	
215 220 225	
ttc cac atc caa gta cca gag ctg ggg ctt cac gcc aca gtc aac aag	835
Phe His Ile Gln Val Pro Glu Leu Gly Leu His Ala Thr Val Asn Lys	
230 235 240 245	
gat gaa agc atg ctg gag gct ttg caa aag gct ggg gcg aat atg atg	883
Asp Glu Ser Met Leu Glu Ala Leu Gln Lys Ala Gly Ala Asn Met Met	
250 255 260	
ttt gat tgt cga aaa ggc gaa tgt ggt ttg tgc cag gtt cgc gtt cta	931
Phe Asp Cys Arg Lys Gly Glu Cys Gly Leu Cys Gln Val Arg Val Leu	
265 270 275	
gaa gtc gat ggc cag gtt gat cac cgc gat gtg ttc ttc tct gat cgt	979
Glu Val Asp Gly Gln Val Asp His Arg Asp Val Phe Phe Ser Asp Arg	
280 285 290	
caa aaa gaa tcc gac gca aag gca tgc gcc tgc gtg tct cga gta gtc	1027
Gln Lys Glu Ser Asp Ala Lys Ala Cys Ala Cys Val Ser Arg Val Val	
295 300 305	
tcc tcc cct tcc tcg tcc cca acc tcg acc att acg gtc gcc ctc tcc	1075
Ser Ser Pro Ser Ser Ser Pro Thr Ser Thr Ile Thr Val Ala Leu Ser	
310 315 320 325	
taaaggagcc tggcatggat atc	1098

<211> 325

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 440

Met Asn Ser Gln Trp Gln Asp Ala His Val Val Ser Ser Glu Ile Ile
 1 5 10 15

Ala Ala Asp Ile Arg Arg Ile Glu Leu Ser Pro Lys Phe Ala Ile Pro
 20 25 30

Val Lys Pro Gly Glu His Leu Lys Ile Met Val Pro Leu Lys Thr Gly
 35 40 45

Gln Glu Lys Arg Ser Tyr Ser Ile Val Asp Ala Arg His Asp Gly Ser
 50 55 60

Thr Leu Ala Leu Ser Val Leu Lys Thr Arg Asn Ser Arg Gly Gly Ser
 65 70 75 80

Glu Phe Met His Thr Leu Arg Ala Gly Asp Thr Val Thr Val Ser Arg
 85 90 95

Pro Ser Gln Asp Phe Pro Leu Arg Val Gly Ala Pro Glu Tyr Val Leu
 100 105 110

Val Ala Gly Gly Ile Gly Ile Thr Ala Ile Arg Ser Met Ala Ser Leu
 115 120 125

Leu Lys Lys Leu Gly Ala Asn Tyr Arg Ile His Phe Ala Ala Arg Ser
 130 135 140

Leu Asp Ala Met Ala Tyr Lys Asp Glu Leu Val Ala Glu His Gly Asp
 145 150 155 160

Lys Leu His Leu His Leu Asp Ser Glu Gly Thr Thr Ile Asp Val Pro
 165 170 175

Ala Leu Ile Glu Thr Leu Asn Pro His Thr Glu Leu Tyr Met Cys Gly
 180 185 190

Pro Ile Arg Leu Met Asp Ala Ile Arg Arg Ala Trp Asn Thr Arg Gly
 195 200 205

Leu Asp Pro Thr Asn Leu Arg Phe Glu Thr Phe Gly Asn Ser Gly Trp
 210 215 220

Phe Ser Pro Glu Val Phe His Ile Gln Val Pro Glu Leu Gly Leu His
 225 230 235 240

Ala Thr Val Asn Lys Asp Glu Ser Met Leu Glu Ala Leu Gln Lys Ala
 245 250 255

Gly Ala Asn Met Met Phe Asp Cys Arg Lys Gly Glu Cys Gly Leu Cys
 260 265 270

Gln Val Arg Val Leu Glu Val Asp Gly Gln Val Asp His Arg Asp Val
 275 280 285

Phe Phe Ser Asp Arg Gln Lys Glu Ser Asp Ala Lys Ala Cys Ala Cys
 290 295 300

Val Ser Arg Val Val Ser Ser Pro Ser Ser Ser Pro Thr Ser Thr Ile
305 310 315 320

Thr Val Ala Leu Ser
325

<210> 441
<211> 1278
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1255)
<223> RXA02535

<400> 441
aggattgggt gaggagggag gcgtcgaaaa gcaagaaacg cctgacacgc gtagccgtgg 60
ctgcgcacct tttaccttga ttaggtgcac aatagggagt gtg aca cct cgc cct 115
Val Thr Pro Arg Pro
1 5
gtt tct tct gtt gcg cga ctc gtt gag gat aac gcg caa gat ttt ctt 163
Val Ser Ser Val Ala Arg Leu Val Glu Asp Asn Ala Gln Asp Phe Leu
10 15 20
cgc gcc gtt cag gcg aaa ctt tta acg ctc gcg cca cag gct cgt ggg 211
Arg Ala Val Gln Ala Lys Leu Leu Thr Leu Ala Pro Gln Ala Arg Gly
25 30 35
cat ttt ccc act gcg gat gat gcg act cat atc agc atc gcc gaa atg 259
His Phe Pro Thr Ala Asp Asp Ala Thr His Ile Ser Ile Ala Glu Met
40 45 50
gtg agt gcg ctg ttg gaa ggc act ggt gag gaa ggg aaa gta gac gac 307
Val Ser Ala Leu Leu Glu Gly Thr Gly Glu Glu Gly Lys Val Asp Asp
55 60 65
aaa aca ctg gag ttc ttt aaa gaa gcg gcg tta gat gcg cgt cga ttt 355
Lys Thr Leu Glu Phe Phe Lys Glu Ala Ala Leu Asp Ala Arg Arg Phe
70 75 80 85
ggc ctg acc cca gaa atg cac agc gct ttg ggt gag gcc gtg cgc agc 403
Gly Leu Thr Pro Glu Met His Ser Ala Leu Gly Glu Ala Val Arg Ser
90 95 100
gaa cta ttg tca tta tgc gag gat ctt ccc ttt gaa aat gtg ctg ttt 451
Glu Leu Leu Ser Leu Cys Glu Asp Leu Pro Phe Glu Asn Val Leu Phe
105 110 115
gcc gag cgt gcg att gct gca acc acg gct gtt tcc gtc gag gcg gtt 499
Ala Glu Arg Ala Ile Ala Ala Thr Thr Ala Val Ser Val Glu Ala Val
120 125 130
cgt gaa gct gat gag gca cac att cct gcc tca tat cag gca gaa att 547
Arg Glu Ala Asp Glu Ala His Ile Pro Ala Ser Tyr Gln Ala Glu Ile
135 140 145

gta gaa gtt gaa aag cgc agc cgt agg ttc acc gtc gtg cgc atg caa	595
Val Glu Val Glu Lys Arg Ser Arg Arg Phe Thr Val Val Arg Met Gln	
150 155 160 165	
gct gaa acg caa ctg ccc tac cta ccg gga caa tat ctt gca gca act	643
Ala Glu Thr Gln Leu Pro Tyr Leu Pro Gly Gln Tyr Leu Ala Ala Thr	
170 175 180	
gcg gat ttt ctg ccc aac aca tgg cgc tac ctg tgc cct tcg atc ccc	691
Ala Asp Phe Leu Pro Asn Thr Trp Arg Tyr Leu Cys Pro Ser Ile Pro	
185 190 195	
act aac gaa tgg ggg cag gtg gag ttt cac atc caa tca gac gca gat	739
Thr Asn Glu Trp Gly Gln Val Glu Phe His Ile Gln Ser Asp Ala Asp	
200 205 210	
gat atc gct gga ctt tta gcc acc aca cgc ctt ggc gat aaa tgg cga	787
Asp Ile Ala Gly Leu Leu Ala Thr Thr Arg Leu Gly Asp Lys Trp Arg	
215 220 225	
ctt ggc ccc ggt cgt gga gat ttc gga caa agc aaa att agt tcc ggc	835
Leu Gly Pro Gly Arg Gly Asp Phe Gly Gln Ser Lys Ile Ser Ser Gly	
230 235 240 245	
aat gat ttg tta ttt att gca cat gga acg ggc cta gct cct ctt cgc	883
Asn Asp Leu Leu Phe Ile Ala His Gly Thr Gly Leu Ala Pro Leu Arg	
250 255 260	
gct tac atg ttt gag ctg atg aac caa gca gca cct cca cgt ttg cac	931
Ala Tyr Met Phe Glu Leu Met Asn Gln Ala Ala Pro Pro Arg Leu His	
265 270 275	
ttt ttc gtc ggt gcc gac tac ccc ggt gag ctg tat gaa ctc acc ggc	979
Phe Phe Val Gly Ala Asp Tyr Pro Gly Glu Leu Tyr Glu Leu Thr Gly	
280 285 290	
atg tgg aat ttt gct gca gcc agc cca tgg ctt tct gtc gta ccg gtg	1027
Met Trp Asn Phe Ala Ala Ala Ser Pro Trp Leu Ser Val Val Pro Val	
295 300 305	
tca acg cat gac aag gat gcg tgg tgg gtt caa gcc acc gaa gca tcg	1075
Ser Thr His Asp Lys Asp Ala Trp Trp Val Gln Ala Thr Glu Ala Ser	
310 315 320 325	
cag cca ccg agg ggt ttg cat ttg cat caa acg ggt tcg atg gcg aag	1123
Gln Pro Pro Arg Gly Leu His Leu His Gln Thr Gly Ser Met Ala Lys	
330 335 340	
atc gtc acc gaa gca ggt gct tgg gcc gac cgc gac gtg tta att gct	1171
Ile Val Thr Glu Ala Gly Ala Trp Ala Asp Arg Asp Val Leu Ile Ala	
345 350 355	
ggc cct gaa tcg tgg gct cgg gat gtt cgg cgc gcg atg att agg cgt	1219
Gly Pro Glu Ser Trp Ala Arg Asp Val Arg Arg Ala Met Ile Arg Arg	
360 365 370	
gga act ccg gcc cag cag att gag att tta ggg ttc taggttgacct	1265
Gly Thr Pro Ala Gln Gln Ile Glu Ile Leu Gly Phe	
375 380 385	
caccgggctg acc	1278

<210> 442

<211> 385

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 442

Val Thr Pro Arg Pro Val Ser Ser Val Ala Arg Leu Val Glu Asp Asn
 1 5 10 15

Ala Gln Asp Phe Leu Arg Ala Val Gln Ala Lys Leu Leu Thr Leu Ala
 20 25 30

Pro Gln Ala Arg Gly His Phe Pro Thr Ala Asp Asp Ala Thr His Ile
 35 40 45

Ser Ile Ala Glu Met Val Ser Ala Leu Leu Glu Gly Thr Gly Glu Glu
 50 55 60

Gly Lys Val Asp Asp Lys Thr Leu Glu Phe Phe Lys Glu Ala Ala Leu
 65 70 75 80

Asp Ala Arg Arg Phe Gly Leu Thr Pro Glu Met His Ser Ala Leu Gly
 85 90 95

Glu Ala Val Arg Ser Glu Leu Leu Ser Leu Cys Glu Asp Leu Pro Phe
 100 105 110

Glu Asn Val Leu Phe Ala Glu Arg Ala Ile Ala Ala Thr Thr Ala Val
 115 120 125

Ser Val Glu Ala Val Arg Glu Ala Asp Glu Ala His Ile Pro Ala Ser
 130 135 140

Tyr Gln Ala Glu Ile Val Glu Val Glu Lys Arg Ser Arg Arg Phe Thr
 145 150 155 160

Val Val Arg Met Gln Ala Glu Thr Gln Leu Pro Tyr Leu Pro Gly Gln
 165 170 175

Tyr Leu Ala Ala Thr Ala Asp Phe Leu Pro Asn Thr Trp Arg Tyr Leu
 180 185 190

Cys Pro Ser Ile Pro Thr Asn Glu Trp Gly Gln Val Glu Phe His Ile
 195 200 205

Gln Ser Asp Ala Asp Asp Ile Ala Gly Leu Leu Ala Thr Thr Arg Leu
 210 215 220

Gly Asp Lys Trp Arg Leu Gly Pro Gly Arg Gly Asp Phe Gly Gln Ser
 225 230 235 240

Lys Ile Ser Ser Gly Asn Asp Leu Leu Phe Ile Ala His Gly Thr Gly
 245 250 255

Leu Ala Pro Leu Arg Ala Tyr Met Phe Glu Leu Met Asn Gln Ala Ala
 260 265 270

Pro Pro Arg Leu His Phe Phe Val Gly Ala Asp Tyr Pro Gly Glu Leu
 275 280 285

Tyr Glu Leu Thr Gly Met Trp Asn Phe Ala Ala Ala Ser Pro Trp Leu
 290 295 300
 Ser Val Val Pro Val Ser Thr His Asp Lys Asp Ala Trp Trp Val Gln
 305 310 315 320
 Ala Thr Glu Ala Ser Gln Pro Pro Arg Gly Leu His Leu His Gln Thr
 325 330 335
 Gly Ser Met Ala Lys Ile Val Thr Glu Ala Gly Ala Trp Ala Asp Arg
 340 345 350
 Asp Val Leu Ile Ala Gly Pro Glu Ser Trp Ala Arg Asp Val Arg Arg
 355 360 365
 Ala Met Ile Arg Arg Gly Thr Pro Ala Gln Gln Ile Glu Ile Leu Gly
 370 375 380

Phe
 385

<210> 443
 <211> 1248
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1225)
 <223> RXA00964

<400> 443
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 tcatacgcat ctacaacatc cgtaaaggag gactccaaca atg ggc gcc cca ggt 115
 Met Gly Ala Pro Gly
 1 5
 aaa aac gat tac gca act gaa cac gtc aag caa gaa gtc cca ccc gca 163
 Lys Asn Asp Tyr Ala Thr Glu His Val Lys Gln Glu Val Pro Pro Ala
 10 15 20
 act cca gaa gag cag gca gag ctg gac acc atg tat aaa cgc atg gat 211
 Thr Pro Glu Glu Gln Ala Glu Leu Asp Thr Met Tyr Lys Arg Met Asp
 25 30 35
 gac ctg cat cta aag ccc ctg tgg act caa atc ggt ggg ttg atg cca 259
 Asp Leu His Leu Lys Pro Leu Trp Thr Gln Ile Gly Gly Leu Met Pro
 40 45 50
 aac cac ccg gaa cca cga gct gtg gca cac aag tgg gat tgg gcg gaa 307
 Asn His Pro Glu Pro Arg Ala Val Ala His Lys Trp Asp Trp Ala Glu
 55 60 65
 ctc ctg aag ctc gcg cag cgc tcc ggt gaa ctc gtt cca gtt ggg cgc 355
 Leu Leu Lys Leu Ala Gln Arg Ser Gly Glu Leu Val Pro Val Gly Arg
 70 75 80 85
 ggt ggc gaa cgc cgt gcc att ggc ctg gca aac cca ggt tta gac ggc 403

Gly	Gly	Glu	Arg	Arg	Ala	Ile	Gly	Leu	Ala	Asn	Pro	Gly	Leu	Asp	Gly		
				90					95					100			
aat	acc	tac	atc	tcc	cct	acc	ctg	tgg	gca	gca	att	cag	tac	ctc	gct	451	
Asn	Thr	Tyr	Ile	Ser	Pro	Thr	Leu	Trp	Ala	Ala	Ile	Gln	Tyr	Leu	Ala		
			105					110					115				
ccg	ggt	gag	aac	gct	cca	gag	cac	cgc	cac	tca	caa	aac	gca	ttc	cgc	499	
Pro	Gly	Glu	Asn	Ala	Pro	Glu	His	Arg	His	Ser	Gln	Asn	Ala	Phe	Arg		
		120					125					130					
ttt	gtt	atc	gaa	ggc	gaa	ggc	gtg	tgg	act	gtc	gtt	aac	ggc	gat	cca	547	
Phe	Val	Ile	Glu	Gly	Glu	Gly	Val	Trp	Thr	Val	Val	Asn	Gly	Asp	Pro		
	135					140					145						
gta	cca	atg	cga	cgc	ggc	gac	ttc	ctg	ctc	acc	cca	ggc	tgg	aac	tac	595	
Val	Pro	Met	Arg	Arg	Gly	Asp	Phe	Leu	Leu	Thr	Pro	Gly	Trp	Asn	Tyr		
150					155					160					165		
cac	ggc	cac	cac	aac	atc	gcg	acc	gag	cca	atg	gcc	tgg	cta	gac	ggg	643	
His	Gly	His	His	Asn	Ile	Ala	Thr	Glu	Pro	Met	Ala	Trp	Leu	Asp	Gly		
				170					175					180			
ctc	gat	atc	cca	ttt	gcc	tac	caa	atg	gac	acc	gga	ttc	ttt	gag	tac	691	
Leu	Asp	Ile	Pro	Phe	Ala	Tyr	Gln	Met	Asp	Thr	Gly	Phe	Phe	Glu	Tyr		
			185					190					195				
ggc	acc	gaa	aaa	ctc	act	gac	gaa	tcc	acc	cca	gac	ctc	tcc	cgt	tca	739	
Gly	Thr	Glu	Lys	Leu	Thr	Asp	Glu	Ser	Thr	Pro	Asp	Leu	Ser	Arg	Ser		
		200					205					210					
gaa	cgc	ctg	tgg	gcc	cac	cca	gga	ctt	cgc	cca	gtc	tcc	ttc	cca	gga	787	
Glu	Arg	Leu	Trp	Ala	His	Pro	Gly	Leu	Arg	Pro	Val	Ser	Phe	Pro	Gly		
	215					220					225						
aaa	act	tcc	tac	tca	cca	att	ggg	cgc	tac	gcc	tgg	gag	cac	acc	gac	835	
Lys	Thr	Ser	Tyr	Ser	Pro	Ile	Gly	Arg	Tyr	Ala	Trp	Glu	His	Thr	Asp		
230					235					240					245		
gca	gca	ctc	aac	gat	cag	ctg	gca	ttg	gaa	gaa	gca	gga	cac	cca	gga	883	
Ala	Ala	Leu	Asn	Asp	Gln	Leu	Ala	Leu	Glu	Glu	Ala	Gly	His	Pro	Gly		
				250					255					260			
aca	gtc	gcg	ccg	gga	cat	gct	gcg	att	cgc	ttc	tcc	aac	cca	act	acc	931	
Thr	Val	Ala	Pro	Gly	His	Ala	Ala	Ile	Arg	Phe	Ser	Asn	Pro	Thr	Thr		
			265					270					275				
ggt	ggc	gat	gtc	atg	acc	acc	atc	cgc	gcg	gag	ttc	cac	cgc	ctg	cgc	979	
Gly	Gly	Asp	Val	Met	Thr	Thr	Ile	Arg	Ala	Glu	Phe	His	Arg	Leu	Arg		
		280					285					290					
cca	ggt	gca	tcc	act	gcc	ccc	att	cat	gag	gta	gga	aac	cgt	tgc	ttc	1027	
Pro	Gly	Ala	Ser	Thr	Ala	Pro	Ile	His	Glu	Val	Gly	Asn	Arg	Cys	Phe		
	295					300					305						
cag	gta	ttt	gag	ggt	tcc	gca	aca	atc	aat	gtt	gga	gat	aaa	acc	ttt	1075	
Gln	Val	Phe	Glu	Gly	Ser	Ala	Thr	Ile	Asn	Val	Gly	Asp	Lys	Thr	Phe		
310					315					320					325		
gaa	gct	aac	cac	ggc	gat	gtg	atc	aat	gta	ccg	tcg	tgg	cag	aag	tgg	1123	
Glu	Ala	Asn	His	Gly	Asp	Val	Ile	Asn	Val	Pro	Ser	Trp	Gln	Lys	Trp		

330										335					340					
aat atc gtc gct ggc tct gac ggc gtc gac ttg ttc tgc ttc tct gat	1171																			
Asn Ile Val Ala Gly Ser Asp Gly Val Asp Leu Phe Cys Phe Ser Asp																				
345 350 355																				
aca cca att ttc gag gcc ctt aac ctc gca cgt act ttt act ccg gaa	1219																			
Thr Pro Ile Phe Glu Ala Leu Asn Leu Ala Arg Thr Phe Thr Pro Glu																				
360 365 370																				
gga atc tagaacttat gcgtcttgca aca	1248																			
Gly Ile																				
375																				

<210> 444

<211> 375

<212> PRT

<213> Corynebacterium glutamicum

<400> 444

Met Gly Ala Pro Gly Lys Asn Asp Tyr Ala Thr Glu His Val Lys Gln	
1 5 10 15	
Glu Val Pro Pro Ala Thr Pro Glu Glu Gln Ala Glu Leu Asp Thr Met	
20 25 30	
Tyr Lys Arg Met Asp Asp Leu His Leu Lys Pro Leu Trp Thr Gln Ile	
35 40 45	
Gly Gly Leu Met Pro Asn His Pro Glu Pro Arg Ala Val Ala His Lys	
50 55 60	
Trp Asp Trp Ala Glu Leu Leu Lys Leu Ala Gln Arg Ser Gly Glu Leu	
65 70 75 80	
Val Pro Val Gly Arg Gly Gly Glu Arg Arg Ala Ile Gly Leu Ala Asn	
85 90 95	
Pro Gly Leu Asp Gly Asn Thr Tyr Ile Ser Pro Thr Leu Trp Ala Ala	
100 105 110	
Ile Gln Tyr Leu Ala Pro Gly Glu Asn Ala Pro Glu His Arg His Ser	
115 120 125	
Gln Asn Ala Phe Arg Phe Val Ile Glu Gly Glu Gly Val Trp Thr Val	
130 135 140	
Val Asn Gly Asp Pro Val Pro Met Arg Arg Gly Asp Phe Leu Leu Thr	
145 150 155 160	
Pro Gly Trp Asn Tyr His Gly His His Asn Ile Ala Thr Glu Pro Met	
165 170 175	
Ala Trp Leu Asp Gly Leu Asp Ile Pro Phe Ala Tyr Gln Met Asp Thr	
180 185 190	
Gly Phe Phe Glu Tyr Gly Thr Glu Lys Leu Thr Asp Glu Ser Thr Pro	
195 200 205	
Asp Leu Ser Arg Ser Glu Arg Leu Trp Ala His Pro Gly Leu Arg Pro	

210	215	220
Val Ser Phe Pro Gly Lys Thr Ser Tyr Ser Pro Ile Gly Arg Tyr Ala		
225	230	235 240
Trp Glu His Thr Asp Ala Ala Leu Asn Asp Gln Leu Ala Leu Glu Glu		
	245	250 255
Ala Gly His Pro Gly Thr Val Ala Pro Gly His Ala Ala Ile Arg Phe		
	260	265 270
Ser Asn Pro Thr Thr Gly Gly Asp Val Met Thr Thr Ile Arg Ala Glu		
	275	280 285
Phe His Arg Leu Arg Pro Gly Ala Ser Thr Ala Pro Ile His Glu Val		
	290	295 300
Gly Asn Arg Cys Phe Gln Val Phe Glu Gly Ser Ala Thr Ile Asn Val		
305	310	315 320
Gly Asp Lys Thr Phe Glu Ala Asn His Gly Asp Val Ile Asn Val Pro		
	325	330 335
Ser Trp Gln Lys Trp Asn Ile Val Ala Gly Ser Asp Gly Val Asp Leu		
	340	345 350
Phe Cys Phe Ser Asp Thr Pro Ile Phe Glu Ala Leu Asn Leu Ala Arg		
	355	360 365
Thr Phe Thr Pro Glu Gly Ile		
370	375	

<210> 445
 <211> 1083
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1060)
 <223> RXN01466

<400> 445
 aatccatgat cccaaactac ctcaaagcgc ttgtaggcta agacttatgg atacacaacg 60

cggctcattg cggggaaaag ctcataaagc aaggctaaag atg acg cca aat ggt 115
 Met Thr Pro Asn Gly
 1 5

cgc agg caa ctc ctc ctg gag cgt ggc gca gca ttt agc aaa aac cgt 163
 Arg Arg Gln Leu Leu Leu Glu Arg Gly Ala Ala Phe Ser Lys Asn Arg
 10 15 20

acc ccg ggt cta aaa cac gtc gac cgc cac acc atc gtg gac tcc gac 211
 Thr Pro Gly Leu Lys His Val Asp Arg His Thr Ile Val Asp Ser Asp
 25 30 35

ggc ctc agc atc cac acg tac atg gtt ggc cat gcc gaa aat gcc acg 259
 Gly Leu Ser Ile His Thr Tyr Met Val Gly His Ala Glu Asn Ala Thr
 40 45 50

gca acg gtc gtg ttc atc cac ggc ttc acc ctc gcc gcc gaa gtg tat	307
Ala Thr Val Val Phe Ile His Gly Phe Thr Leu Ala Ala Glu Val Tyr	
55 60 65	
tac atg cag gtc gac tac cta caa acc ttt tac cca aat att aaa agc	355
Tyr Met Gln Val Asp Tyr Leu Gln Thr Phe Tyr Pro Asn Ile Lys Ser	
70 75 80 85	
gtg ctt atc gac gcc cgc ggc cac ggc gcc acc ggc cag atc cgc cca	403
Val Leu Ile Asp Ala Arg Gly His Gly Ala Thr Gly Gln Ile Arg Pro	
90 95 100	
gag ctc tgc acc atc gaa gga aca gcg aac gat gtt ctc gca gcc atc	451
Glu Leu Cys Thr Ile Glu Gly Thr Ala Asn Asp Val Leu Ala Ala Ile	
105 110 115	
cac gaa cac gca ccg acc ggc ccg ctc att ttg gtt ggg cat tcc ctc	499
His Glu His Ala Pro Thr Gly Pro Leu Ile Leu Val Gly His Ser Leu	
120 125 130	
ggc gga ctc acg gca ctt aac ctg gtt aaa cgg gca gat cac tca ctt	547
Gly Gly Leu Thr Ala Leu Asn Leu Val Lys Arg Ala Asp His Ser Leu	
135 140 145	
cgg aag agg atc gtc ggc atg gtt cta gtc gcc aca tcg atc gaa tca	595
Arg Lys Arg Ile Val Gly Met Val Leu Val Ala Thr Ser Ile Glu Ser	
150 155 160 165	
tta tcc acc caa ggt cta cca caa gtc ctg gca tca ccc ctt gcc gac	643
Leu Ser Thr Gln Gly Leu Pro Gln Val Leu Ala Ser Pro Leu Ala Asp	
170 175 180	
aac atc aaa aac gcc gtc gaa gca gcc ccc aac gat gcc caa aaa ttc	691
Asn Ile Lys Asn Ala Val Glu Ala Ala Pro Asn Asp Ala Gln Lys Phe	
185 190 195	
cgc caa tac gcc acc aca ttt cta gcc ccc acc ctg gcc acc gca gtc	739
Arg Gln Tyr Ala Thr Thr Phe Leu Ala Pro Thr Leu Ala Thr Ala Val	
200 205 210	
ttc caa cga gac aca aac gat gaa gtc atc gat ttc cac gcc gcc atg	787
Phe Gln Arg Asp Thr Asn Asp Glu Val Ile Asp Phe His Ala Ala Met	
215 220 225	
atc cac gaa acc ccc ttg gat acc ttc gtc ggt ttc ttc gac gac ctc	835
Ile His Glu Thr Pro Leu Asp Thr Phe Val Gly Phe Phe Asp Asp Leu	
230 235 240 245	
caa gaa cac gac gaa ctc gat gcc gca cca gca ttg gaa ggc ctc aaa	883
Gln Glu His Asp Glu Leu Asp Ala Ala Pro Ala Leu Glu Gly Leu Lys	
250 255 260	
ggc tac gtc ctt gcc ggc gaa tta gat gat gtc acc cca att agc caa	931
Gly Tyr Val Leu Ala Gly Glu Leu Asp Asp Val Thr Pro Ile Ser Gln	
265 270 275	
gcc gac cgc atc tgc gaa gtc tgg ccc ggc gca cgc ctt caa atc gca	979
Ala Asp Arg Ile Cys Glu Val Trp Pro Gly Ala Arg Leu Gln Ile Ala	
280 285 290	

gaa gga gca ggt cat atg ctt ccg ctt gaa gcg cca gga atc ctc aat 1027
 Glu Gly Ala Gly His Met Leu Pro Leu Glu Ala Pro Gly Ile Leu Asn
 295 300 305

aat gcg atc ggc aac att ttg gac ggg ctg ggc tgaggaacct ggttcgggacg 1080
 Asn Ala Ile Gly Asn Ile Leu Asp Gly Leu Gly
 310 315 320

tgg 1083

<210> 446

<211> 320

<212> PRT

<213> Corynebacterium glutamicum

<400> 446

Met Thr Pro Asn Gly Arg Arg Gln Leu Leu Leu Glu Arg Gly Ala Ala
 1 5 10 15

Phe Ser Lys Asn Arg Thr Pro Gly Leu Lys His Val Asp Arg His Thr
 20 25 30

Ile Val Asp Ser Asp Gly Leu Ser Ile His Thr Tyr Met Val Gly His
 35 40 45

Ala Glu Asn Ala Thr Ala Thr Val Val Phe Ile His Gly Phe Thr Leu
 50 55 60

Ala Ala Glu Val Tyr Tyr Met Gln Val Asp Tyr Leu Gln Thr Phe Tyr
 65 70 75 80

Pro Asn Ile Lys Ser Val Leu Ile Asp Ala Arg Gly His Gly Ala Thr
 85 90 95

Gly Gln Ile Arg Pro Glu Leu Cys Thr Ile Glu Gly Thr Ala Asn Asp
 100 105 110

Val Leu Ala Ala Ile His Glu His Ala Pro Thr Gly Pro Leu Ile Leu
 115 120 125

Val Gly His Ser Leu Gly Gly Leu Thr Ala Leu Asn Leu Val Lys Arg
 130 135 140

Ala Asp His Ser Leu Arg Lys Arg Ile Val Gly Met Val Leu Val Ala
 145 150 155 160

Thr Ser Ile Glu Ser Leu Ser Thr Gln Gly Leu Pro Gln Val Leu Ala
 165 170 175

Ser Pro Leu Ala Asp Asn Ile Lys Asn Ala Val Glu Ala Ala Pro Asn
 180 185 190

Asp Ala Gln Lys Phe Arg Gln Tyr Ala Thr Thr Phe Leu Ala Pro Thr
 195 200 205

Leu Ala Thr Ala Val Phe Gln Arg Asp Thr Asn Asp Glu Val Ile Asp
 210 215 220

Phe His Ala Ala Met Ile His Glu Thr Pro Leu Asp Thr Phe Val Gly
 225 230 235 240

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<210> 447
<211> 922
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(922)
<223> FRXA01466
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<400> 447
aatccatgat cccaaactac ctcaaagcgc ttgtaggcta agacttatgg atacacaacg 60
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cggctcattg cggggaaaag ctcataaaagc aaggctaaga atg acg cca aat ggt 115
Met Thr Pro Asn Gly
 1 5

cgc agg caa ctc ctc ctg gag cgt ggc gca gca ttt agc aaa aac cgt 163
 Arg Arg Gln Leu Leu Leu Glu Arg Gly Ala Ala Phe Ser Lys Asn Arg
 10 15 20

acc ccg ggt cta aaa cac gtc gac cgc cac acc atc gtg gac tcc gac 211
Thr Pro Gly Leu Lys His Val Asp Arg His Thr Ile Val Asp Ser Asp
25 30 35

ggc ctc agc atc cac acg tac atg gtt ggc cat gcc gaa aat gcc acg 259
Gly Leu Ser Ile His Thr Tyr Met Val Gly His Ala Glu Asn Ala Thr
40 45 50

gca acg gtc gtg ttc atc cac ggc ttc acc ctc gcc gcc gaa gtg tat 307
Ala Thr Val Val Phe Ile His Gly Phe Thr Leu Ala Ala Glu Val Tyr
55 60 65

tac	atg	cag	gtc	gac	tac	cta	caa	acc	ttt	tac	cca	aat	att	aaa	agc	355
Tyr	Met	Gln	Val	Asp	Tyr	Leu	Gln	Thr	Phe	Tyr	Pro	Asn	Ile	Lys	Ser	
70					75					80					85	

gtg ctt atc gac gcc cgc ggc cac ggc gcc acc ggc cag atc cgc cca 403
Val Leu Ile Asp Ala Arg Gly His Gly Ala Thr Gly Gln Ile Arg Pro
90 95 100

gag ctc tgc acc atc gaa gga aca gcg aac gat gtt ctc gca gcc atc 451
Glu Leu Cys Thr Ile Glu Gly Thr Ala Asn Asp Val Leu Ala Ala Ile
105 110 115

cac gaa cac gca ccg acc ggc ccg ctc att ttg gtt ggg cat tcc ctc 499
 His Glu His Ala Pro Thr Gly Pro Leu Ile Leu Val Gly His Ser Leu
 120 125 130
 ggc gga ctc acg gca ctt aac ctg gtt aaa cgg gca gat cac tca ctt 547
 Gly Gly Leu Thr Ala Leu Asn Leu Val Lys Arg Ala Asp His Ser Leu
 135 140 145
 cgg aag agg atc gtc ggc atg gtt cta gtc gcc aca tcg atc gaa tca 595
 Arg Lys Arg Ile Val Gly Met Val Leu Val Ala Thr Ser Ile Glu Ser
 150 155 160 165
 tta tcc acc caa ggt cta cca caa gtc ctg gca tca ccc ctt gcc gac 643
 Leu Ser Thr Gln Gly Leu Pro Gln Val Leu Ala Ser Pro Leu Ala Asp
 170 175 180
 aac atc aaa aac gcc gtc gaa gca gcc ccc aac gat gcc caa aaa ttc 691
 Asn Ile Lys Asn Ala Val Glu Ala Ala Pro Asn Asp Ala Gln Lys Phe
 185 190 195
 cgc caa tac gcc acc aca ttt cta gcc ccc acc ctg gcc acc gca gtc 739
 Arg Gln Tyr Ala Thr Thr Phe Leu Ala Pro Thr Leu Ala Thr Ala Val
 200 205 210
 ttc caa cga gac aca aac gat gaa gtc atc gat ttc cac gcc gcc atg 787
 Phe Gln Arg Asp Thr Asn Asp Glu Val Ile Asp Phe His Ala Ala Met
 215 220 225
 atc cac gaa acc ccc ttg gat acc ttc gtc ggt ttc ttc gac gac ctt 835
 Ile His Glu Thr Pro Leu Asp Thr Phe Val Gly Phe Phe Asp Asp Leu
 230 235 240 245
 caa gaa cac gac gaa ctc gat gcc gca cca aca ttg gaa ggc ctc aaa 883
 Gln Glu His Asp Glu Leu Asp Ala Ala Pro Thr Leu Glu Gly Leu Lys
 250 255 260
 ggc tac gtc ctt gcc ggc gaa tta gat gat gtc acc cca 922
 Gly Tyr Val Leu Ala Gly Glu Leu Asp Asp Val Thr Pro
 265 270

<210> 448

<211> 274

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 448

Met Thr Pro Asn Gly Arg Arg Gln Leu Leu Leu Glu Arg Gly Ala Ala
 1 5 10 15

Phe Ser Lys Asn Arg Thr Pro Gly Leu Lys His Val Asp Arg His Thr
 20 25 30

Ile Val Asp Ser Asp Gly Leu Ser Ile His Thr Tyr Met Val Gly His
 35 40 45

Ala Glu Asn Ala Thr Ala Thr Val Val Phe Ile His Gly Phe Thr Leu
 50 55 60

Ala Ala Glu Val Tyr Tyr Met Gln Val Asp Tyr Leu Gln Thr Phe Tyr

```

65              70              75              80
Pro Asn Ile Lys Ser Val Leu Ile Asp Ala Arg Gly His Gly Ala Thr
      85              90              95
Gly Gln Ile Arg Pro Glu Leu Cys Thr Ile Glu Gly Thr Ala Asn Asp
      100             105             110
Val Leu Ala Ala Ile His Glu His Ala Pro Thr Gly Pro Leu Ile Leu
      115             120             125
Val Gly His Ser Leu Gly Gly Leu Thr Ala Leu Asn Leu Val Lys Arg
      130             135             140
Ala Asp His Ser Leu Arg Lys Arg Ile Val Gly Met Val Leu Val Ala
      145             150             155             160
Thr Ser Ile Glu Ser Leu Ser Thr Gln Gly Leu Pro Gln Val Leu Ala
      165             170             175
Ser Pro Leu Ala Asp Asn Ile Lys Asn Ala Val Glu Ala Ala Pro Asn
      180             185             190
Asp Ala Gln Lys Phe Arg Gln Tyr Ala Thr Thr Phe Leu Ala Pro Thr
      195             200             205
Leu Ala Thr Ala Val Phe Gln Arg Asp Thr Asn Asp Glu Val Ile Asp
      210             215             220
Phe His Ala Ala Met Ile His Glu Thr Pro Leu Asp Thr Phe Val Gly
      225             230             235             240
Phe Phe Asp Asp Leu Gln Glu His Asp Glu Leu Asp Ala Ala Pro Thr
      245             250             255
Leu Glu Gly Leu Lys Gly Tyr Val Leu Ala Gly Glu Leu Asp Asp Val
      260             265             270
Thr Pro

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<210> 449
<211> 766
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(766)
<223> RXN03036

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<400> 449
tagaaaaatc tacccagtaa gcattcagga accattcaga atcttttctt agcatgtctc 60

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tatcagcgta aacgtccgaa catgaaaggc tagaaaagcc atg gct gag cag ttg 115
Met Ala Glu Gln Leu
      1              5

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cgt caa ttt gaa ggc agg gtc ctc cct aat caa tcc gag gac ttg gaa 163
Arg Gln Phe Glu Gly Arg Val Leu Pro Asn Gln Ser Glu Asp Leu Glu

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	10	15	20	
gat cag ggt ttg gga ttt gac ctg gga acc gtt ttc tcc cgc agg aag				211
Asp Gln Gly Leu Gly Phe Asp Leu Gly Thr Val Phe Ser Arg Arg Lys	25	30	35	
ggt ttg gga ttc atc ggt gtt ggt gga gca ggt gtg gca ctt gct gct				259
Val Leu Gly Phe Ile Gly Val Gly Gly Ala Gly Val Ala Leu Ala Ala	40	45	50	
tgt tca cct tct ggt tct tcc gcg gca tcg agc acc tca agc gcg tcc				307
Cys Ser Pro Ser Gly Ser Ser Ala Ala Ser Ser Thr Ser Ser Ala Ser	55	60	65	
agc agc gca gct gca acc acc agt gca gca gca gag act ttg act gag				355
Ser Ser Ala Ala Ala Thr Thr Ser Ala Ala Ala Glu Thr Leu Thr Glu	70	75	80	85
atg aag tcg gag act gct ggt ccg tac ccg ggc gat ggt tcg aat ggt				403
Met Lys Ser Glu Thr Ala Gly Pro Tyr Pro Gly Asp Gly Ser Asn Gly	90	95	100	
ccg gat gtg ttg gag gtc tcc ggt gtg gag cgc cag gac atc acc aag				451
Pro Asp Val Leu Glu Val Ser Gly Val Glu Arg Gln Asp Ile Thr Lys	105	110	115	
tcg att gat tct gac acc gtg gca gag ggc gta cct ctg acg ttg act				499
Ser Ile Asp Ser Asp Thr Val Ala Glu Gly Val Pro Leu Thr Leu Thr	120	125	130	
atg acc att ttg gac atg aac aac aac aat cag cca atg gag ggt gct				547
Met Thr Ile Leu Asp Met Asn Asn Asn Asn Gln Pro Met Glu Gly Ala	135	140	145	
gcg gtg tac gtg tgg cac tgt gat gcg ccg ggt cga tat tcg atg tac				595
Ala Val Tyr Val Trp His Cys Asp Ala Pro Gly Arg Tyr Ser Met Tyr	150	155	160	165
gac tct gag ctg gaa gat gag acc tat tta cgc ggt gtg cag att acc				643
Asp Ser Glu Leu Glu Asp Glu Thr Tyr Leu Arg Gly Val Gln Ile Thr	170	175	180	
gat aag tat ggc cag gtc acg ttc gat acc att ttc cct ggt tgt tat				691
Asp Lys Tyr Gly Gln Val Thr Phe Asp Thr Ile Phe Pro Gly Cys Tyr	185	190	195	
gcg ggc cgt tgg gtg cat att cat ttc gag gtg ttc ccg gat cga gac				739
Ala Gly Arg Trp Val His Ile His Phe Glu Val Phe Pro Asp Arg Asp	200	205	210	
agc atc acg gat tcc acg aac aac att				766
Ser Ile Thr Asp Ser Thr Asn Asn Ile	215	220		

<210> 450

<211> 222

<212> PRT

<213> Corynebacterium glutamicum

<400> 450

Met Ala Glu Gln Leu Arg Gln Phe Glu Gly Arg Val Leu Pro Asn Gln
 1 5 10 15

Ser Glu Asp Leu Glu Asp Gln Gly Leu Gly Phe Asp Leu Gly Thr Val
 20 25 30

Phe Ser Arg Arg Lys Val Leu Gly Phe Ile Gly Val Gly Gly Ala Gly
 35 40 45

Val Ala Leu Ala Ala Cys Ser Pro Ser Gly Ser Ser Ala Ala Ser Ser
 50 55 60

Thr Ser Ser Ala Ser Ser Ser Ala Ala Ala Thr Thr Ser Ala Ala Ala
 65 70 75 80

Glu Thr Leu Thr Glu Met Lys Ser Glu Thr Ala Gly Pro Tyr Pro Gly
 85 90 95

Asp Gly Ser Asn Gly Pro Asp Val Leu Glu Val Ser Gly Val Glu Arg
 100 105 110

Gln Asp Ile Thr Lys Ser Ile Asp Ser Asp Thr Val Ala Glu Gly Val
 115 120 125

Pro Leu Thr Leu Thr Met Thr Ile Leu Asp Met Asn Asn Asn Asn Gln
 130 135 140

Pro Met Glu Gly Ala Ala Val Tyr Val Trp His Cys Asp Ala Pro Gly
 145 150 155 160

Arg Tyr Ser Met Tyr Asp Ser Glu Leu Glu Asp Glu Thr Tyr Leu Arg
 165 170 175

Gly Val Gln Ile Thr Asp Lys Tyr Gly Gln Val Thr Phe Asp Thr Ile
 180 185 190

Phe Pro Gly Cys Tyr Ala Gly Arg Trp Val His Ile His Phe Glu Val
 195 200 205

Phe Pro Asp Arg Asp Ser Ile Thr Asp Ser Thr Asn Asn Ile
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<210> 451

<211> 766

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(766)

<223> FRXA02895

<400> 451

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tatcagcgta aacgtccgaa catgaaaggc tagaaaagcc atg gct gag cag ttg 115
 Met Ala Glu Gln Leu
 1 5

cgt caa ttt gaa ggc agg gtc ctc cct aat caa tcc gag gac ttg gaa 163

Arg	Gln	Phe	Glu	Gly	Arg	Val	Leu	Pro	Asn	Gln	Ser	Glu	Asp	Leu	Glu		
				10					15					20			
gat	cag	ggt	ttg	gga	ttt	gac	ctg	gga	acc	gtt	ttc	tcc	cgc	agg	aag	211	
Asp	Gln	Gly	Leu	Gly	Phe	Asp	Leu	Gly	Thr	Val	Phe	Ser	Arg	Arg	Lys		
			25					30					35				
gtt	ttg	gga	ttc	atc	ggt	gtt	ggt	gga	gca	ggt	gtg	gca	ctt	gct	gct	259	
Val	Leu	Gly	Phe	Ile	Gly	Val	Gly	Gly	Ala	Gly	Val	Ala	Leu	Ala	Ala		
			40				45					50					
tgt	tca	cct	tct	ggt	tct	tcc	gcg	gca	tcg	agc	acc	tca	agc	gcg	tcc	307	
Cys	Ser	Pro	Ser	Gly	Ser	Ser	Ala	Ala	Ser	Ser	Thr	Ser	Ser	Ala	Ser		
	55					60					65						
agc	agc	gca	gct	gca	acc	acc	agt	gca	gca	gca	gag	act	ttg	act	gag	355	
Ser	Ser	Ala	Ala	Ala	Thr	Thr	Ser	Ala	Ala	Ala	Glu	Thr	Leu	Thr	Glu		
	70				75				80						85		
atg	aag	tcg	gag	act	gct	ggt	ccg	tac	ccg	ggc	gat	ggt	tcg	aat	ggt	403	
Met	Lys	Ser	Glu	Thr	Ala	Gly	Pro	Tyr	Pro	Gly	Asp	Gly	Ser	Asn	Gly		
				90				95						100			
ccg	gat	gtg	ttg	gag	gtc	tcc	ggt	gtg	gag	cgc	cag	gac	atc	acc	aag	451	
Pro	Asp	Val	Leu	Glu	Val	Ser	Gly	Val	Glu	Arg	Gln	Asp	Ile	Thr	Lys		
			105					110					115				
tcg	att	gat	tct	gac	acc	gtg	gca	gag	ggc	gta	cct	ctg	acg	ttg	act	499	
Ser	Ile	Asp	Ser	Asp	Thr	Val	Ala	Glu	Gly	Val	Pro	Leu	Thr	Leu	Thr		
		120					125					130					
atg	acc	att	ttg	gac	atg	aac	aac	aac	aat	cag	cca	atg	gag	ggt	gct	547	
Met	Thr	Ile	Leu	Asp	Met	Asn	Asn	Asn	Asn	Gln	Pro	Met	Glu	Gly	Ala		
	135					140					145						
gcg	gtg	tac	gtg	tgg	cac	tgt	gat	gcg	ccg	ggt	cga	tat	tcg	atg	tac	595	
Ala	Val	Tyr	Val	Trp	His	Cys	Asp	Ala	Pro	Gly	Arg	Tyr	Ser	Met	Tyr		
	150				155				160						165		
gac	tct	gag	ctg	gaa	gat	gag	acc	tat	tta	cgc	ggt	gtg	cag	att	acc	643	
Asp	Ser	Glu	Leu	Glu	Asp	Glu	Thr	Tyr	Leu	Arg	Gly	Val	Gln	Ile	Thr		
			170					175						180			
gat	aag	tat	ggc	cag	gtc	acg	ttc	gat	acc	att	ttc	cct	ggt	tgt	tat	691	
Asp	Lys	Tyr	Gly	Gln	Val	Thr	Phe	Asp	Thr	Ile	Phe	Pro	Gly	Cys	Tyr		
			185					190					195				
gcg	ggc	cgt	tgg	gtg	cat	att	cat	ttc	gag	gtg	ttc	ccg	gat	cga	gac	739	
Ala	Gly	Arg	Trp	Val	His	Ile	His	Phe	Glu	Val	Phe	Pro	Asp	Arg	Asp		
		200					205					210					
agc	atc	acg	gat	tcc	acg	aac	aac	att								766	
Ser	Ile	Thr	Asp	Ser	Thr	Asn	Asn	Ile									
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<212> PRT

<213> Corynebacterium glutamicum

<400> 452

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Ser Glu Asp Leu Glu Asp Gln Gly Leu Gly Phe Asp Leu Gly Thr Val
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Phe Ser Arg Arg Lys Val Leu Gly Phe Ile Gly Val Gly Gly Ala Gly
 35 40 45

Val Ala Leu Ala Ala Cys Ser Pro Ser Gly Ser Ser Ala Ala Ser Ser
 50 55 60

Thr Ser Ser Ala Ser Ser Ser Ala Ala Ala Thr Thr Ser Ala Ala Ala
 65 70 75 80

Glu Thr Leu Thr Glu Met Lys Ser Glu Thr Ala Gly Pro Tyr Pro Gly
 85 90 95

Asp Gly Ser Asn Gly Pro Asp Val Leu Glu Val Ser Gly Val Glu Arg
 100 105 110

Gln Asp Ile Thr Lys Ser Ile Asp Ser Asp Thr Val Ala Glu Gly Val
 115 120 125

Pro Leu Thr Leu Thr Met Thr Ile Leu Asp Met Asn Asn Asn Asn Gln
 130 135 140

Pro Met Glu Gly Ala Ala Val Tyr Val Trp His Cys Asp Ala Pro Gly
 145 150 155 160

Arg Tyr Ser Met Tyr Asp Ser Glu Leu Glu Asp Glu Thr Tyr Leu Arg
 165 170 175

Gly Val Gln Ile Thr Asp Lys Tyr Gly Gln Val Thr Phe Asp Thr Ile
 180 185 190

Phe Pro Gly Cys Tyr Ala Gly Arg Trp Val His Ile His Phe Glu Val
 195 200 205

Phe Pro Asp Arg Asp Ser Ile Thr Asp Ser Thr Asn Asn Ile
 210 215 220

<210> 453

<211> 1026

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1003)

<223> RXA02449

<400> 453

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tactcagtaa ctaaccggc gatttttcaa ggagaaaatc atg aca acc acc acc 115
 Met Thr Thr Thr Thr
 1 5

gca gac cac aac atc agc gcg cag caa aag gct gtt gaa gaa aat ctg	163
Ala Asp His Asn Ile Ser Ala Gln Gln Lys Ala Val Glu Glu Asn Leu	
10 15 20	
gtg aac cgt gtc ctc caa tct ttt gat gcg tgt gaa aac ccg cgc ctc	211
Val Asn Arg Val Leu Gln Ser Phe Asp Ala Cys Glu Asn Pro Arg Leu	
25 30 35	
aag cag ctg atg gaa tcg ctg gtt gtg cat ctg cac gat ttc atc cgg	259
Lys Gln Leu Met Glu Ser Leu Val Val His Leu His Asp Phe Ile Arg	
40 45 50	
gat gtg cgc ctc acc gag gat gag tgg aat tac gcc att gat ttc ctc	307
Asp Val Arg Leu Thr Glu Asp Glu Trp Asn Tyr Ala Ile Asp Phe Leu	
55 60 65	
aca gcg gtt ggc cac att act gat gac aag cgc caa gag ttt gtg ttg	355
Thr Ala Val Gly His Ile Thr Asp Asp Lys Arg Gln Glu Phe Val Leu	
70 75 80 85	
ctt tcc gat acc ttg ggc gcc tcg atg cag acc atc gcg gtg aac aac	403
Leu Ser Asp Thr Leu Gly Ala Ser Met Gln Thr Ile Ala Val Asn Asn	
90 95 100	
gaa gcg tat gaa aac tca acg gaa gct aca gtc ttt ggt cca ttc ttc	451
Glu Ala Tyr Glu Asn Ser Thr Glu Ala Thr Val Phe Gly Pro Phe Phe	
105 110 115	
ctc gat gac gct cct gag gtt gag ctg ggt gga gat atc gcc ggc ggc	499
Leu Asp Asp Ala Pro Glu Val Glu Leu Gly Gly Asp Ile Ala Gly Gly	
120 125 130	
gcc cag ggg cag gca gcg tgg att gaa gga acc gtc acc gac act gaa	547
Ala Gln Gly Gln Ala Ala Trp Ile Glu Gly Thr Val Thr Asp Thr Glu	
135 140 145	
ggc aat ccc gtt ccg aat gct cgt atc gag gtg tgg gag tgc gat gaa	595
Gly Asn Pro Val Pro Asn Ala Arg Ile Glu Val Trp Glu Cys Asp Glu	
150 155 160 165	
gat gga ctc tac gat gtc caa tat gcc gat gag cgc atg gcg ggt cgc	643
Asp Gly Leu Tyr Asp Val Gln Tyr Ala Asp Glu Arg Met Ala Gly Arg	
170 175 180	
gcg tat atg cac acc gac gcc aat ggc gat tac cgc ttc tgg ggt ctg	691
Ala Tyr Met His Thr Asp Ala Asn Gly Asp Tyr Arg Phe Trp Gly Leu	
185 190 195	
act ccg gtt cct tat cca atc ccc cac gat ggc ccc gtg ggc aac atg	739
Thr Pro Val Pro Tyr Pro Ile Pro His Asp Gly Pro Val Gly Asn Met	
200 205 210	
ctc aag gcg gtt ggt cgt tcg ccg gtg cgc tgc gcc cac ctt cac ttc	787
Leu Lys Ala Val Gly Arg Ser Pro Val Arg Cys Ala His Leu His Phe	
215 220 225	
atg gtg acc gct cct gaa ttg cgc acc ttg gtc act cac att ttc gtt	835
Met Val Thr Ala Pro Glu Leu Arg Thr Leu Val Thr His Ile Phe Val	
230 235 240 245	
gag ggt gat ccg cag cta gaa atc ggc gat tcc gtc ttc ggg gtc aag	883

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<210> 454
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<213> Corynebacterium glutamicum
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			20					25					30		
Glu	Asn	Pro	Arg	Leu	Lys	Gln	Leu	Met	Glu	Ser	Leu	Val	Val	His	Leu
		35					40					45			
His	Asp	Phe	Ile	Arg	Asp	Val	Arg	Leu	Thr	Glu	Asp	Glu	Trp	Asn	Tyr
	50					55					60				
Ala	Ile	Asp	Phe	Leu	Thr	Ala	Val	Gly	His	Ile	Thr	Asp	Asp	Lys	Arg
65					70					75					80
Gln	Glu	Phe	Val	Leu	Leu	Ser	Asp	Thr	Leu	Gly	Ala	Ser	Met	Gln	Thr
				85					90					95	
Ile	Ala	Val	Asn	Asn	Glu	Ala	Tyr	Glu	Asn	Ser	Thr	Glu	Ala	Thr	Val
			100					105					110		
Phe	Gly	Pro	Phe	Phe	Leu	Asp	Asp	Ala	Pro	Glu	Val	Glu	Leu	Gly	Gly
		115					120					125			
Asp	Ile	Ala	Gly	Gly	Ala	Gln	Gly	Gln	Ala	Ala	Trp	Ile	Glu	Gly	Thr
	130					135					140				
Val	Thr	Asp	Thr	Glu	Gly	Asn	Pro	Val	Pro	Asn	Ala	Arg	Ile	Glu	Val
145				150						155					160
Trp	Glu	Cys	Asp	Glu	Asp	Gly	Leu	Tyr	Asp	Val	Gln	Tyr	Ala	Asp	Glu
				165					170					175	
Arg	Met	Ala	Gly	Arg	Ala	Tyr	Met	His	Thr	Asp	Ala	Asn	Gly	Asp	Tyr
			180					185					190		
Arg	Phe	Trp	Gly	Leu	Thr	Pro	Val	Pro	Tyr	Pro	Ile	Pro	His	Asp	Gly
		195					200					205			

Pro Val Gly Asn Met Leu Lys Ala Val Gly Arg Ser Pro Val Arg Cys
 210 215 220

Ala His Leu His Phe Met Val Thr Ala Pro Glu Leu Arg Thr Leu Val
 225 230 235 240

Thr His Ile Phe Val Glu Gly Asp Pro Gln Leu Glu Ile Gly Asp Ser
 245 250 255

Val Phe Gly Val Lys Asp Ser Leu Ile Lys Lys Phe Glu Glu Gln Ala
 260 265 270

Pro Gly Thr Pro Thr Pro Asp Gly Arg Asp Leu Gly Asp Gln Thr Trp
 275 280 285

Ala Arg Thr Arg Phe Asp Ile Val Leu Ala Pro Gly Ala
 290 295 300

<210> 455

<211> 1008

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(985)

<223> RXN00178

<400> 455

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aacggcgacg atccagcaac tttgaattaa ggagaccaac atg act att tca gca 115
 Met Thr Ile Ser Ala
 1 5

caa cag caa gca gtg gaa gaa gac ctt gta gag cgc gta ctc gca tct 163
 Gln Gln Gln Ala Val Glu Glu Asp Leu Val Glu Arg Val Leu Ala Ser
 10 15 20

ttt gat tcg tgt gaa aac cct cgc ctc aaa cta gtg atg aaa tcc ctg 211
 Phe Asp Ser Cys Glu Asn Pro Arg Leu Lys Leu Val Met Lys Ser Leu
 25 30 35

act gtg cat ctc cat gat ttc atc cgc gat gtt cga ctc act gaa gaa 259
 Thr Val His Leu His Asp Phe Ile Arg Asp Val Arg Leu Thr Glu Glu
 40 45 50

gag tgg aac tac gcc att gat ttc ctc acc aag gtt ggg cat atc acc 307
 Glu Trp Asn Tyr Ala Ile Asp Phe Leu Thr Lys Val Gly His Ile Thr
 55 60 65

gac gat aag cgc caa gaa ttc gtg ttg ctc tct gac acc ttg ggt gca 355
 Asp Asp Lys Arg Gln Glu Phe Val Leu Leu Ser Asp Thr Leu Gly Ala
 70 75 80 85

tcc atg cag acc atc gct gtt aat aac gaa gca tat gaa gac gct acc 403
 Ser Met Gln Thr Ile Ala Val Asn Asn Glu Ala Tyr Glu Asp Ala Thr
 90 95 100

gaa gca aca gtc ttt ggc ccc ttc ttt gtc gat gat gcg cca ctg gtc 451

Glu	Ala	Thr	Val	Phe	Gly	Pro	Phe	Phe	Val	Asp	Asp	Ala	Pro	Leu	Val		
			105					110					115				
caa	aac	gga	gat	gac	att	gcc	ttt	ggc	gca	gtc	ggc	cag	ccg	gca	tgg	499	
Gln	Asn	Gly	Asp	Asp	Ile	Ala	Phe	Gly	Ala	Val	Gly	Gln	Pro	Ala	Trp		
		120					125					130					
gtg	gag	gga	acg	gtc	aaa	gac	act	gaa	gga	aac	ccc	att	ccc	aat	gca	547	
Val	Glu	Gly	Thr	Val	Lys	Asp	Thr	Glu	Gly	Asn	Pro	Ile	Pro	Asn	Ala		
	135					140					145						
cgc	att	gaa	gta	tgg	gaa	tgc	gat	gaa	gat	gga	ctt	tat	gat	gtg	caa	595	
Arg	Ile	Glu	Val	Trp	Glu	Cys	Asp	Glu	Asp	Gly	Leu	Tyr	Asp	Val	Gln		
150					155					160					165		
tac	gcc	gat	gag	cgc	agt	gct	gga	cgc	gca	cac	ctg	tat	tca	gat	gaa	643	
Tyr	Ala	Asp	Glu	Arg	Ser	Ala	Gly	Arg	Ala	His	Leu	Tyr	Ser	Asp	Glu		
				170					175						180		
aac	ggc	gaa	tac	cac	ttc	tgg	gga	cta	act	ccc	gtg	cca	tat	ccc	atc	691	
Asn	Gly	Glu	Tyr	His	Phe	Trp	Gly	Leu	Thr	Pro	Val	Pro	Tyr	Pro	Ile		
			185					190					195				
cca	cac	gat	ggt	cca	gta	gga	caa	atg	ctc	caa	gca	gtt	ggt	cgt	tcc	739	
Pro	His	Asp	Gly	Pro	Val	Gly	Gln	Met	Leu	Gln	Ala	Val	Gly	Arg	Ser		
		200					205					210					
ccc	gtt	cgt	tgc	gcg	cac	cta	cac	ttc	atg	gtg	act	gcg	cca	gag	aag	787	
Pro	Val	Arg	Cys	Ala	His	Leu	His	Phe	Met	Val	Thr	Ala	Pro	Glu	Lys		
	215					220					225						
cga	acc	ttg	gta	acc	cat	atc	ttc	gtt	gag	ggc	gat	ccg	cag	cta	gag	835	
Arg	Thr	Leu	Val	Thr	His	Ile	Phe	Val	Glu	Gly	Asp	Pro	Gln	Leu	Glu		
230					235					240					245		
atc	ggc	gat	tcc	gtg	ttt	ggc	gtg	aag	gac	tca	ctg	att	aag	aaa	ttc	883	
Ile	Gly	Asp	Ser	Val	Phe	Gly	Val	Lys	Asp	Ser	Leu	Ile	Lys	Lys	Phe		
				250					255					260			
gtt	gag	caa	cct	gca	gga	acc	gca	act	cca	gat	ggt	cgc	gat	gtg	ggt	931	
Val	Glu	Gln	Pro	Ala	Gly	Thr	Ala	Thr	Pro	Asp	Gly	Arg	Asp	Val	Gly		
			265					270					275				
gat	caa	acc	tgg	gca	cgc	aca	cgt	ttt	gat	att	gtg	ctc	gcc	ccc	ggc	979	
Asp	Gln	Thr	Trp	Ala	Arg	Thr	Arg	Phe	Asp	Ile	Val	Leu	Ala	Pro	Gly		
		280					285					290					
aat	gtc	taagtagaag	cagcaaaaaa	cca												1008	
Asn	Val																
		295															

<210> 456

<211> 295

<212> PRT

<213> ~~Corynebacterium-glutamicum~~

<400> 456

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Arg Val Leu Ala Ser Phe Asp Ser Cys Glu Asn Pro Arg Leu Lys Leu
 20 25 30
 Val Met Lys Ser Leu Thr Val His Leu His Asp Phe Ile Arg Asp Val
 35 40 45
 Arg Leu Thr Glu Glu Glu Trp Asn Tyr Ala Ile Asp Phe Leu Thr Lys
 50 55 60
 Val Gly His Ile Thr Asp Asp Lys Arg Gln Glu Phe Val Leu Leu Ser
 65 70 75 80
 Asp Thr Leu Gly Ala Ser Met Gln Thr Ile Ala Val Asn Asn Glu Ala
 85 90 95
 Tyr Glu Asp Ala Thr Glu Ala Thr Val Phe Gly Pro Phe Phe Val Asp
 100 105 110
 Asp Ala Pro Leu Val Gln Asn Gly Asp Asp Ile Ala Phe Gly Ala Val
 115 120 125
 Gly Gln Pro Ala Trp Val Glu Gly Thr Val Lys Asp Thr Glu Gly Asn
 130 135 140
 Pro Ile Pro Asn Ala Arg Ile Glu Val Trp Glu Cys Asp Glu Asp Gly
 145 150 155 160
 Leu Tyr Asp Val Gln Tyr Ala Asp Glu Arg Ser Ala Gly Arg Ala His
 165 170 175
 Leu Tyr Ser Asp Glu Asn Gly Glu Tyr His Phe Trp Gly Leu Thr Pro
 180 185 190
 Val Pro Tyr Pro Ile Pro His Asp Gly Pro Val Gly Gln Met Leu Gln
 195 200 205
 Ala Val Gly Arg Ser Pro Val Arg Cys Ala His Leu His Phe Met Val
 210 215 220
 Thr Ala Pro Glu Lys Arg Thr Leu Val Thr His Ile Phe Val Glu Gly
 225 230 235 240
 Asp Pro Gln Leu Glu Ile Gly Asp Ser Val Phe Gly Val Lys Asp Ser
 245 250 255
 Leu Ile Lys Lys Phe Val Glu Gln Pro Ala Gly Thr Ala Thr Pro Asp
 260 265 270
 Gly Arg Asp Val Gly Asp Gln Thr Trp Ala Arg Thr Arg Phe Asp Ile
 275 280 285
 Val Leu Ala Pro Gly Asn Val
 290 295

<210> 457

<211> 1008

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(985)

<223> FRXA00178

<400> 457

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aacggcgacg atccagcaac tttgaattaa ggagaccaac atg act att tca gca 115
Met Thr Ile Ser Ala
1 5

caa cag caa gca gtg gaa gaa gac ctt gta gag cgc gta ctc gca tct 163
Gln Gln Gln Ala Val Glu Glu Asp Leu Val Glu Arg Val Leu Ala Ser
10 15 20

ttt gat tcg tgt gaa aac cct cgc ctc aaa cta gtg atg aaa tcc ctg 211
Phe Asp Ser Cys Glu Asn Pro Arg Leu Lys Leu Val Met Lys Ser Leu
25 30 35

act gtg cat ctc cat gat ttc atc cgc gat gtt cga ctc act gaa gaa 259
Thr Val His Leu His Asp Phe Ile Arg Asp Val Arg Leu Thr Glu Glu
40 45 50

gag tgg aac tac gcc att gat ttc ctc acc aag gtt ggg cat atc acc 307
Glu Trp Asn Tyr Ala Ile Asp Phe Leu Thr Lys Val Gly His Ile Thr
55 60 65

gac gat aag cgc caa gaa ttc gtg ttg ctc tct gac acc ttg ggt gca 355
Asp Asp Lys Arg Gln Glu Phe Val Leu Leu Ser Asp Thr Leu Gly Ala
70 75 80 85

tcc atg cag acc atc gct gtt aat aac gaa gca tat gaa gac gct acc 403
Ser Met Gln Thr Ile Ala Val Asn Asn Glu Ala Tyr Glu Asp Ala Thr
90 95 100

gaa gca aca gtc ttt ggc ccc ttc ttt gtc gat gat gcg cca ctg gtc 451
Glu Ala Thr Val Phe Gly Pro Phe Phe Val Asp Asp Ala Pro Leu Val
105 110 115

caa aac gga gat gac att gcc ttt ggc gca gtc ggc cag ccg gca tgg 499
Gln Asn Gly Asp Asp Ile Ala Phe Gly Ala Val Gly Gln Pro Ala Trp
120 125 130

gtg gag gga acg gtc aaa gac act gaa gga aac ccc att ccc aat gca 547
Val Glu Gly Thr Val Lys Asp Thr Glu Gly Asn Pro Ile Pro Asn Ala
135 140 145

cgc att gaa gta tgg gaa tgc gat gaa gat gga ctt tat gat gtg caa 595
Arg Ile Glu Val Trp Glu Cys Asp Glu Asp Gly Leu Tyr Asp Val Gln
150 155 160 165

tac gcc gat gag cgc agt gct gga cgc gca cac ctg tat tca gat gaa 643
Tyr Ala Asp Glu Arg Ser Ala Gly Arg Ala His Leu Tyr Ser Asp Glu
170 175 180

aac ggc gaa tac cac ttc tgg gga cta act ccc gtg cca tat ccc atc 691
Asn Gly Glu Tyr His Phe Trp Gly Leu Thr Pro Val Pro Tyr Pro Ile
185 190 195

cca cac gat ggt cca gta gga caa atg ctc caa gca gtt ggt cgt tcc 739
Pro His Asp Gly Pro Val Gly Gln Met Leu Gln Ala Val Gly Arg Ser

200	205	210	
ccc gtt cgt tgc gcg cac cta cac ttc atg gtg act gcg cca gag aag			787
Pro Val Arg Cys Ala His Leu His Phe Met Val Thr Ala Pro Glu Lys			
215	220	225	
cga acc ttg gta acc cat atc ttc gtt gag ggc gat ccg cag cta gag			835
Arg Thr Leu Val Thr His Ile Phe Val Glu Gly Asp Pro Gln Leu Glu			
230	235	240	245
atc ggc gat tcc gtg ttt ggc gtg aag gac tca ctg att aag aaa ttc			883
Ile Gly Asp Ser Val Phe Gly Val Lys Asp Ser Leu Ile Lys Lys Phe			
250	255	260	
gtt gag caa cct gca gga acc gca act cca gat ggt cgc gat gtg ggt			931
Val Glu Gln Pro Ala Gly Thr Ala Thr Pro Asp Gly Arg Asp Val Gly			
265	270	275	
gat caa acc tgg gca cgc aca cgt ttt gat att gtg ctc gcc ccc ggc			979
Asp Gln Thr Trp Ala Arg Thr Arg Phe Asp Ile Val Leu Ala Pro Gly			
280	285	290	
aat gtc taagtagaag cagcaaaaaa cca			1008
Asn Val			
295			

<210> 458

<211> 295

<212> PRT

<213> Corynebacterium glutamicum

<400> 458

Met Thr Ile Ser Ala Gln Gln Gln Ala Val Glu Glu Asp Leu Val Glu
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Arg Val Leu Ala Ser Phe Asp Ser Cys Glu Asn Pro Arg Leu Lys Leu
20 25 30

Val Met Lys Ser Leu Thr Val His Leu His Asp Phe Ile Arg Asp Val
35 40 45

Arg Leu Thr Glu Glu Glu Trp Asn Tyr Ala Ile Asp Phe Leu Thr Lys
50 55 60

Val Gly His Ile Thr Asp Asp Lys Arg Gln Glu Phe Val Leu Leu Ser
65 70 75 80

Asp Thr Leu Gly Ala Ser Met Gln Thr Ile Ala Val Asn Asn Glu Ala
85 90 95

Tyr Glu Asp Ala Thr Glu Ala Thr Val Phe Gly Pro Phe Phe Val Asp
100 105 110

Asp Ala Pro Leu Val Gln Asn Gly Asp Asp Ile Ala Phe Gly Ala Val
115 120 125

Gly Gln Pro Ala Trp Val Glu Gly Thr Val Lys Asp Thr Glu Gly Asn
130 135 140

Pro Ile Pro Asn Ala Arg Ile Glu Val Trp Glu Cys Asp Glu Asp Gly

145		150		155		160
Leu Tyr Asp Val Gln Tyr Ala Asp Glu Arg Ser Ala Gly Arg Ala His						
	165			170		175
Leu Tyr Ser Asp Glu Asn Gly Glu Tyr His Phe Trp Gly Leu Thr Pro						
	180			185		190
Val Pro Tyr Pro Ile Pro His Asp Gly Pro Val Gly Gln Met Leu Gln						
	195			200		205
Ala Val Gly Arg Ser Pro Val Arg Cys Ala His Leu His Phe Met Val						
	210			215		220
Thr Ala Pro Glu Lys Arg Thr Leu Val Thr His Ile Phe Val Glu Gly						
	225			230		235
Asp Pro Gln Leu Glu Ile Gly Asp Ser Val Phe Gly Val Lys Asp Ser						
	245			250		255
Leu Ile Lys Lys Phe Val Glu Gln Pro Ala Gly Thr Ala Thr Pro Asp						
	260			265		270
Gly Arg Asp Val Gly Asp Gln Thr Trp Ala Arg Thr Arg Phe Asp Ile						
	275			280		285
Val Leu Ala Pro Gly Asn Val						
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<211> 1407

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1384)

<223> RXA02111

<400> 459

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	Met Thr Thr Ser Ile	
	1 5	

acc cca tct gtc aac ctt gca ttg aaa aat gcc aat agc tgc aac agt	163
Thr Pro Ser Val Asn Leu Ala Leu Lys Asn Ala Asn Ser Cys Asn Ser	
	10 15 20

gaa ctc aaa gac gga ccc tgg ttc ctc gac cag ccc gga atg ccg gat	211
Glu Leu Lys Asp Gly Pro Trp Phe Leu Asp Gln Pro Gly Met Pro Asp	
	25 30 35

gtc-tac-ggc-ccc-ggc-gcg-tca-caa-aac-gat-ccg-ata-cct-gcg-cat-gct	259
Val Tyr Gly Pro Gly Ala Ser Gln Asn Asp Pro Ile Pro Ala His Ala	
	40 45 50

ccg cgc cag cag gtt ctc ccc gag gag tac cag cgc gca agt gat gac	307
Pro Arg Gln Gln Val Leu Pro Glu Glu Tyr Gln Arg Ala Ser Asp Asp	

55	60	65	
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Glu Leu His Arg Arg Ile Arg Glu Ala Lys Asp Thr Leu Gly Asp Lys			
70	75	80	85
gtg gtt atc cta gga cac ttc tac cag cgc gat gaa gtt atc caa cac			403
Val Val Ile Leu Gly His Phe Tyr Gln Arg Asp Glu Val Ile Gln His			
	90	95	100
gca gat ttt gtt ggt gac tct ttc caa ctt gcc cgc gct gcc aaa acc			451
Ala Asp Phe Val Gly Asp Ser Phe Gln Leu Ala Arg Ala Ala Lys Thr			
	105	110	115
cga ccc gag gcg gaa gcg att gtg ttc tgc ggt gtg cac ttc atg gct			499
Arg Pro Glu Ala Glu Ala Ile Val Phe Cys Gly Val His Phe Met Ala			
	120	125	130
gaa acc gct gat ctg tta tcc acg gat gaa caa tca gtg atc ctc ccc			547
Glu Thr Ala Asp Leu Leu Ser Thr Asp Glu Gln Ser Val Ile Leu Pro			
	135	140	145
aac ctt gcc gca ggt tgc tcc atg gca gac atg gct gac ctt gat tcc			595
Asn Leu Ala Ala Gly Cys Ser Met Ala Asp Met Ala Asp Leu Asp Ser			
	150	155	160
gtc gaa gac tgc tgg gag caa ctc acc tca att tat ggc gat gac acc			643
Val Glu Asp Cys Trp Glu Gln Leu Thr Ser Ile Tyr Gly Asp Asp Thr			
	170	175	180
ctg atc cct gtg acc tac atg aat tcc tct gca gcg ctc aaa ggt ttc			691
Leu Ile Pro Val Thr Tyr Met Asn Ser Ser Ala Ala Leu Lys Gly Phe			
	185	190	195
gtg ggt gag cac ggc gga att gta tgc acc tcc tca aat gca cgt tcc			739
Val Gly Glu His Gly Gly Ile Val Cys Thr Ser Ser Asn Ala Arg Ser			
	200	205	210
gta ttg gag tgg gcg ttt gaa cgc ggc caa cga gtc ctg ttc ttc ccc			787
Val Leu Glu Trp Ala Phe Glu Arg Gly Gln Arg Val Leu Phe Phe Pro			
	215	220	225
gat cag cac ttg ggt cga aac acc gcg aaa gcc atg ggc att ggg atc			835
Asp Gln His Leu Gly Arg Asn Thr Ala Lys Ala Met Gly Ile Gly Ile			
	230	235	240
gat caa atg ccc ctg tgg aat ccc aac aaa cca ctg ggt ggc aac acc			883
Asp Gln Met Pro Leu Trp Asn Pro Asn Lys Pro Leu Gly Gly Asn Thr			
	250	255	260
gtt tcc gag cta gaa aac gca aag gta ctg ctc tgg cat ggt ttc tgc			931
Val Ser Glu Leu Glu Asn Ala Lys Val Leu Leu Trp His Gly Phe Cys			
	265	270	275
tct gta cac aag cgc ttt act gtc gag cag atc aac aaa gcc cgc gcc			979
Ser Val His Lys Arg Phe Thr Val Glu Gln Ile Asn Lys Ala Arg Ala			
	280	285	290
gag tac ccc gac gtt cac gtc atc gtg cac cct gaa tcc ccc atg cca			1027
Glu Tyr Pro Asp Val His Val Ile Val His Pro Glu Ser Pro Met Pro			
	295	300	305

gtt gtt gac gcc gcc gac tca tcc gga tcc act gac ttc att gtg aaa 1075
 Val Val Asp Ala Ala Asp Ser Ser Gly Ser Thr Asp Phe Ile Val Lys
 310 315 320 325

gcc att caa gca gca ccg gca gga tct acc ttt gcg atc ggc acc gaa 1123
 Ala Ile Gln Ala Ala Pro Ala Gly Ser Thr Phe Ala Ile Gly Thr Glu
 330 335 340

atc aac ttg gtt cag cgc ctg gca gcc cag tac ccg cag cac acc atc 1171
 Ile Asn Leu Val Gln Arg Leu Ala Ala Gln Tyr Pro Gln His Thr Ile
 345 350 355

ttc tgc ctc gac cct gtc atc tgc cca tgc tcc acc atg tat cgc att 1219
 Phe Cys Leu Asp Pro Val Ile Cys Pro Cys Ser Thr Met Tyr Arg Ile
 360 365 370

cac cct ggt tac ctg gcc tgg gca ctt gag gag ttg gtg gct gga aac 1267
 His Pro Gly Tyr Leu Ala Trp Ala Leu Glu Glu Leu Val Ala Gly Asn
 375 380 385

gtg att aac cag att tct gtc tct gaa tcc gtg gcg gca ccg gcg cga 1315
 Val Ile Asn Gln Ile Ser Val Ser Glu Ser Val Ala Ala Pro Ala Arg
 390 395 400 405

gtc gct ttg gaa agg atg cta tct gtt gtt cca gca gct cct gtt act 1363
 Val Ala Leu Glu Arg Met Leu Ser Val Val Pro Ala Ala Pro Val Thr
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cct agc tcc tcg aag gat gcg taatttatga ctacccatat tga 1407
 Pro Ser Ser Ser Lys Asp Ala
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<210> 460

<211> 428

<212> PRT

<213> Corynebacterium glutamicum

<400> 460

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Pro Gly Met Pro Asp Val Tyr Gly Pro Gly Ala Ser Gln Asn Asp Pro
 35 40 45

Ile Pro Ala His Ala Pro Arg Gln Gln Val Leu Pro Glu Glu Tyr Gln
 50 55 60

Arg Ala Ser Asp Asp Glu Leu His Arg Arg Ile Arg Glu Ala Lys Asp
 65 70 75 80

Thr Leu Gly Asp Lys Val Val Ile Leu Gly His Phe Tyr Gln Arg Asp
 85 90 95

Glu Val Ile Gln His Ala Asp Phe Val Gly Asp Ser Phe Gln Leu Ala
 100 105 110

Arg	Ala	Lys	Thr	Arg	Pro	Glu	Ala	Glu	Ala	Ile	Val	Phe	Cys	Gly	
	115					120					125				
Val	His	Phe	Met	Ala	Glu	Thr	Ala	Asp	Leu	Leu	Ser	Thr	Asp	Glu	Gln
	130					135					140				
Ser	Val	Ile	Leu	Pro	Asn	Leu	Ala	Ala	Gly	Cys	Ser	Met	Ala	Asp	Met
145					150					155					160
Ala	Asp	Leu	Asp	Ser	Val	Glu	Asp	Cys	Trp	Glu	Gln	Leu	Thr	Ser	Ile
				165					170					175	
Tyr	Gly	Asp	Asp	Thr	Leu	Ile	Pro	Val	Thr	Tyr	Met	Asn	Ser	Ser	Ala
			180					185					190		
Ala	Leu	Lys	Gly	Phe	Val	Gly	Glu	His	Gly	Gly	Ile	Val	Cys	Thr	Ser
		195					200					205			
Ser	Asn	Ala	Arg	Ser	Val	Leu	Glu	Trp	Ala	Phe	Glu	Arg	Gly	Gln	Arg
	210					215					220				
Val	Leu	Phe	Phe	Pro	Asp	Gln	His	Leu	Gly	Arg	Asn	Thr	Ala	Lys	Ala
225					230					235					240
Met	Gly	Ile	Gly	Ile	Asp	Gln	Met	Pro	Leu	Trp	Asn	Pro	Asn	Lys	Pro
				245					250					255	
Leu	Gly	Gly	Asn	Thr	Val	Ser	Glu	Leu	Glu	Asn	Ala	Lys	Val	Leu	Leu
			260					265					270		
Trp	His	Gly	Phe	Cys	Ser	Val	His	Lys	Arg	Phe	Thr	Val	Glu	Gln	Ile
		275					280					285			
Asn	Lys	Ala	Arg	Ala	Glu	Tyr	Pro	Asp	Val	His	Val	Ile	Val	His	Pro
	290					295					300				
Glu	Ser	Pro	Met	Pro	Val	Val	Asp	Ala	Ala	Asp	Ser	Ser	Gly	Ser	Thr
305					310					315					320
Asp	Phe	Ile	Val	Lys	Ala	Ile	Gln	Ala	Ala	Pro	Ala	Gly	Ser	Thr	Phe
				325					330					335	
Ala	Ile	Gly	Thr	Glu	Ile	Asn	Leu	Val	Gln	Arg	Leu	Ala	Ala	Gln	Tyr
			340					345					350		
Pro	Gln	His	Thr	Ile	Phe	Cys	Leu	Asp	Pro	Val	Ile	Cys	Pro	Cys	Ser
		355					360					365			
Thr	Met	Tyr	Arg	Ile	His	Pro	Gly	Tyr	Leu	Ala	Trp	Ala	Leu	Glu	Glu
	370					375					380				
Leu	Val	Ala	Gly	Asn	Val	Ile	Asn	Gln	Ile	Ser	Val	Ser	Glu	Ser	Val
385					390					395					400
Ala	Ala	Pro	Ala	Arg	Val	Ala	Leu	Glu	Arg	Met	Leu	Ser	Val	Val	Pro
				405					410					415	
Ala	Ala	Pro	Val	Thr	Pro	Ser	Ser	Ser	Lys	Asp	Ala				
			420					425							

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Ile Asn Arg Val Pro Tyr Ala Ala Ala Lys Gly Gly Val Asn Gly Ile
      170                      175                      180

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gtt tct gcc atg gcc cgc gaa gct gca ccg cat aat gtg cgc gtg gtg 691
 Val Ser Ala Met Ala Arg Glu Ala Ala Pro His Asn Val Arg Val Val
 185 190 195

gca acg gct ccc ggt ggc acg ctc gct ccg gaa cgt gcc gtc aaa cga 739
 Ala Thr Ala Pro Gly Gly Thr Leu Ala Pro Glu Arg Ala Val Lys Arg
 200 205 210

ggc cct ggg cca gag ggc gaa ttg gaa gaa aag tgg tat cag caa atc 787
 Gly Pro Gly Pro Glu Gly Glu Leu Glu Glu Lys Trp Tyr Gln Gln Ile
 215 220 225

gtt gat caa acc att gat tcc agt ttg atg aag cgc tac ggc acc cta 835
 Val Asp Gln Thr Ile Asp Ser Ser Leu Met Lys Arg Tyr Gly Thr Leu
 230 235 240 245

gag gag cag gtc gcg ccg atc tgt ttc ctc gct tct gag gaa gct tcc 883
 Glu Glu Gln Val Ala Pro Ile Cys Phe Leu Ala Ser Glu Glu Ala Ser
 250 255 260

tac atc act gga tca gtc atg cca gtc ggt gga ggc gac cag gga 928
 Tyr Ile Thr Gly Ser Val Met Pro Val Gly Gly Gly Asp Gln Gly
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taacccttgg tcaatcttag gga 951

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<211> 276

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<213> Corynebacterium glutamicum

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Thr Pro Glu Arg Phe Phe Gly Gln Gly Val Val Val Thr Gly Ala Ala
 20 25 30

Gln Gly Ile Gly Met Ala Val Ala His Arg Ile Ala Tyr Glu Asp Gly
 35 40 45

Asn Leu Val Leu Val Asp Arg Ser Pro Leu Val His Glu Val Ala Glu
 50 55 60

Glu Leu Arg Lys Ala Gly Ala Gly Thr Val Asp Ser Phe Ile Ala Asp
 65 70 75 80

Leu Glu Thr Phe Glu Gly Ala Thr Asp Ala Leu Glu Phe Ala Gly Gln
 85 90 95

Lys Leu Lys Asn Leu Asp Val Val Ile Asn Asn Val Gly Gly Thr Ile
 100 105 110

Trp Ala Lys Pro Tyr Gln Glu Tyr Ser Glu Glu Glu Ile Arg Lys Glu
 115 120 125

Ile Asn Arg Ser Leu Phe Pro Thr Leu Trp Met Cys Arg Ala Ala Leu
 130 135 140

Pro Ile Leu Ile Gly Asn Gly Gly Gly Thr Ile Val Asn Val Ser Ser

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Met Ser Leu Gln Phe															
1 5															
gat cat gaa acc ctc ggt caa cga gtt ctg ttc ggt tca ggt gag gcg															163
Asp His Glu Thr Leu Gly Gln Arg Val Leu Phe Gly Ser Gly Glu Ala															
10 15 20															
gcg caa aat ctc gcc gct gaa att agc cga ctc gat gcc aaa aac gtc															211
Ala Gln Asn Leu Ala Ala Glu Ile Ser Arg Leu Asp Ala Lys Asn Val															
25 30 35															
atg gtg gtt gcc ggt gat ttc gag ctt ccc atg gca cgg caa gta gca															259
Met Val Val Ala Gly Asp Phe Glu Leu Pro Met Ala Arg Gln Val Ala															
40 45 50															
gca gat att gat gtc aag gtg tgg cat tca aat gtc gtg atg cat gtg															307
Ala Asp Ile Asp Val Lys Val Trp His Ser Asn Val Val Met His Val															
55 60 65															
ccc atc gaa aca gca gaa gaa gca cgc agt gtt gcg aaa gaa aac gac															355

Pro	Ile	Glu	Thr	Ala	Glu	Glu	Ala	Arg	Ser	Val	Ala	Lys	Glu	Asn	Asp	
70					75					80					85	
att	gat	gtt	gtg	gtg	tgt	gtg	ggc	ggg	gga	tcc	aca	aca	ggg	cta	gct	403
Ile	Asp	Val	Val	Val	Cys	Val	Gly	Gly	Gly	Ser	Thr	Thr	Gly	Leu	Ala	
				90					95					100		
aaa	gcg	att	gcc	atg	acc	acc	gca	ttg	ccg	atc	att	gcg	gta	ccc	act	451
Lys	Ala	Ile	Ala	Met	Thr	Thr	Ala	Leu	Pro	Ile	Ile	Ala	Val	Pro	Thr	
			105					110					115			
act	tat	gca	ggg	tct	gaa	gca	aca	aat	gtg	tgg	gga	ttg	acc	gaa	gcc	499
Thr	Tyr	Ala	Gly	Ser	Glu	Ala	Thr	Asn	Val	Trp	Gly	Leu	Thr	Glu	Ala	
		120					125					130				
gcg	cgc	aaa	aca	act	ggg	gtt	gat	aac	aaa	gtg	ctg	cca	gtg	aca	gtt	547
Ala	Arg	Lys	Thr	Thr	Gly	Val	Asp	Asn	Lys	Val	Leu	Pro	Val	Thr	Val	
	135					140					145					
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Ile	Tyr	Asp	Ser	Ala	Leu	Thr	Met	Ser	Leu	Pro	Val	Glu	Met	Ser	Val	
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Ala	Ser	Gly	Leu	Asn	Gly	Leu	Ala	His	Cys	Ile	Asp	Ser	Leu	Trp	Gly	
				170					175					180		
ccg	aag	gcg	gat	ccc	atc	aat	gcg	gct	atg	gct	gct	gag	gga	att	cga	691
Pro	Lys	Ala	Asp	Pro	Ile	Asn	Ala	Ala	Met	Ala	Ala	Glu	Gly	Ile	Arg	
			185					190					195			
gca	ctt	tct	gct	ggc	ctt	ccc	aag	att	gtg	gca	gat	gct	cag	gac	gta	739
Ala	Leu	Ser	Ala	Gly	Leu	Pro	Lys	Ile	Val	Ala	Asp	Ala	Gln	Asp	Val	
		200					205				210					
gat	ggg	cgc	gat	gaa	gcg	ctc	tac	ggg	gcc	tac	ctg	gct	gcg	gtg	tct	787
Asp	Gly	Arg	Asp	Glu	Ala	Leu	Tyr	Gly	Ala	Tyr	Leu	Ala	Ala	Val	Ser	
	215					220					225					
ttt	gcc	tct	gct	ggc	tct	ggg	ctc	cac	cac	aag	atc	tgc	cac	gtg	ttg	835
Phe	Ala	Ser	Ala	Gly	Ser	Gly	Leu	His	His	Lys	Ile	Cys	His	Val	Leu	
	230				235					240				245		
ggg	gga	act	ttt	aac	ctt	cca	cac	gcg	caa	acc	cat	gca	aca	gta	ctg	883
Gly	Gly	Thr	Phe	Asn	Leu	Pro	His	Ala	Gln	Thr	His	Ala	Thr	Val	Leu	
				250					255					260		
cct	tat	gtt	ctt	gcc	ttc	aac	gcg	cca	tat	gcg	cca	cag	gca	gaa	caa	931
Pro	Tyr	Val	Leu	Ala	Phe	Asn	Ala	Pro	Tyr	Ala	Pro	Gln	Ala	Glu	Gln	
			265					270				275				
cgc	gca	gcg	gca	gct	ttc	ggg	tct	gcg	aca	gca	ctt	gaa	gga	ttg	caa	979
Arg	Ala	Ala	Ala	Phe	Gly	Ser	Ala	Thr	Ala	Leu	Glu	Gly	Leu	Gln		
		280				285					290					
cag	ctg	cgt	gcc	caa	gtg	gga	gca	cca	cag	cga	cta	tcc	gat	tac	gga	1027
Gln	Leu	Arg	Ala	Gln	Val	Gly	Ala	Pro	Gln	Arg	Leu	Ser	Asp	Tyr	Gly	
	295					300					305					
ttc	acc	gca	gca	gga	atc	cca	gag	gca	gtg	gaa	atc	atc	ttg	gag	aaa	1075
Phe	Thr	Ala	Ala	Gly	Ile	Pro	Glu	Ala	Val	Glu	Ile	Ile	Leu	Glu	Lys	

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Gly	Ser	Gly	Glu 20	Ala	Ala	Gln	Asn	Leu 25	Ala	Ala	Glu	Ile	Ser 30	Arg	Leu
Asp	Ala	Lys 35	Asn	Val	Met	Val	Val 40	Ala	Gly	Asp	Phe	Glu 45	Leu	Pro	Met
Ala	Arg 50	Gln	Val	Ala	Ala	Asp 55	Ile	Asp	Val	Lys	Val 60	Trp	His	Ser	Asn
Val 65	Val	Met	His	Val	Pro 70	Ile	Glu	Thr	Ala	Glu 75	Glu	Ala	Arg	Ser	Val 80
Ala	Lys	Glu	Asn	Asp 85	Ile	Asp	Val	Val 90	Val	Cys	Val	Gly	Gly	Gly 95	Ser
Thr	Thr	Gly	Leu 100	Ala	Lys	Ala	Ile	Ala 105	Met	Thr	Thr	Ala	Leu 110	Pro	Ile
Ile	Ala	Val 115	Pro	Thr	Thr	Tyr	Ala 120	Gly	Ser	Glu	Ala 125	Thr	Asn	Val	Trp
Gly	Leu 130	Thr	Glu	Ala	Ala	Arg 135	Lys	Thr	Thr	Gly	Val 140	Asp	Asn	Lys	Val
Leu 145	Pro	Val	Thr	Val	Ile 150	Tyr	Asp	Ser	Ala	Leu 155	Thr	Met	Ser	Leu	Pro 160
Val	Glu	Met	Ser	Val 165	Ala	Ser	Gly	Leu 170	Asn	Gly	Leu	Ala	His 175	Cys	Ile
Asp	Ser	Leu	Trp 180	Gly	Pro	Lys	Ala	Asp 185	Pro	Ile	Asn	Ala	Ala 190	Met	Ala
Ala	Glu	Gly	Ile	Arg	Ala	Leu	Ser	Ala	Gly	Leu	Pro	Lys	Ile	Val	Ala
195 200 205															
Asp	Ala 210	Gln	Asp	Val	Asp	Gly 215	Arg	Asp	Glu	Ala	Leu 220	Tyr	Gly	Ala	Tyr

Leu Ala Ala Val Ser Phe Ala Ser Ala Gly Ser Gly Leu His His Lys
 225 230 235 240

Ile Cys His Val Leu Gly Gly Thr Phe Asn Leu Pro His Ala Gln Thr
 245 250 255

His Ala Thr Val Leu Pro Tyr Val Leu Ala Phe Asn Ala Pro Tyr Ala
 260 265 270

Pro Gln Ala Glu Gln Arg Ala Ala Ala Ala Phe Gly Ser Ala Thr Ala
 275 280 285

Leu Glu Gly Leu Gln Gln Leu Arg Ala Gln Val Gly Ala Pro Gln Arg
 290 295 300

Leu Ser Asp Tyr Gly Phe Thr Ala Ala Gly Ile Pro Glu Ala Val Glu
 305 310 315 320

Ile Ile Leu Glu Lys Val Pro Ala Asn Asn Pro Arg Thr Val Thr Glu
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Glu Asn Leu Thr Ala Leu Leu Thr Thr Ala Leu Asn Gly Asp Asp Pro
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Ala Thr Leu Asn
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<223> FRXA00177

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 Gln Arg Ala Ala Ala Phe Gly Ser Ala Thr Ala Leu Glu Gly Leu
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caa cag ctg cgt gcc caa gtg gga gca cca cag cga cta tcc gat tac 144
 Gln Gln Leu Arg Ala Gln Val Gly Ala Pro Gln Arg Leu Ser Asp Tyr
 35 40 45

gga ttc acc gca gca gga atc cca gag gca gtg gaa atc atc ttg gag 192
 Gly Phe Thr Ala Ala Gly Ile Pro Glu Ala Val Glu Ile Ile Leu Glu
 50 55 60

---aaa-gta-ccg-gcg-aat-aat-cca-cgg-acg-gtc-aca-gaa-gaa-aac-ctc-act 240
 Lys Val Pro Ala Asn Asn Pro Arg Thr Val Thr Glu Glu Asn Leu Thr
 65 70 75 80

gcg ctg ctt acc aca gcg ctc aac ggc gac gat cca gca act ttg aat 288
 Ala Leu Leu Thr Thr Ala Leu Asn Gly Asp Asp Pro Ala Thr Leu Asn

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 20 25 30
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 35 40 45
 Gly Phe Thr Ala Ala Gly Ile Pro Glu Ala Val Glu Ile Ile Leu Glu
 50 55 60
 Lys Val Pro Ala Asn Asn Pro Arg Thr Val Thr Glu Glu Asn Leu Thr
 65 70 75 80
 Ala Leu Leu Thr Thr Ala Leu Asn Gly Asp Asp Pro Ala Thr Leu Asn
 85 90 95

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 <223> RXA02448

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 Val Asn Asn Ser Leu
 1 5
 gca ttc aac cac gac acc ctc cca cag aaa gtc atg ttt gga tat ggc 163
 Ala Phe Asn His Asp Thr Leu Pro Gln Lys Val Met Phe Gly Tyr Gly
 10 15 20
 aag tcc agt gca ttc tta aag cag gaa gtt gaa cgc cgc ggc tca gcc 211
 Lys Ser Ser Ala Phe Leu Lys Gln Glu Val Glu Arg Arg Gly Ser Ala
 25 30 35
 aag gtc atg gtc att gcg ggt gaa cga gaa atg tcg atc gcc cat aag 259
 Lys Val Met Val Ile Ala Gly Glu Arg Glu Met Ser Ile Ala His Lys
 40 45 50
 gtg gcc tca gaa att gag gtg gcg atc tgg cac gac gaa gtt gtc atg 307
 Val Ala Ser Glu Ile Glu Val Ala Ile Trp His Asp Glu Val Val Met

55	60	65	
cac gtg ccc atc gaa gta gcc gaa cgt gcg cgt gca gtg gca acc gac			355
His Val Pro Ile Glu Val Ala Glu Arg Ala Arg Ala Val Ala Thr Asp			
70	75	80	85
aat gag att gat ctg ctg gtg tgt gtt ggc ggc gga tcc acc ata ggt			403
Asn Glu Ile Asp Leu Leu Val Cys Val Gly Gly Gly Ser Thr Ile Gly			
	90	95	100
ttg gcc aaa gca att gcc atg acc act gcc ctg ccc atc gtc gcg atc			451
Leu Ala Lys Ala Ile Ala Met Thr Thr Ala Leu Pro Ile Val Ala Ile			
	105	110	115
ccc acc acc tac gca gga tcg gaa gca acc aac gtg tgg ggt ctg acg			499
Pro Thr Thr Tyr Ala Gly Ser Glu Ala Thr Asn Val Trp Gly Leu Thr			
	120	125	130
gaa gca gcg cgc aaa aca acc ggt gtt gat ctg aag gtg ctc ccc gaa			547
Glu Ala Ala Arg Lys Thr Thr Gly Val Asp Leu Lys Val Leu Pro Glu			
	135	140	145
aca gtc att tac gat tcc gaa ctc acc atg tcg ctt cca gtg gag atg			595
Thr Val Ile Tyr Asp Ser Glu Leu Thr Met Ser Leu Pro Val Glu Met			
	150	155	160
tcc gtg gca tcc gga ctc aac ggc ctg gcg cac tgc att gat tct ttg			643
Ser Val Ala Ser Gly Leu Asn Gly Leu Ala His Cys Ile Asp Ser Leu			
	170	175	180
tgg gga ccc aac gcc gat ccc atc aac gca gtg ctt gca gcc gaa gga			691
Trp Gly Pro Asn Ala Asp Pro Ile Asn Ala Val Leu Ala Ala Glu Gly			
	185	190	195
atc cgc gca ctc aac cag gga ctg ccg aaa att gtt gcg aac ccg cac			739
Ile Arg Ala Leu Asn Gln Gly Leu Pro Lys Ile Val Ala Asn Pro His			
	200	205	210
agc atc gaa gga cgc gac gaa gcc ctc tac ggc gcc tac ctc gca gca			787
Ser Ile Glu Gly Arg Asp Glu Ala Leu Tyr Gly Ala Tyr Leu Ala Ala			
	215	220	225
gta tcc ttc gcc tcc gca ggc tcc gga cta cac cac aaa atc tgc cac			835
Val Ser Phe Ala Ser Ala Gly Ser Gly Leu His His Lys Ile Cys His			
	230	235	240
acc ttg gga ggc acc ttc aac ctc ccc cac gcc caa acc cac gca acc			883
Thr Leu Gly Gly Thr Phe Asn Leu Pro His Ala Gln Thr His Ala Thr			
	250	255	260
gtg ctg ccg tat gtt ttg gca ttc aac gca ggc gac gca cca gaa gct			931
Val Leu Pro Tyr Val Leu Ala Phe Asn Ala Gly Asp Ala Pro Glu Ala			
	265	270	275
gaa cgc cgc gca gcc gca gcc ttt gga act gac acc gca cta gaa ggc			979
Glu Arg Arg Ala Ala Ala Ala Phe Gly Thr Asp Thr Ala Leu Glu Gly			
	280	285	290
ctg caa cgc ctc cgc ttg tca gtc aac gca ccg aaa cga ctt tcc gac			1027
Leu Gln Arg Leu Arg Leu Ser Val Asn Ala Pro Lys Arg Leu Ser Asp			
	295	300	305

tac ggc ttc gag gct tca gga att gct gag gca gtg gac gtc acg ttg 1075
 Tyr Gly Phe Glu Ala Ser Gly Ile Ala Glu Ala Val Asp Val Thr Leu
 310 315 320 325
 gag aaa gtt ccc gcc aac aat cct cgc cca gtg acc cgg gaa aac ctc 1123
 Glu Lys Val Pro Ala Asn Asn Pro Arg Pro Val Thr Arg Glu Asn Leu
 330 335 340
 agc aga ttg ctc gaa gca gca ctc aac ggt gag gat ccg gca gtt ctt 1171
 Ser Arg Leu Leu Glu Ala Ala Leu Asn Gly Glu Asp Pro Ala Val Leu
 345 350 355
 agc gca gta ctc agt aac taacccggcg atttttcaag gag 1212
 Ser Ala Val Leu Ser Asn
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<210> 468

<211> 363

<212> PRT

<213> Corynebacterium glutamicum

<400> 468

Val Asn Asn Ser Leu Ala Phe Asn His Asp Thr Leu Pro Gln Lys Val
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 Met Phe Gly Tyr Gly Lys Ser Ser Ala Phe Leu Lys Gln Glu Val Glu
 20 25 30
 Arg Arg Gly Ser Ala Lys Val Met Val Ile Ala Gly Glu Arg Glu Met
 35 40 45
 Ser Ile Ala His Lys Val Ala Ser Glu Ile Glu Val Ala Ile Trp His
 50 55 60
 Asp Glu Val Val Met His Val Pro Ile Glu Val Ala Glu Arg Ala Arg
 65 70 75 80
 Ala Val Ala Thr Asp Asn Glu Ile Asp Leu Leu Val Cys Val Gly Gly
 85 90 95
 Gly Ser Thr Ile Gly Leu Ala Lys Ala Ile Ala Met Thr Thr Ala Leu
 100 105 110
 Pro Ile Val Ala Ile Pro Thr Thr Tyr Ala Gly Ser Glu Ala Thr Asn
 115 120 125
 Val Trp Gly Leu Thr Glu Ala Ala Arg Lys Thr Thr Gly Val Asp Leu
 130 135 140
 Lys Val Leu Pro Glu Thr Val Ile Tyr Asp Ser Glu Leu Thr Met Ser
 145 150 155 160
 Leu Pro Val Glu Met Ser Val Ala Ser Gly Leu Asn Gly Leu Ala His
 165 170 175
 Cys Ile Asp Ser Leu Trp Gly Pro Asn Ala Asp Pro Ile Asn Ala Val
 180 185 190
 Leu Ala Ala Glu Gly Ile Arg Ala Leu Asn Gln Gly Leu Pro Lys Ile

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<210> 469
<211> 1782
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(1759)  
<223> RXA00048
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tggaatgggg gtattgtaaa atctgaaccc ttgttcattt atg aat cat gat tca 115
Met Asn His Asp Ser
1 5

gaa tgt gat cta gat aat gtt gtt cag ttc act att caa gaa ggg tta 163
Glu Cys Asp Leu Asp Asn Val Val Gln Phe Thr Ile Gln Glu Gly Leu
10 15 20

gat ccc atg tca ccc aat aac ttc gat acc gat gtc tgc atc gtc ggt 211
Asp-Pro-Met-Ser-Pro-Asn-Asn-Phe-Asp-Thr-Asp-Val-Cys-Ile-Val-Gly
25 30 35

gga ggt cct acc gga acg ctc ctt gca gta ctg ctc ggc caa aaa ggt 259
Gly Gly Pro Thr Gly Thr Leu Leu Ala Val Leu Leu Gly Gln Lys Gly
40 45 50

cac	cgc	gtc	acc	atc	ctg	gaa	aag	tgg	cca	aca	ttc	tac	gaa	cga	cct	307
His	Arg	Val	Thr	Ile	Leu	Glu	Lys	Trp	Pro	Thr	Phe	Tyr	Glu	Arg	Pro	
	55					60					65					
cgt	gca	gtc	acc	ttt	gac	cac	gaa	atc	gca	cgg	atc	ctt	gga	tac	att	355
Arg	Ala	Val	Thr	Phe	Asp	His	Glu	Ile	Ala	Arg	Ile	Leu	Gly	Tyr	Ile	
	70				75					80					85	
ggc	att	gat	tct	gaa	aac	gac	gaa	gcc	atc	gat	tac	cac	tcc	gac	agc	403
Gly	Ile	Asp	Ser	Glu	Asn	Asp	Glu	Ala	Ile	Asp	Tyr	His	Ser	Asp	Ser	
				90					95					100		
tac	gac	tgg	aag	aac	gca	gcg	ggg	gag	acg	ctt	ttg	gaa	gtc	gat	tgg	451
Tyr	Asp	Trp	Lys	Asn	Ala	Ala	Gly	Glu	Thr	Leu	Leu	Glu	Val	Asp	Trp	
			105					110					115			
acc	tcc	atg	aca	gat	tcc	gga	tgg	cgc	acc	cga	tac	tgg	ttc	tac	cag	499
Thr	Ser	Met	Thr	Asp	Ser	Gly	Trp	Arg	Thr	Arg	Tyr	Trp	Phe	Tyr	Gln	
		120					125					130				
cca	gaa	ctt	gaa	aag	cgt	ctg	cgc	gat	ctg	gcc	ctg	acc	atg	gat	ttt	547
Pro	Glu	Leu	Glu	Lys	Arg	Leu	Arg	Asp	Leu	Ala	Leu	Thr	Met	Asp	Phe	
	135					140					145					
gta	gat	att	cgc	tgt	ggc	ttc	acc	gct	gtc	gga	ttg	tcc	caa	gat	gaa	595
Val	Asp	Ile	Arg	Cys	Gly	Phe	Thr	Ala	Val	Gly	Leu	Ser	Gln	Asp	Glu	
	150				155					160					165	
aac	tcc	gcc	atc	att	cac	ggc	att	gtc	act	gat	acc	cca	gag	aac	att	643
Asn	Ser	Ala	Ile	Ile	His	Gly	Ile	Val	Thr	Asp	Thr	Pro	Glu	Asn	Ile	
				170				175						180		
cca	gca	gat	gct	cag	cgc	gaa	gat	atc	cga	gcg	aag	tat	gtc	atc	ggc	691
Pro	Ala	Asp	Ala	Gln	Arg	Glu	Asp	Ile	Arg	Ala	Lys	Tyr	Val	Ile	Gly	
			185					190					195			
gca	gac	gga	gct	aac	agt	ttc	gtg	cgt	aac	tcc	ctt	ggc	tta	gag	atg	739
Ala	Asp	Gly	Ala	Asn	Ser	Phe	Val	Arg	Asn	Ser	Leu	Gly	Leu	Glu	Met	
		200					205					210				
aat	gat	ctt	gga	tac	ttc	ttc	gac	tgg	ctg	atc	ctg	gac	ctc	aag	cca	787
Asn	Asp	Leu	Gly	Tyr	Phe	Phe	Asp	Trp	Leu	Ile	Leu	Asp	Leu	Lys	Pro	
	215					220					225					
act	cag	gac	att	gac	tac	gga	aca	gat	cac	tgg	caa	ctg	tgt	gat	ccc	835
Thr	Gln	Asp	Ile	Asp	Tyr	Gly	Thr	Asp	His	Trp	Gln	Leu	Cys	Asp	Pro	
	230				235					240					245	
aag	cgc	cca	acc	acc	atc	gtt	cct	gga	ggc	ccc	ggc	cgc	cga	cgt	tgg	883
Lys	Arg	Pro	Thr	Thr	Ile	Val	Pro	Gly	Gly	Pro	Gly	Arg	Arg	Arg	Trp	
				250				255						260		
gaa	ttc	atg	gcg	ctg	cct	ggc	gaa	gat	ctc	aag	gaa	ctc	gct	tct	gaa	931
Glu	Phe	Met	Ala	Leu	Pro	Gly	Glu	Asp	Leu	Lys	Glu	Leu	Ala	Ser	Glu	
			265				270					275				
gaa	agc	gcg	tgg	aat	cta	ctt	gag	cca	tgg	gat	gtc	aca	cct	ggc	aag	979
Glu	Ser	Ala	Trp	Asn	Leu	Leu	Glu	Pro	Trp	Asp	Val	Thr	Pro	Gly	Lys	
		280					285					290				

gcc att ctc gag cgc tcc gca gtg tat cga ttc caa gct cgc tgg gcc	1027
Ala Ile Leu Glu Arg Ser Ala Val Tyr Arg Phe Gln Ala Arg Trp Ala	
295 300 305	
cag gaa tgg cgc tcc gga aga gct ctc atc gca ggc gat gcc gct cac	1075
Gln Glu Trp Arg Ser Gly Arg Ala Leu Ile Ala Gly Asp Ala Ala His	
310 315 320 325	
ctc atg cca cct ttc gca ggt gaa ggc atg tgc gct ggc ctg aga gac	1123
Leu Met Pro Pro Phe Ala Gly Glu Gly Met Cys Ala Gly Leu Arg Asp	
330 335 340	
tca ctg gcg ttg gca tgg cgt ctt gat ttg gtg ctg agc gga aaa tca	1171
Ser Leu Ala Leu Ala Trp Arg Leu Asp Leu Val Leu Ser Gly Lys Ser	
345 350 355	
gat gat gca ttg cta gac acc tac gga gaa gaa cgc cgc gaa cac gtc	1219
Asp Asp Ala Leu Leu Asp Thr Tyr Gly Glu Glu Arg Arg Glu His Val	
360 365 370	
cac tac tac att gat ttc tcc atg gac ctg ggc aat gtc atc tgc att	1267
His Tyr Tyr Ile Asp Phe Ser Met Asp Leu Gly Asn Val Ile Cys Ile	
375 380 385	
act gat gaa gat gaa gca cgt ttg cgc gat gag cgc atg att aaa gag	1315
Thr Asp Glu Asp Glu Ala Arg Leu Arg Asp Glu Arg Met Ile Lys Glu	
390 395 400 405	
ctt gaa gca caa gac ggg gtc cct gtt aat acc gat gtc gca cac ttg	1363
Leu Glu Ala Gln Asp Gly Val Pro Val Asn Thr Asp Val Ala His Leu	
410 415 420	
gga ccg gga att tgg gat aaa gat tct tcc cat ggt ggc gag cta gcg	1411
Gly Pro Gly Ile Trp Asp Lys Asp Ser Ser His Gly Gly Glu Leu Ala	
425 430 435	
aag cag ggc ata gtg gaa tac caa ggt cga aag gcg cgt ttc gac gac	1459
Lys Gln Gly Ile Val Glu Tyr Gln Gly Arg Lys Ala Arg Phe Asp Asp	
440 445 450	
gca gtc ggc cgt ggc tgg gca gtt tta ggc ctc aac act gat cca cga	1507
Ala Val Gly Arg Gly Trp Ala Val Leu Gly Leu Asn Thr Asp Pro Arg	
455 460 465	
gaa gtg ctt gat gag gat tgc ctt gtg gca ctt gac gcc atc ggt gca	1555
Glu Val Leu Asp Glu Asp Ser Leu Val Ala Leu Asp Ala Ile Gly Ala	
470 475 480 485	
atc gtc gaa tca gta ggt gat gca act tcc gca gtt tta gat gtt gaa	1603
Ile Val Glu Ser Val Gly Asp Ala Thr Ser Ala Val Leu Asp Val Glu	
490 495 500	
ggt ctt tac act cgc tgg ctc aag gaa gcc ggg gca aca ttt att att	1651
Gly Leu Tyr Thr Arg Trp Leu Lys Glu Ala Gly Ala Thr Phe Ile Ile	
505 510 515	
acc cgc ccc gat ttc tac gtc tat tcc aca gca gtg gac gct gaa caa	1699
Thr Arg Pro Asp Phe Tyr Val Tyr Ser Thr Ala Val Asp Ala Glu Gln	
520 525 530	
ctt caa aca cag att aag cag cta tgc gat cta ctt cac ctc aac tca	1747

Leu Gln Thr Gln Ile Lys Gln Leu Ser Asp Leu Leu His Leu Asn Ser
 535 540 545

gtt gtc gga gca taggagctaa aaatgtcttt aca
 Val Val Gly Ala
 550

1782

<210> 470

<211> 553

<212> PRT

<213> Corynebacterium glutamicum

<400> 470

Met Asn His Asp Ser Glu Cys Asp Leu Asp Asn Val Val Gln Phe Thr
 1 5 10 15

Ile Gln Glu Gly Leu Asp Pro Met Ser Pro Asn Asn Phe Asp Thr Asp
 20 25 30

Val Cys Ile Val Gly Gly Gly Pro Thr Gly Thr Leu Leu Ala Val Leu
 35 40 45

Leu Gly Gln Lys Gly His Arg Val Thr Ile Leu Glu Lys Trp Pro Thr
 50 55 60

Phe Tyr Glu Arg Pro Arg Ala Val Thr Phe Asp His Glu Ile Ala Arg
 65 70 75 80

Ile Leu Gly Tyr Ile Gly Ile Asp Ser Glu Asn Asp Glu Ala Ile Asp
 85 90 95

Tyr His Ser Asp Ser Tyr Asp Trp Lys Asn Ala Ala Gly Glu Thr Leu
 100 105 110

Leu Glu Val Asp Trp Thr Ser Met Thr Asp Ser Gly Trp Arg Thr Arg
 115 120 125

Tyr Trp Phe Tyr Gln Pro Glu Leu Glu Lys Arg Leu Arg Asp Leu Ala
 130 135 140

Leu Thr Met Asp Phe Val Asp Ile Arg Cys Gly Phe Thr Ala Val Gly
 145 150 155 160

Leu Ser Gln Asp Glu Asn Ser Ala Ile Ile His Gly Ile Val Thr Asp
 165 170 175

Thr Pro Glu Asn Ile Pro Ala Asp Ala Gln Arg Glu Asp Ile Arg Ala
 180 185 190

Lys Tyr Val Ile Gly Ala Asp Gly Ala Asn Ser Phe Val Arg Asn Ser
 195 200 205

Leu Gly Leu Glu Met Asn Asp Leu Gly Tyr Phe Phe Asp Trp Leu Ile
 210 215 220

Leu Asp Leu Lys Pro Thr Gln Asp Ile Asp Tyr Gly Thr Asp His Trp
 225 230 235 240

Gln Leu Cys Asp Pro Lys Arg Pro Thr Thr Ile Val Pro Gly Gly Pro
 245 250 255

Gly Arg Arg Arg Trp Glu Phe Met Ala Leu Pro Gly Glu Asp Leu Lys
 260 265 270
 Glu Leu Ala Ser Glu Glu Ser Ala Trp Asn Leu Leu Glu Pro Trp Asp
 275 280 285
 Val Thr Pro Gly Lys Ala Ile Leu Glu Arg Ser Ala Val Tyr Arg Phe
 290 295 300
 Gln Ala Arg Trp Ala Gln Glu Trp Arg Ser Gly Arg Ala Leu Ile Ala
 305 310 315 320
 Gly Asp Ala Ala His Leu Met Pro Pro Phe Ala Gly Glu Gly Met Cys
 325 330 335
 Ala Gly Leu Arg Asp Ser Leu Ala Leu Ala Trp Arg Leu Asp Leu Val
 340 345 350
 Leu Ser Gly Lys Ser Asp Asp Ala Leu Leu Asp Thr Tyr Gly Glu Glu
 355 360 365
 Arg Arg Glu His Val His Tyr Tyr Ile Asp Phe Ser Met Asp Leu Gly
 370 375 380
 Asn Val Ile Cys Ile Thr Asp Glu Asp Glu Ala Arg Leu Arg Asp Glu
 385 390 395 400
 Arg Met Ile Lys Glu Leu Glu Ala Gln Asp Gly Val Pro Val Asn Thr
 405 410 415
 Asp Val Ala His Leu Gly Pro Gly Ile Trp Asp Lys Asp Ser Ser His
 420 425 430
 Gly Gly Glu Leu Ala Lys Gln Gly Ile Val Glu Tyr Gln Gly Arg Lys
 435 440 445
 Ala Arg Phe Asp Asp Ala Val Gly Arg Gly Trp Ala Val Leu Gly Leu
 450 455 460
 Asn Thr Asp Pro Arg Glu Val Leu Asp Glu Asp Ser Leu Val Ala Leu
 465 470 475 480
 Asp Ala Ile Gly Ala Ile Val Glu Ser Val Gly Asp Ala Thr Ser Ala
 485 490 495
 Val Leu Asp Val Glu Gly Leu Tyr Thr Arg Trp Leu Lys Glu Ala Gly
 500 505 510
 Ala Thr Phe Ile Ile Thr Arg Pro Asp Phe Tyr Val Tyr Ser Thr Ala
 515 520 525
 Val Asp Ala Glu Gln Leu Gln Thr Gln Ile Lys Gln Leu Ser Asp Leu
 530 535 540

~~Leu His Leu Asn Ser Val Val Gly Ala~~
 545 550

<210> 471
 <211> 583

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(564)

<223> RXA01126

<400> 471

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Ser Ala Glu Ser Leu Pro Pro Thr Leu Phe Leu Lys Pro Pro Thr Ala	
1 5 10 15	

gtc acc gga cca gag tcc cca atc cga atc cct tcc ttt gcc acc aag	96
Val Thr Gly Pro Glu Ser Pro Ile Arg Ile Pro Ser Phe Ala Thr Lys	
20 25 30	

gtg gaa ttc gaa ggt gag ctc gca gta gtt atc ggc aag ccc tgc aag	144
Val Glu Phe Glu Gly Glu Leu Ala Val Val Ile Gly Lys Pro Cys Lys	
35 40 45	

aac gtc aag gct gat gac tgg aag tct gtc gtt ttg ggc ttc acc atc	192
Asn Val Lys Ala Asp Asp Trp Lys Ser Val Val Leu Gly Phe Thr Ile	
50 55 60	

atc aac gac gtc tcc tcc cgt gac ctc cag ttc gct gac ggc cag tgg	240
Ile Asn Asp Val Ser Ser Arg Asp Leu Gln Phe Ala Asp Gly Gln Trp	
65 70 75 80	

gca cgc gct aag ggc att gac acc ttc ggc ccc atc gga cca tgg att	288
Ala Arg Ala Lys Gly Ile Asp Thr Phe Gly Pro Ile Gly Pro Trp Ile	
85 90 95	

gaa act gac atc aac tcc atc gac ttg gac aac ctg ccc atc aag gca	336
Glu Thr Asp Ile Asn Ser Ile Asp Leu Asp Asn Leu Pro Ile Lys Ala	
100 105 110	

cgc ctc acc cac gac ggc gaa acc caa ttg aag cag gac tcc aac tcc	384
Arg Leu Thr His Asp Gly Glu Thr Gln Leu Lys Gln Asp Ser Asn Ser	
115 120 125	

aac cag atg atc atg aag atg ggc gaa att atc gag ttc atc acc gcc	432
Asn Gln Met Ile Met Lys Met Gly Glu Ile Ile Glu Phe Ile Thr Ala	
130 135 140	

tcc atg acc ctg ctc cca ggc gac gtt att gca acc ggt tct cca gca	480
Ser Met Thr Leu Leu Pro Gly Asp Val Ile Ala Thr Gly Ser Pro Ala	
145 150 155 160	

ggc acc gaa gca atg gtt gac ggc gac tac atc gaa atc gaa att cca	528
Gly Thr Glu Ala Met Val Asp Gly Asp Tyr Ile Glu Ile Glu Ile Pro	
165 170 175	

ggc atc ggc aag ctg ggc aac cca gtt gtg gac gcc taaaatggat	574
Gly Ile Gly Lys Leu Gly Asn Pro Val Val Asp Ala	

180

185

caccaccat

583

<210> 472

<211> 188

<212> PRT

<213> Corynebacterium glutamicum

<400> 472

Ser Ala Glu Ser Leu Pro Pro Thr Leu Phe Leu Lys Pro Pro Thr Ala
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Val Thr Gly Pro Glu Ser Pro Ile Arg Ile Pro Ser Phe Ala Thr Lys
 20 25 30

Val Glu Phe Glu Gly Glu Leu Ala Val Val Ile Gly Lys Pro Cys Lys
 35 40 45

Asn Val Lys Ala Asp Asp Trp Lys Ser Val Val Leu Gly Phe Thr Ile
 50 55 60

Ile Asn Asp Val Ser Ser Arg Asp Leu Gln Phe Ala Asp Gly Gln Trp
 65 70 75 80

Ala Arg Ala Lys Gly Ile Asp Thr Phe Gly Pro Ile Gly Pro Trp Ile
 85 90 95

Glu Thr Asp Ile Asn Ser Ile Asp Leu Asp Asn Leu Pro Ile Lys Ala
 100 105 110

Arg Leu Thr His Asp Gly Glu Thr Gln Leu Lys Gln Asp Ser Asn Ser
 115 120 125

Asn Gln Met Ile Met Lys Met Gly Glu Ile Ile Glu Phe Ile Thr Ala
 130 135 140

Ser Met Thr Leu Leu Pro Gly Asp Val Ile Ala Thr Gly Ser Pro Ala
 145 150 155 160

Gly Thr Glu Ala Met Val Asp Gly Asp Tyr Ile Glu Ile Glu Ile Pro
 165 170 175

Gly Ile Gly Lys Leu Gly Asn Pro Val Val Asp Ala
 180 185

<210> 473

<211> 864

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(841)

<223> RXA01117

<400> 473

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cccttggtgea-tatgatgaac-attacgttag-catgtctcac-atg-att-aac-aag-agc 115
 Met Ile Asn Lys Ser
 1 5

att tct tcc act gct gaa gcg gtg gcc gat atc cca gac ggt gcg tcc 163
 Ile Ser Ser Thr Ala Glu Ala Val Ala Asp Ile Pro Asp Gly Ala Ser

tct aac taatgacttg ggatcataac caa 864
Ser Asn

<210> 474
 <211> 247
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 474
 Met Ile Asn Lys Ser Ile Ser Ser Thr Ala Glu Ala Val Ala Asp Ile
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 Pro Asp Gly Ala Ser Ile Ala Val Gly Gly Phe Gly Leu Val Gly Ile
 20 25 30
 Pro Thr Ala Leu Ile Leu Ala Leu Arg Glu Gln Gly Ala Gly Asp Leu
 35 40 45
 Thr Ile Ile Ser Asn Asn Leu Gly Thr Asp Gly Phe Gly Leu Gly Leu
 50 55 60
 Leu Leu Leu Asp Lys Lys Ile Ser Lys Ser Ile Gly Ser Tyr Leu Gly
 65 70 75 80
 Ser Asn Lys Glu Tyr Ala Arg Gln Tyr Leu Glu Gly Glu Leu Thr Val
 85 90 95
 Glu Phe Thr Pro Gln Gly Thr Leu Ala Glu Arg Leu Arg Ala Gly Gly
 100 105 110
 Ala Gly Ile Pro Ala Phe Tyr Thr Thr Ala Gly Val Gly Thr Gln Val
 115 120 125
 Ala Glu Gly Gly Leu Pro Gln Arg Tyr Asn Thr Asp Gly Thr Val Ala
 130 135 140
 Val Val Ser Gln Pro Lys Glu Thr Arg Glu Phe Asn Gly Gln Leu Tyr
 145 150 155 160
 Val Met Glu Glu Gly Ile Arg Ala Asp Tyr Ala Leu Val His Ala His
 165 170 175
 Lys Ala Asp Arg Phe Gly Asn Leu Val Phe Arg Lys Thr Ala Gln Asn
 180 185 190
 Phe Asn Pro Asp Ala Ala Met Ser Gly Lys Ile Thr Ile Ala Gln Val
 195 200 205
 Glu His Phe Val Asp Glu Leu His Pro Asp Glu Ile Asp Leu Pro Gly
 210 215 220
 Ile Tyr Val Asn Arg Val Val His Val Gly Pro Gln Glu Thr Gly Ile
 225 230 235 240
 Glu Asn Arg Thr Val Ser Asn
 245

<210> 475
 <211> 1629
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1606)

<223> RXA00772

<400> 475

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gaaaaatttg aaaaagtccg attacctgag gaggtattca atg tct gat cgc att 115
                                         Met Ser Asp Arg Ile
                                         1 5
gct tca gaa aag ctg cgc tcc aag ctc atg tcc gcc gac gag gcg gca 163
Ala Ser Glu Lys Leu Arg Ser Lys Leu Met Ser Ala Asp Glu Ala Ala
                        10 15 20
cag ttt gtt aac cac ggt gac aag gtt ggt ttc tcc ggc ttc acc ggc 211
Gln Phe Val Asn His Gly Asp Lys Val Gly Phe Ser Gly Phe Thr Gly
                        25 30 35
gct ggc tac cca aag gca ctg cct acg gca atc gct aac cgg gct aaa 259
Ala Gly Tyr Pro Lys Ala Leu Pro Thr Ala Ile Ala Asn Arg Ala Lys
                        40 45 50
gaa gca cac ggt gca ggc aac gac tac gca atc gac ctg ttc act ggc 307
Glu Ala His Gly Ala Gly Asn Asp Tyr Ala Ile Asp Leu Phe Thr Gly
                        55 60 65
gca tcg acc gcc cct gac tgc gat ggc gta ctt gca gaa gct gac gct 355
Ala Ser Thr Ala Pro Asp Cys Asp Gly Val Leu Ala Glu Ala Asp Ala
                        70 75 80 85
atc cgc tgg cgc atg cca tac gca tct gat cca atc atg cgt aac aag 403
Ile Arg Trp Arg Met Pro Tyr Ala Ser Asp Pro Ile Met Arg Asn Lys
                        90 95 100
atc aac tcc ggc tcc atg gga tac tcc gat atc cac ctg tcc cac tcc 451
Ile Asn Ser Gly Ser Met Gly Tyr Ser Asp Ile His Leu Ser His Ser
                        105 110 115
ggc cag cag gtt gaa gag ggc ttc ttc ggc cag ctc aac gta gct gtc 499
Gly Gln Gln Val Glu Glu Gly Phe Phe Gly Gln Leu Asn Val Ala Val
                        120 125 130
att gaa atc acc cgc atc act gaa gag ggc tac atc atc cct tct tcc 547
Ile Glu Ile Thr Arg Ile Thr Glu Glu Gly Tyr Ile Ile Pro Ser Ser
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Ser Val Gly Asn Asn Val Glu Trp Leu Asn Ala Ala Glu Lys Val Ile
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Leu Glu Val Asn Ser Trp Gln Ser Glu Asp Leu Glu Gly Met His Asp
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Ile Trp Ser Val Pro Ala Leu Pro Asn Arg Ile Ala Val Pro Ile Asn
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Phe Lys Pro Val Asp Asp Ile Ser Lys Lys Ile Ala Gly Asn Phe Leu	
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Tyr Ile Met Gln Ser Gly Val Gly Asn Val Pro Asn Ala Val Met Ala	
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Gly Leu Leu Glu Ser Lys Phe Glu Asn Ile Gln Ala Tyr Thr Glu Val	
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Ala Ser Ala Thr Ser Phe Ser Leu Ser Pro Glu Tyr Ala Glu Lys Met	
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Gln Ile Ser Asn His Pro Glu Val Ile Arg Arg Val Gly Leu Ile Ala	
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Thr Asn Gly Leu Ile Glu Ala Asp Ile Tyr Gly Asn Val Asn Ser Thr	
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Phe Thr Arg Asn Gly Tyr Ile Ser Ser Phe Ile Thr Pro Ser Glu Ala	
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Lys Gly Gly Ala Ile Ser Ala Ile Val Pro Phe Ala Ser His Ile Asp	
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 Ile Met Arg Asn Lys Ile Asn Ser Gly Ser Met Gly Tyr Ser Asp Ile
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 His Leu Ser His Ser Gly Gln Gln Val Glu Glu Gly Phe Phe Gly Gln
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 Ile Ile Pro Ser Ser Ser Val Gly Asn Asn Val Glu Trp Leu Asn Ala
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 Glu Gly Met His Asp Ile Trp Ser Val Pro Ala Leu Pro Asn Arg Ile
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Ala Val Pro Ile Asn Lys Pro Gly Asp Arg Ile Gly Lys Thr Tyr Ile
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 Glu Phe Asp Thr Asp Lys Val Val Ala Val Val Glu Thr Asn Thr Ala
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 Asp Arg Asn Ala Pro Phe Lys Pro Val Asp Asp Ile Ser Lys Lys Ile
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 Ala Gly Asn Phe Leu Asp Phe Leu Glu Ser Glu Val Ala Ala Gly Arg
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 Leu Ser Tyr Ala Gly Tyr Ile Met Gln Ser Gly Val Gly Asn Val Pro
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 Asn Ala Val Met Ala Gly Leu Leu Glu Ser Lys Phe Glu Asn Ile Gln
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 Ala Tyr Thr Glu Val Ile Gln Asp Gly Met Val Asp Leu Ile Asp Ala
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 Gly Lys Met Thr Val Ala Ser Ala Thr Ser Phe Ser Leu Ser Pro Glu
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 Tyr Ala Glu Lys Met Asn Asn Glu Ala Lys Arg Tyr Arg Glu Ser Ile
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 Val Gly Leu Ile Ala Thr Asn Gly Leu Ile Glu Ala Asp Ile Tyr Gly
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 Asn Val Asn Ser Thr Asn Val Ser Gly Ser Arg Val Met Asn Gly Ile
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 Gly Gly Ser Gly Asp Phe Thr Arg Asn Gly Tyr Ile Ser Ser Phe Ile
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 Thr Pro Ser Glu Ala Lys Gly Gly Ala Ile Ser Ala Ile Val Pro Phe
 405 410 415
 Ala Ser His Ile Asp His Thr Glu His Asp Val Met Val Val Ile Ser
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 Glu Tyr Gly Tyr Ala Asp Leu Arg Gly Leu Ala Pro Arg Glu Arg Val
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 Ala Lys Met Ile Gly Leu Ala His Pro Asp Tyr Arg Pro Leu Leu Glu
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 Asn Gly Ser Met Lys Ala
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Val Val Ile Thr Glu Tyr Gly Tyr Ala Asp Leu Arg Gly Leu Ser Pro
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Lys Gln Arg Val Pro Lys Met Ile Ala Ile Ala His Pro Asp Tyr Arg
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Pro Leu Leu Glu Ala Tyr Phe Asp Arg Ala Leu Asn Ser Ala Asp Ser
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Tyr Gln His Thr Leu His Asp Leu Arg Thr Ala Phe Asp Phe His Asn
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